GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2000, 01:28:41 ; Search time 4946.18 Seconds
(without alignments)
-1936.192 Million cell updates/sec

Title: US-09-030-832-41
Perfect score: 3154
Sequence: 1 CGCGACCTCCGCGCAGGTGG.....AGCAAAAAGAAAAAAAAAAA 3154

Scoring table: IDENTITY_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl:*

Word size : 0

Number of hits that pass the threshold : 1642386

1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pr1:*
10: gb_pr2:*
11: gb_pr3:*
12: gb_ro:*
13: gb_sts:*
14: gb_sy:*
15: gb_un:*
16: gb_vi:*
17: em_fun:*
18: em_hum1:*
19: em_hum2:*
20: em_in:*
21: em_om:*
22: em_or:*
23: em_ov:*
24: em_pat:*
25: em_ph:*
26: em_pl:*
27: em_ro:*
28: em_sts:*
29: em_sy:*
30: em_un:*
31: em_vi:*
32: gb_htg1:*
33: gb_htg2:*
34: gb_in1:*
35: gb_in2:*
36: em_ba1:*
37: em_ba2:*
38: em_hum3:*
39: em_hum4:*
40: gb_pr4:*
41: gb_htg3:*
42: gb_htg4:*
43: gb_htg5:*
44: gb_htg6:*
45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3154	100.0	3154	10	HSU66661	U66661 Human GABA-
2	3120.2	98.9	3150	10	HSY09765	Y09765 Homo sapien
3	2975.8	94.4	3153	9	HSGABACHL	Y07637 H.sapiens m
4	2284	72.4	6146	11	HSU92285	U92285 Human GABA-
c 5	1963	62.2	158898	11	U82696	U82696 Homo sapien
6	1943.6	61.6	10897	10	HSY09764	Y09764 Homo sapien
7	1771.2	56.2	9631	11	HSGABRE3	U92283 Human GABA-
8	438	13.9	1572	4	GGGABAA	X73533 G.domesticu
9	364	11.5	1598	12	MMGSGABA	X59300 Mouse mRNA
10	364	11.5	1930	12	RNGABAG3	X63324 R.norvegicu
11	362.4	11.5	1654	12	RATGABAA	M81142 Rat GABA-A
12	357.6	11.3	1565	5	A46959	A46959 Sequence 7
13	357.6	11.3	1536	10	S82769	S82769 GABAA recep
14	350.8	11.1	2231	12	MUSGABAAG2	M62374 Mus musculu
15	349.6	11.1	2036	12	MUSGABAAR	M86572 Mouse gamma
16	346.8	11.0	1428	3	BOVGABAARG	M55563 Bovine gamm
17	345.6	11.0	1838	12	RATGABAAI	L08497 Rattus ratt
18	341.4	10.8	2206	4	GDGABAAR	X54944 Chicken mRN
19	335.6	10.6	1745	9	HSGABAAS	X15376 Human mRNA
20	320.2	10.2	1739	12	RNGABA	X57514 R.norvegicu
21	311.6	9.9	1336	4	GLGABABRA	Z25467 Gallus dome
22	309.2	9.8	1995	12	MMGABAG1	X55272 Mouse mRNA
23	287.2	9.1	714	11	HUMZD71B07	AF086385 Homo sapi
24	283.2	9.0	1843	12	RATGABAAE	L08493 Rattus ratt
25	283.2	9.0	1843	12	S55933	S55933 GABAA recep
26	281	8.9	1345	4	CAGABANTS	X94342 C.auratus m
27	278.8	8.8	1707	5	A50024	A50024 Sequence 7
28	277.2	8.8	1679	10	HSU30461	U30461 Human GABAA
c 29	269.2	8.5	596	13	G60680	G60680 SHGC-57595
30	264.6	8.4	1408	5	A28106	A28106 Human GABAa
31	264.6	8.4	1408	5	A39278	A39278 Sequence 3
32	264.6	8.4	1732	5	I88880	I88880 Sequence 17
33	263	8.3	1732	10	S81944	S81944 gamma-amino
34	261.8	8.3	2310	5	A28104	A28104 Human GABAa
35	261.8	8.3	2310	5	A39276	A39276 Sequence 1
36	261.8	8.3	2310	5	I88879	I88879 Sequence 15
37	261.8	8.3	2318	9	HUMGABRA5Y	L08485 Human GABA-
38	261.8	8.3	346	12	AF090376	AF090376 Mus muscu
39	260.4	8.3	1439	4	GGGABAA6S	X94343 G.gallus mR
40	255.2	8.1	2111	12	RATGABAAG	L08495 Rattus ratt
41	255.2	8.1	1805	12	RNGABAA6A	X55742 R.norvegicu
42	252.6	8.0	1908	3	BTGABAA	X61456 Bovine GABA
43	244	7.7	2591	12	RNGABAA5	X51992 R.norvegicu
44	242.4	7.7	1874	12	RATGABAAF	L08494 Rattus ratt
45	237.6	7.5	1637	5	A28102	A28102 Human GABAa

ALIGNMENTS

RESULT 1
HSU66661
LOCUS HSU66661 3154 bp mRNA PRI 11-MAR-1997
DEFINITION Human GABA-A receptor epsilon subunit mRNA, complete cds.
ACCESSION U66661
VERSION U66661.1 GI:1857125
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3154)

Sequence Comparison A

This PAGE BLANK (USPTO)

```
  AUTHORS   Davies,P.A., Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Insensitivity to anaesthetic agents conferred by a class of GABA(A)
            receptor subunit
  JOURNAL   Nature 385 (6619), 820-823 (1997)   2/27/97
  MEDLINE   97192095
REFERENCE   2  (bases 1 to 3154)
  AUTHORS   Davies,P.A., Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-1996) Department of Cellular and Molecular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .3154
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             41. .1561
                     /codon_start=1
                     /product="GABA-A receptor epsilon subunit"
                     /protein_id="AAB49284.1"
                     /db_xref="GI:1857126"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIA
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRR
                     FGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV
                     SYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRA
                     RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWC
                     KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
BASE COUNT      725 a    886 c    686 g    857 t
ORIGIN
```

Query Match 100.0%; Score 3154; DB 10; Length 3154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 CGCGACCTCCGCGCAGGTGGTCGCGCCGGTCTCCGCGGAAATGTTGTCCAAAGTTCTTCC 60
Db       1 CGCGACCTCCGCGCAGGTGGTCGCGCCGGTCTCCGCGGAAATGTTGTCCAAAGTTCTTCC 60

Qy      61 AGTCCTCCTAGGCATCTTATTGATCCTCCAGTCGAGGGTCGAGGGACCTCAGACTGAATC 120
Db      61 AGTCCTCCTAGGCATCTTATTGATCCTCCAGTCGAGGGTCGAGGGACCTCAGACTGAATC 120

Qy     121 AAAGAATGAAGCCTCTTCCCGTGATGTTGTCTATGGCCCCCAGCCCCAGCCTCTGGAAAA 180
Db     121 AAAGAATGAAGCCTCTTCCCGTGATGTTGTCTATGGCCCCCAGCCCCAGCCTCTGGAAAA 180

Qy     181 TCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAA 240
Db     181 TCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAA 240

Qy     241 ACTGCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCG 300
Db     241 ACTGCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCG 300

Qy     301 CCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGG 360
Db     301 CCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGG 360

Qy     361 TCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTA 420
Db     361 TCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTA 420

Qy     421 CGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGT 480
Db     421 CGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGT 480

Qy     481 GAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGA 540
Db     481 GAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGA 540

Qy     541 GATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAAT 600
Db     541 GATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAAT 600

Qy     601 TAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCA 660
Db     601 TAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCA 660

Qy     661 CTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTG 720
Db     661 CTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTG 720

Qy     721 GGAAAATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 780
Db     721 GGAAAATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 780

Qy     781 TACAGGAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCAT 840
Db     781 TACAGGAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCAT 840

Qy     841 GACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCC 900
Db     841 GACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCC 900

Qy     901 TTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCC 960
Db     901 TTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCC 960

Qy     961 AGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTC 1020
Db     961 AGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTC 1020

Qy    1021 TCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTG 1080
Db    1021 TCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTG 1080

Qy    1081 CTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAA 1140
Db    1081 CTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAA 1140

Qy    1141 CCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCA 1200
Db    1141 CCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCA 1200

Qy    1201 TGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTG 1260
Db    1201 TGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTG 1260

Qy    1261 CCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCA 1320
Db    1261 CCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCA 1320

Qy    1321 GCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTG 1380
Db    1321 GCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTG 1380

Qy    1381 TGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTAC 1440
Db    1381 TGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTAC 1440

Qy    1441 CTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGT 1500
Db    1441 CTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGT 1500

Qy    1501 TTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTA 1560
Db    1501 TTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTA 1560

Qy    1561 GGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTT 1620
Db    1561 GGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTT 1620

Qy    1621 GCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCC 1680
```

THIS PAGE BLANK (USPTO)

```
Db  1621 GCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCC 1680
Qy  1681 CATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGC 1740
Db  1681 CATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGC 1740
Qy  1741 CCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCT 1800
Db  1741 CCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCT 1800
Qy  1801 CTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGC 1860
Db  1801 CTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGC 1860
Qy  1861 TCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCA 1920
Db  1861 TCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCA 1920
Qy  1921 GACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTT 1980
Db  1921 GACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTT 1980
Qy  1981 CTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAG 2040
Db  1981 CTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAG 2040
Qy  2041 ATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGT 2100
Db  2041 ATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGT 2100
Qy  2101 TCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCC 2160
Db  2101 TCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCC 2160
Qy  2161 CTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTG 2220
Db  2161 CTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTG 2220
Qy  2221 CTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAAT 2280
Db  2221 CTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAAT 2280
Qy  2281 GCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTA 2340
Db  2281 GCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTA 2340
Qy  2341 TATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGAC 2400
Db  2341 TATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGAC 2400
Qy  2401 TTCCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAG 2460
Db  2401 TTCCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAG 2460
Qy  2461 GAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACT 2520
Db  2461 GAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACT 2520
Qy  2521 GTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCG 2580
Db  2521 GTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCG 2580
Qy  2581 GGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAA 2640
Db  2581 GGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAA 2640
Qy  2641 CTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGAC 2700
Db  2641 CTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGAC 2700
Qy  2701 ATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTC 2760
Db  2701 ATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTC 2760
Qy  2761 TGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCAC 2820
Db  2761 TGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCAC 2820
Qy  2821 ATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACAC 2880
Db  2821 ATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACAC 2880
Qy  2881 CAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTC 2940
Db  2881 CAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTC 2940
Qy  2941 AGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGAC 3000
Db  2941 AGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGAC 3000
Qy  3001 ATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGA 3060
Db  3001 ATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGA 3060
Qy  3061 TAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAAT 3120
Db  3061 TAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAAT 3120
Qy  3121 AAATATATCAGCAAAGCAAAAAGAAAAAAAAAAA 3154
Db  3121 AAATATATCAGCAAAGCAAAAAGAAAAAAAAAAA 3154
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:26:38 ; Search time 22.24 Seconds
(without alignments)
679.479 Million cell updates/sec

Title: US-09-030-832-42
Perfect score: 2691
Sequence: 1 MLSKVLPVLLGILLILQSRV.....VFPVTFFFFNVLYWLVCLNL 506

Scoring table: BLOSUM62

Searched: 82229 seqs, 29864866 residues

Database : SwissProt_38:*

Word size : 0

Number of hits that pass the threshold : 82229

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2691	100.0	506	1	GAE_HUMAN	P78334 homo sapien
2	1202.5	44.7	457	1	GAC4_CHICK	P34904 gallus gall
3	1097.5	40.8	467	1	GAC3_MOUSE	P27681 mus musculu
4	1087	40.4	474	1	GAC2_CHICK	P21548 gallus gall
5	1085.5	40.3	467	1	GAC3_HUMAN	Q99928 homo sapien
6	1084.5	40.3	467	1	GAC3_RAT	P28473 rattus norv
7	1082	40.2	475	1	GAC2_BOVIN	P22300 bos taurus
8	1078	40.1	474	1	GAC2_MOUSE	P22723 mus musculu
9	1077	40.0	466	1	GAC2_RAT	P18508 rattus norv
10	1067	39.7	467	1	GAC2_HUMAN	P18507 homo sapien
11	1054	39.2	465	1	GAC1_RAT	P23574 rattus norv
12	861	32.0	465	1	GAA6_CHICK	Q90845 gallus gall
13	858	31.9	453	1	GAA6_RAT	P30191 rattus norv
14	855.5	31.8	552	1	GAA4_RAT	P28471 rattus norv
15	851	31.6	453	1	GAA6_HUMAN	Q16445 homo sapien
16	850	31.6	554	1	GAA4_HUMAN	P48169 homo sapien
17	842	31.3	556	1	GAA4_BOVIN	P20237 bos taurus
18	814	30.2	464	1	GAA5_RAT	P19969 rattus norv
19	813	30.2	462	1	GAA5_HUMAN	P31644 homo sapien
20	808.5	30.0	492	1	GAA3_MOUSE	P26049 mus musculu
21	803	29.8	455	1	GAA1_MOUSE	P18504 mus musculu
22	800	29.7	493	1	GAA3_RAT	P20236 rattus norv
23	800	29.7	443	1	GAA6_MOUSE	P16305 mus musculu
24	799.5	29.7	456	1	GAA1_BOVIN	P08219 bos taurus
25	798.5	29.7	492	1	GAA3_HUMAN	P34903 homo sapien
26	797.5	29.6	455	1	GAA1_CHICK	P19150 gallus gall
27	796.5	29.6	492	1	GAA3_BOVIN	P10064 bos taurus
28	785.5	29.2	456	1	GAA1_HUMAN	P14867 homo sapien
29	782.5	29.1	451	1	GAA2_RAT	P23576 rattus norv
30	781	29.0	451	1	GAA2_BOVIN	P10063 bos taurus
31	781	29.0	451	1	GAA2_HUMAN	P47869 homo sapien
32	778	28.9	451	1	GAA2_MOUSE	P26048 mus musculu
33	709	26.3	488	1	GAB4_CHICK	P24045 gallus gall
34	677.5	25.2	474	1	GAB1_HUMAN	P18505 homo sapien
35	673.5	25.0	474	1	GAB1_BOVIN	P08220 bos taurus
36	671.5	25.0	474	1	GAB1_RAT	P15431 rattus norv
37	668.5	24.8	474	1	GAB1_MOUSE	P50571 mus musculu
38	668	24.8	473	1	GAB3_HUMAN	P28472 homo sapien
39	667	24.8	474	1	GAB2_HUMAN	P47870 homo sapien
40	665	24.7	473	1	GAB3_MOUSE	P15433 mus musculu
41	664	24.7	474	1	GAB2_MOUSE	P15432 mus musculu
42	655	24.3	449	1	GRA1_MOUSE	Q64018 mus musculu
43	652.5	24.2	449	1	GAD_RAT	P18506 rattus norv
44	652	24.2	449	1	GRA1_HUMAN	P23415 homo sapien
45	649.5	24.1	452	1	GRA2_HUMAN	P23416 homo sapien

ALIGNMENTS

RESULT 1
GAE_HUMAN
ID GAE_HUMAN STANDARD; PRT; 506 AA.
AC P78334; O15345;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE GAMMA-AMINOBUTYRIC-ACID RECEPTOR EPSILON SUBUNIT PRECURSOR (GABA(A)
DE RECEPTOR).
GN GABRE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97192095.
RA DAVIES P.A., HANNA M.C., HALES T.G., KIRKNESS E.F.;
RT "Insensitivity to anaesthetic agents conferred by a class of GABA(A)
RT receptor subunit.";
RL Nature 385:820-823(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97480709.
RA WILKE K., GAUL R., KLAUCK S.M., POUSTKA A.;
RT "A gene in human chromosome band Xq28 (GABRE) defines a putative new
RT subunit class of the GABAA neurotransmitter receptor.";
RL Genomics 45:1-10(1997).
CC -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC CHANNEL.
CC -!- SUBUNIT: GENERALLY PENTAMERIC. ASSOCIATES WITH ALPHA AND BETA
CC SUBUNITS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: FOUND IN MANY TISSUE. HIGHEST LEVELS OF
CC EXPRESSION IN ADULT HEART AND PLACENTA.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; U66661; AAB49284.1; -.
DR EMBL; Y09763; CAA70903.1; -.
DR EMBL; Y09764; CAA70903.1; JOINED.
DR MIM; 300093; -.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR PFAM; PF00065; neur_chan; 2.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane.
FT SIGNAL 1 ? POTENTIAL.
FT CHAIN ? 506 GAMMA-AMINOBUTYRIC-ACID RECEPTOR EPSILON
FT SUBUNIT.
FT DOMAIN ? 253 EXTRACELLULAR (PROBABLE).
FT TRANSMEM 254 274 POTENTIAL.
FT TRANSMEM 281 301 POTENTIAL.
FT TRANSMEM 344 364 POTENTIAL.
FT DOMAIN 365 485 CYTOPLASMIC (PROBABLE).

Sequence Comparison B

THIS PAGE BLANK (USPTO)

```
FT   TRANSMEM    486    506       POTENTIAL.
FT   CARBOHYD    134    134       POTENTIAL.
FT   CARBOHYD    252    252       POTENTIAL.
FT   DISULFID    195    209       BY SIMILARITY.
FT   CONFLICT    102    102       A -> S (IN REF. 2).
FT   CONFLICT    245    245       F -> L (IN REF. 2).
FT   CONFLICT    471    471       G -> A (IN REF. 2).
FT   CONFLICT    502    502       V -> F (IN REF. 2).
SQ   SEQUENCE   506 AA;  57955 MW;  6BC8394B CRC32;
```

```
  Query Match           100.0%;  Score 2691;  DB 1;  Length 506;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-202;
  Matches  506;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60

Qy      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120

Qy     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180

Qy     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240

Qy     241 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300

Qy     301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360

Qy     361 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 420

Qy     421 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 480

Qy     481 DNYSRVVFPVTFFFFNVLYWLVCLNL 506
          |||||||||||||||||||||||||||
Db     481 DNYSRVVFPVTFFFFNVLYWLVCLNL 506
```

```
RESULT   2
GAC4_CHICK
ID   GAC4_CHICK     STANDARD;      PRT;   457 AA.
AC   P34904;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG4.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93387470.
RA   HARVEY R.J., KIM H.-C., DARLISON M.G.;
RT   "Molecular cloning reveals the existence of a fourth gamma subunit of
RT   the vertebrate brain GABAA receptor.";
RL   FEBS Lett. 331:211-216(1993).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: ABUNDANT IN SEVERAL BRAIN REGIONS, INCLUDING
CC       THE ECTOSTRIATUM, NUCLEUS ROTUNDUS AND HYPERSTRIATUM VENTRALE.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X73533; CAA51939.1; -.
DR   PIR; S38296; S38296.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    457       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4
FT                                SUBUNIT.
FT   DOMAIN       22    256       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    257    279       PROBABLE.
FT   TRANSMEM    283    305       PROBABLE.
FT   TRANSMEM    317    339       PROBABLE.
FT   DOMAIN      340    433       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    434    457       PROBABLE.
FT   CARBOHYD     35     35       POTENTIAL.
FT   CARBOHYD    112    112       POTENTIAL.
FT   CARBOHYD    230    230       POTENTIAL.
FT   DISULFID    173    187       BY SIMILARITY.
SQ   SEQUENCE   457 AA;  53183 MW;  1571332B CRC32;
```

```
  Query Match           44.7%;  Score 1202.5;  DB 1;  Length 457;
  Best Local Similarity  48.1%;  Pred. No. 1.4e-86;
  Matches  218;  Conservative   82;  Mismatches   94;  Indels   59;  Gaps    5;

Qy      70 EASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDE 129
           :|::|||::| |||:|||| || ||| : |:| |||:||:|:: ||||||| |:|||||
Db      48 DATQILNSLLKNYDNKLRPDIGIKPTFIDVDIYVNSIGPVSVIQMEYTIDIFFAQTWYDR 107

Qy     130 RLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
           || :| | ::| || |:||::|||||||||||||   | || |||::||: |||||||:|:
Db     108 RLRFNSTLKALTLNTNMVSRIWIPDTFFRNSKRADSHWITTPNQLLRIWNDGKVLYTLRL 167

Qy     190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
           ||:| | | :  ||||:||||| |||: ||  |::|:|  : :|:::: :|:|:||||||
Db     168 TIEAECLLQLQNFPMDTHSCPLVFSSYGYPREEIVYRWRRYSIEVSDQRTWRLYQFDFTG 227

Qy     250 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 309
           : | :|:: |  |::|||||: |::||| || | | |:|  :| :|||||||| :| |||
Db     228 LRNTSEVLRTGAGEYMVMTVSFDLSRRMGYFAIQTYIPCILTVVLSWVSFWIKRDSTPAR 287

Qy     310 TSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQT 369
           ||||||:|||||||  | |||: |||||||||:| ::::||:|  | ||:|:| ||:|: |:
Db     288 TSLGITTVLTMTTLSTISRKHLPRVSYITAMDLFVSVCFIFVFAALMEYATLNYLVGNKK 347

Qy     370 K-AHASPKLRHP---------------RINSRAHARTRARSRACARQHQEAFVCQIVTTE 413
              |:| | | |                ||:  |
Db     348 PLEHSSRKARLPPAGAQVMPSFTAININNINMH------------------------- 382

Qy     414 GSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRL 473
                 |    :   ||||          | |  |  :::|| : ||:   |::||:
Db     382 -----WPPEIEEDEDDDPGSP----------CLEG-KECERFFCCIEDCQTGMWREGRV 424
```

THIS PAGE BLANK (USPTO)

```
Db    3074 TAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAAT 3133

Qy    3121 AAATATATCAGCAAAGC 3137
           |||||||||||||||||
Db    3134 AAATATATCAGCAAAGC 3150
```

Sequence Comparison C

```
RESULT   3
HSGABACHL
LOCUS       HSGABACHL    3153 bp    mRNA            PRI       03-MAR-1997
DEFINITION  H.sapiens mRNA for putative GABA-gated chloride channel.
ACCESSION   Y07637
VERSION     Y07637.1  GI:1747370
KEYWORDS    GABA-gated chloride channel.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3153)
  AUTHORS   Garret,M., Bascles,L., Boue-Grabot,E., Sartor,P., Charron,G.,
            Bloch,B. and Margolskee,R.F.
  TITLE     An mRNA encoding a putative GABA-gated chloride channel is
            expressed in the human cardiac conduction system
  JOURNAL   J. Neurochem. 68 (4), 1382-1389 (1997)
  MEDLINE   97238072
REFERENCE   2  (bases 1 to 3153)
  AUTHORS   Garret,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-AUG-1996) M. Garret, CNRS UMR5543, Laboratoire de
            Neurophysiologie, Universite de Bordeaux2, 146 rue Leo Saignat,
            33076 Bordeaux Cedex, FRANCE
FEATURES             Location/Qualifiers
     source          1. .3153
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             51. .1568
                     /function="expressed in cardiac conduction system"
                     /codon_start=1
                     /product="putative GABA-gated chloride channel"
                     /protein_id="CAA68914.1"
                     /db_xref="GI:1747371"
                     /db_xref="SPTREMBL:Q99520"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIA
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPGDFMVMTIFFNVSRRF
                     GYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVS
                     YITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRAR
                     SRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCK
                     RFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
     polyA_signal    3118. .3123
BASE COUNT      726 a    885 c    687 g    855 t
ORIGIN
```

```
  Query Match           94.4%;  Score 2975.8;  DB 9;  Length 3153;
  Best Local Similarity  98.7%;  Pred. No. 0;
  Matches 3117;  Conservative    0;  Mismatches   22;  Indels   18;  Gaps   11;

Qy       1 CGCGACCTCCGCGCAGGTGGTCGCGCCGGTCTCCGCGGAAATGTTGTCCAAAGTTCTTCC 60
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db      11 CGCGACCTCCGCGCAGGTGGTGGCGCCGGTCTCCGCGGAAATGTTGTCCAAAGTTCTTCC 70

Qy      61 AGTCCTCCTAGGCATCTTATTGATCCTCCAGTCGAGGGTCGAGGGACCTCAGACTGAATC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      71 AGTCCTCCTAGGCATCTTATTGATCCTCCAGTCGAGGGTCGAGGGACCTCAGACTGAATC 130

Qy     121 AAAGAATGAAGCCTCTTCCCGTGATGTTGTCTATGGCCCCCAGCCCCAGCCTCTGGAAAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131 AAAGAATGAAGCCTCTTCCCGTGATGTTGTCTATGGCCCCCAGCCCCAGCCTCTGGAAAA 190

Qy     181 TCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAA 240
```

THIS PAGE BLANK (USPTO)

```
Db    191 TCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAA 250
Qy    241 ACTGCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCG 300
Db    251 ACTGCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCG 310
Qy    301 CCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGG 360
Db    311 CCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGG 370
Qy    361 TCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTA 420
Db    371 TCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTA 430
Qy    421 CGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGT 480
Db    431 CGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGT 490
Qy    481 GAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGA 540
Db    491 GAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGA 550
Qy    541 GATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAAT 600
Db    551 GATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAAT 610
Qy    601 TAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCA 660
Db    611 TAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCA 670
Qy    661 CTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTG 720
Db    671 CTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTG 730
Qy    721 GGAAAATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 780
Db    731 GGAAAATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 790
Qy    781 TACAGGAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCAT 840
Db    791 TACAGGAGTGAGCAACAAAACTGAAATAATCACAACCCCA---GGTGACTTCATGGTCAT 847
Qy    841 GACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCC 900
Db    848 GACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCC 907
Qy    901 TTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCC 960
Db    908 TTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCC 967
Qy    961 AGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTC 1020
Db    968 AGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTC 1027
Qy   1021 TCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTG 1080
Db   1028 TCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTG 1087
Qy   1081 CTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAA 1140
Db   1088 CTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAA 1147
Qy   1141 CCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCA 1200
Db   1148 CCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCA 1207
Qy   1201 TGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTG 1260
Db   1208 TGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTG 1267
Qy   1261 CCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCA 1320
Db   1268 CCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCA 1327
Qy   1321 GCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTG 1380
Db   1328 GCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTG 1387
Qy   1381 TGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTAC 1440
Db   1388 TGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTAC 1447
Qy   1441 CTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGT 1500
Db   1448 CTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGT 1507
Qy   1501 TTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTA 1560
Db   1508 TTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTA 1567
Qy   1561 GGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTT-CCCCAGGAGGTCCAAGCCCCT 1619
Db   1568 GGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCCAGGAGGTCCAAGCCCCT 1627
Qy   1620 TGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCC 1679
Db   1628 TGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCC 1687
Qy   1680 CCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCCCTCTCCCCTACCTGG 1739
Db   1688 CCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCCCTCTCCCCTACCTGG 1747
Qy   1740 CCCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCC 1799
Db   1748 CCCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCC 1807
Qy   1800 TCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAG 1859
Db   1808 TCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAG 1867
Qy   1860 CTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACC 1919
Db   1868 CTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACC 1927
Qy   1920 AGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGT 1979
Db   1928 AGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGT 1987
Qy   1980 TCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAA 2039
Db   1988 TCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAA 2047
Qy   2040 GATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATG 2099
Db   2048 GATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATG 2107
Qy   2100 TTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATC 2159
Db   2108 TTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATC 2167
Qy   2160 CCTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCT 2219
Db   2168 CCTTTAGGAAGGGGGGGGGGCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCT 2227
Qy   2220 GCTGCTGTGACATCTCCCTCTCCTTGCTGG-CTCCATCTTTCGTCTGCACTACCAATTCA 2278
Db   2228 CCTGCTGTGACATCTCCCTCTCCTTGCTGGCCTCCATCTTTCGTCTGCACTACCAATTCA 2287
Qy   2279 ATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTT 2338
Db   2288 ATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTT 2347
Qy   2339 TATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTG 2398
Db   2348 TATATGCC-CCCTCTTCCTTCTCTTTACCCCCTGTGACTCTTTCTGT-ACTTTCCCAGTG 2405
```

THIS PAGE BLANK (USPTO)

```
Qy   2399 ACTTCCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTA 2458
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2406 ACTTGCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTA 2465

Qy   2459 AGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACA 2518
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   2466 AGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATT-GTGCCCACCCAGGGCACA 2524

Qy   2519 CTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACC 2578
          |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2525 CTGATGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACC 2584

Qy   2579 CGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGG 2638
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2585 CGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGG 2644

Qy   2639 AACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTG 2698
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2645 AACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTG 2704

Qy   2699 ACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATG-AAAACCCTGAGTCACAGAT 2757
          |||||||   |||||||||||||||||||||||||||| ||||||||||||| |||||
Db   2705 ACATCTT--AGGCAGGATTCTTATCCCCATTTTGCAGATGAAAAACCCTGAGTCTCAGAT 2762

Qy   2758 TTCTGTGGGACTGTGGATCTCACTGGAAG-CTATCCAAGAGCCCACTGTCACCTTCTAGA 2816
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   2763 TTCTGTGGGACTGTGGATCTCACTGGAAGCCTATCCAAGAGCCCACTGTCACCTTCTAGA 2822

Qy   2817 CCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGC 2876
          |||||||||||||||||||||||||||||||||||     | |     ||||||||||
Db   2823 CCACATGATAGGGCTAGACAGCTCAGTTCACCATGAT----CTTTTGTCACTCTGCTGGC 2878

Qy   2877 ACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGT 2936
          ||||||||||||||||    |  ||||||||||||||||||||||||||||||||||||
Db   2879 ACACCAGTGGCAAGGCC--AGAATGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGT 2936

Qy   2937 GCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTT 2996
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2937 GCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTT 2996

Qy   2997 GGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGG 3056
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2997 GGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGG 3056

Qy   3057 TGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGT 3116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3057 TGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGT 3116

Qy   3117 AAATAAATATATCAGCAAAGCAAAAAGAAAAAAAAAA 3153
          |||||||||||||||||||||||| ||||||||||
Db   3117 AAATAAATATATCAGCAAAGCAAAAAAAAAAAAAAAA 3153
```

```
RESULT   4
HSU92285
LOCUS       HSU92285     6146 bp    mRNA            PRI       04-FEB-1998
DEFINITION  Human GABA-A receptor epsilon subunit (GABRE) RNA, alternative
            transcript.
ACCESSION   U92285
VERSION     U92285.1  GI:2735330
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 6146)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6146)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .6146
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq28"
     misc_RNA        1. .6146
                     /gene="GABRE"
                     /note="RNA transcript is initiated from within the GABRE
                     gene, and therefore contains intron sequence with respect
                     to the subunit transcript"
     misc_feature    1. .3863
                     /gene="GABRE"
                     /note="intron 6 of GABRE; GABRE gene sequence deposited in
                     GenBank Accession Number U92283"
     gene            1. .6146
                     /gene="GABRE"
     stem_loop       12. .96
                     /gene="GABRE"
     stem_loop       1065. .1147
                     /gene="GABRE"
     misc_feature    3864. .6146
                     /gene="GABRE"
                     /note="exons 7, 8 and 9 of GABRE; GABRE gene sequence
                     deposited in GenBank Accession Number U92283"
BASE COUNT     1440 a   1519 c   1458 g   1729 t
ORIGIN
```

Query Match 72.4%; Score 2284; DB 11; Length 6146;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    824 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 883
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3863 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 3922

Qy    884 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 943
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3923 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 3982

Qy    944 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 1003
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3983 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 4042

Qy   1004 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGAT 1063
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4043 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGAT 4102

Qy   1064 TTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTC 1123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4103 TTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTC 4162

Qy   1124 AACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGT 1183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4163 AACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGT 4222

Qy   1184 ATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACAT 1243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4223 ATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACAT 4282

Qy   1244 CAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCG 1303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4283 CAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCG 4342

Qy   1304 TCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGC 1363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4343 TCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGC 4402
```

THIS PAGE BLANK (USPTO)

```
Qy    181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240

Qy    241 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300

Qy    301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360

Qy    361 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 420

Qy    421 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 480

Qy    481 DNYSRVVFPVTFFFFNVLYWLVCLNL 506
          |||||||||||||||||||||||||||
Db    481 DNYSRVVFPVTFFFFNVLYWLVCLNL 506
```

RESULT 2
Q99520
ID Q99520 PRELIMINARY; PRT; 505 AA.
AC Q99520;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE PUTATIVE GABA-GATED CHLORIDE CHANNEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97238072.
RA GARRET M., BASCLES L., BOUE-GRABOT E., SARTOR P., CHARRON G.,
RA BLOCH B., MARGOLSKEE R.F.;
RT "An mRNA encoding a putative GABA-gated chloride channel is expressed
RT in the human cardiac conduction system.";
RL J. Neurochem. 68:1382-1389(1997).
DR EMBL; Y07637; CAA68914.1; -.
DR PFAM; PF00065; neur_chan; 2.
DR PRINTS; PR00253; GABAARECEPTR.
SQ SEQUENCE 505 AA; 57856 MW; 1E6B104C CRC32;

Sequence Comparison D

Query Match 99.5%; Score 2676.5; DB 4; Length 505;
Best Local Similarity 99.8%; Pred. No. 1.8e-220;
Matches 505; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy      1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60

Qy     61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120

Qy    121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180

Qy    181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240

Qy    241 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    241 KLFQFDFTGVSNKTEIITTP-GDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 299

Qy    301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 359

Qy    361 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 419

Qy    421 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 479

Qy    481 DNYSRVVFPVTFFFFNVLYWLVCLNL 506
          |||||||||||||||||||||||||||
Db    480 DNYSRVVFPVTFFFFNVLYWLVCLNL 505
```

RESULT 3
O55209
ID O55209 PRELIMINARY; PRT; 384 AA.
AC O55209;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE GABA-A RECEPTOR EPSILON SUBUNIT (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RA HANNA M.C., HALES T.G., KIRKNESS E.F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U92284; AAB93879.1; -.
DR PFAM; PF00065; neur_chan; 2.
FT NON_TER 1 1
SQ SEQUENCE 384 AA; 45465 MW; E5D0E1B9 CRC32;

Query Match 56.3%; Score 1515.5; DB 11; Length 384;
Best Local Similarity 72.1%; Pred. No. 1.6e-121;
Matches 282; Conservative 41; Mismatches 55; Indels 13; Gaps 4;

```
Qy    122 FSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDG 181
          | |||||||||||||||:|:|:||||||||||||||||||| |::||:|||| |:|||
Db      1 FYQTWYDERLCYNDTFETLILHGNVVSQLWIPDTFFRNSKRTQEYDITIPNQMALIHKDG 60

Qy    182 KVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWK 241
          |||||:|||||| |||||| |||||||||||||||| |:||||||||||:|: ||:||
Db     61 KVLYTVRMTIDARCSLHMLNFPMDSHSCPLSFSSFSYDEHEMIYKWENFKLKIDAKNTWK 120

Qy    242 LFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWI 301
          | :||||||:||||||:|||||||||| |||||||||:: ||||:|||||||||||||||
Db    121 LLEFDFTGVNNKTEIISTPVGDFMVMTFFFNVSRRFGFIVFQNYIPSSVTTMLSWVSFWI 180

Qy    302 KTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVL 361
          | |:| || |:|::||||| ||||||||||||||:|||||||||||| ||| |||| ||
Db    181 KIEAAAARASVGVSSVLTMATLGTFSRKNFPRVSYLTALDFYIAICFVLCFCTLLEFTVL 240

Qy    362 NFLIYNQTKAHASPKLRHPRINSRAH------ARTRARSRACARQHQEAFVCQIVTTEGS 415
          ||| ||  :  |||| |||||:|| ||| || |||:||| |
Db    241 NFLTYNNIERQASPKFYQFPTNSRANARTRARARTRARARARQQQEVFVCEIVTYE-E 299

Qy    416 DGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCI 475
          : ||   |  |   |: |  | :  |  :  ||||||| |||::||:|||:||
Db    300 NAEE----GYQWSPRSRRPQCPWRRCGRSYVC--FRVLRKYFCMVPGCEGNSWQRGRICI 353

Qy    476 HVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
          ||||||||||:||:||||||:||::||||
Db    354 HVYRLDNYSRVLFPITFFFFNVVYWVICLNL 384
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:26:38 ; Search time 22.24 Seconds
(without alignments)
679.479 Million cell updates/sec

Title: US-09-030-832-42
Perfect score: 2691
Sequence: 1 MLSKVLPVLLGILLILQSRV.....VFPVTFFFFNVLYWLVCLNL 506

Scoring table: BLOSUM62

Searched: 82229 seqs, 29864866 residues

Database : SwissProt_38:*

Word size : 0

Number of hits that pass the threshold : 82229

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2691	100.0	506	1	GAE_HUMAN	P78334 homo sapien
2	1202.5	44.7	457	1	GAC4_CHICK	P34904 gallus gall
3	1097.5	40.8	467	1	GAC3_MOUSE	P27681 mus musculu
4	1087	40.4	474	1	GAC2_CHICK	P21548 gallus gall
5	1085.5	40.3	467	1	GAC3_HUMAN	Q99928 homo sapien
6	1084.5	40.3	467	1	GAC3_RAT	P28473 rattus norv
7	1082	40.2	475	1	GAC2_BOVIN	P22300 bos taurus
8	1078	40.1	474	1	GAC2_MOUSE	P22723 mus musculu
9	1077	40.0	466	1	GAC2_RAT	P18508 rattus norv
10	1067	39.7	467	1	GAC2_HUMAN	P18507 homo sapien
11	1054	39.2	465	1	GAC1_RAT	P23574 rattus norv
12	861	32.0	465	1	GAA6_CHICK	Q90845 gallus gall
13	858	31.9	453	1	GAA6_RAT	P30191 rattus norv
14	855.5	31.8	552	1	GAA4_RAT	P28471 rattus norv
15	851	31.6	453	1	GAA6_HUMAN	Q16445 homo sapien
16	850	31.6	554	1	GAA4_HUMAN	P48169 homo sapien
17	842	31.3	556	1	GAA4_BOVIN	P20237 bos taurus
18	814	30.2	464	1	GAA5_RAT	P19969 rattus norv
19	813	30.2	462	1	GAA5_HUMAN	P31644 homo sapien
20	808.5	30.0	492	1	GAA3_MOUSE	P26049 mus musculu
21	803	29.8	455	1	GAA1_MOUSE	P18504 mus musculu
22	800	29.7	493	1	GAA3_RAT	P20236 rattus norv
23	800	29.7	443	1	GAA6_MOUSE	P16305 mus musculu
24	799.5	29.7	456	1	GAA1_BOVIN	P08219 bos taurus
25	798.5	29.7	492	1	GAA3_HUMAN	P34903 homo sapien
26	797.5	29.6	455	1	GAA1_CHICK	P19150 gallus gall
27	796.5	29.6	492	1	GAA3_BOVIN	P10064 bos taurus
28	785.5	29.2	456	1	GAA1_HUMAN	P14867 homo sapien
29	782.5	29.1	451	1	GAA2_RAT	P23576 rattus norv
30	781	29.0	451	1	GAA2_BOVIN	P10063 bos taurus
31	781	29.0	451	1	GAA2_HUMAN	P47869 homo sapien
32	778	28.9	451	1	GAA2_MOUSE	P26048 mus musculu
33	709	26.3	488	1	GAB4_CHICK	P24045 gallus gall
34	677.5	25.2	474	1	GAB1_HUMAN	P18505 homo sapien
35	673.5	25.0	474	1	GAB1_BOVIN	P08220 bos taurus
36	671.5	25.0	474	1	GAB1_RAT	P15431 rattus norv
37	668.5	24.8	474	1	GAB1_MOUSE	P50571 mus musculu
38	668	24.8	473	1	GAB3_HUMAN	P28472 homo sapien
39	667	24.8	474	1	GAB2_HUMAN	P47870 homo sapien
40	665	24.7	473	1	GAB3_MOUSE	P15433 mus musculu
41	664	24.7	474	1	GAB2_MOUSE	P15432 mus musculu
42	655	24.3	449	1	GRA1_MOUSE	Q64018 mus musculu
43	652.5	24.2	449	1	GAD_RAT	P18506 rattus norv
44	652	24.2	449	1	GRA1_HUMAN	P23415 homo sapien
45	649.5	24.1	452	1	GRA2_HUMAN	P23416 homo sapien

ALIGNMENTS

Sequence Comparison B

```
RESULT   1
GAE_HUMAN
ID   GAE_HUMAN      STANDARD;      PRT;   506 AA.
AC   P78334; O15345;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR EPSILON SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97192095.
RA   DAVIES P.A., HANNA M.C., HALES T.G., KIRKNESS E.F.;
RT   "Insensitivity to anaesthetic agents conferred by a class of GABA(A)
RT   receptor subunit.";
RL   Nature 385:820-823(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97480709.
RA   WILKE K., GAUL R., KLAUCK S.M., POUSTKA A.;
RT   "A gene in human chromosome band Xq28 (GABRE) defines a putative new
RT   subunit class of the GABAA neurotransmitter receptor.";
RL   Genomics 45:1-10(1997).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. ASSOCIATES WITH ALPHA AND BETA
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: FOUND IN MANY TISSUE. HIGHEST LEVELS OF
CC       EXPRESSION IN ADULT HEART AND PLACENTA.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U66661; AAB49284.1; -.
DR   EMBL; Y09763; CAA70903.1; -.
DR   EMBL; Y09764; CAA70903.1; JOINED.
DR   MIM; 300093; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane.
FT   SIGNAL        1      ?       POTENTIAL.
FT   CHAIN         ?    506       GAMMA-AMINOBUTYRIC-ACID RECEPTOR EPSILON
FT                                SUBUNIT.
FT   DOMAIN        ?    253       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    254    274       POTENTIAL.
FT   TRANSMEM    281    301       POTENTIAL.
FT   TRANSMEM    344    364       POTENTIAL.
FT   DOMAIN      365    485       CYTOPLASMIC (PROBABLE).
```

```
FT   TRANSMEM    486    506       POTENTIAL.
FT   CARBOHYD    134    134       POTENTIAL.
FT   CARBOHYD    252    252       POTENTIAL.
FT   DISULFID    195    209       BY SIMILARITY.
FT   CONFLICT    102    102       A -> S (IN REF. 2).
FT   CONFLICT    245    245       F -> L (IN REF. 2).
FT   CONFLICT    471    471       G -> A (IN REF. 2).
FT   CONFLICT    502    502       V -> F (IN REF. 2).
SQ   SEQUENCE   506 AA;  57955 MW;  6BC8394B CRC32;
```

```
  Query Match           100.0%;  Score 2691;  DB 1;  Length 506;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-202;
  Matches  506;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60

Qy      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120

Qy     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180

Qy     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240

Qy     241 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300

Qy     301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360

Qy     361 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 420

Qy     421 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 480

Qy     481 DNYSRVVFPVTFFFFNVLYWLVCLNL 506
           |||||||||||||||||||||||||
Db     481 DNYSRVVFPVTFFFFNVLYWLVCLNL 506
```

```
RESULT   2
GAC4_CHICK
ID   GAC4_CHICK     STANDARD;      PRT;   457 AA.
AC   P34904;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG4.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93387470.
RA   HARVEY R.J., KIM H.-C., DARLISON M.G.;
RT   "Molecular cloning reveals the existence of a fourth gamma subunit of
RT   the vertebrate brain GABAA receptor.";
RL   FEBS Lett. 331:211-216(1993).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: ABUNDANT IN SEVERAL BRAIN REGIONS, INCLUDING
CC       THE ECTOSTRIATUM, NUCLEUS ROTUNDUS AND HYPERSTRIATUM VENTRALE.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X73533; CAA51939.1; -.
DR   PIR; S38296; S38296.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    457       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4
FT                                SUBUNIT.
FT   DOMAIN       22    256       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    257    279       PROBABLE.
FT   TRANSMEM    283    305       PROBABLE.
FT   TRANSMEM    317    339       PROBABLE.
FT   DOMAIN      340    433       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    434    457       PROBABLE.
FT   CARBOHYD     35     35       POTENTIAL.
FT   CARBOHYD    112    112       POTENTIAL.
FT   CARBOHYD    230    230       POTENTIAL.
FT   DISULFID    173    187       BY SIMILARITY.
SQ   SEQUENCE   457 AA;  53183 MW;  1571332B CRC32;
```

```
  Query Match           44.7%;  Score 1202.5;  DB 1;  Length 457;
  Best Local Similarity  48.1%;  Pred. No. 1.4e-86;
  Matches  218;  Conservative   82;  Mismatches   94;  Indels   59;  Gaps    5;

Qy      70 EASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDE 129
           :|::|||::| |||:|||| || ||| : |:| |||:||:|:: |||||||  |:|||||
Db      48 DATQILNSLLKNYDNKLRPDIGIKPTFIDVDIYVNSIGPVSVIQMEYTIDIFFAQTWYDR 107

Qy     130 RLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
           || :| | ::| || |:||::||||||||||||   | || |||::||: |||||||:|:
Db     108 RLRFNSTLKALTLNTNMVSRIWIPDTFFRNSKRADSHWITTPNQLLRIWNDGKVLYTLRL 167

Qy     190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
           ||:| | | :  ||||:||||| |||: ||  |::|:|  : :|:::: :|:|:||||||
Db     168 TIEAECLLQLQNFPMDTHSCPLVFSSYGYPREEIVYRWRRYSIEVSDQRTWRLYQFDFTG 227

Qy     250 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 309
           : | :|:: |  |::|||||: |::||| || | | |:|  :| :|||||||| :| |||
Db     228 LRNTSEVLRTGAGEYMVMTVSFDLSRRMGYFAIQTYIPCILTVVLSWVSFWIKRDSTPAR 287

Qy     310 TSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQT 369
           ||||||:|||||| | |||: ||||||||:| ::::||:| | ||:|:| ||:|: |:
Db     288 TSLGITTVLTMTTLSTISRKHLPRVSYITAMDLFVSVCFIFVFAALMEYATLNYLVGNKK 347

Qy     370 K-AHASPKLRHP--------------RINSRAHARTRARSRACARQHQEAFVCQIVTTE 413
           |:| | | |                  ||:  |
Db     348 PLEHSSRKARLPPAGAQVMPSFTAININININMH------------------------- 382

Qy     414 GSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRL 473
                 |     :  ||||           | |  |  :::|| : ||:   |::||:
Db     382 -----WPPEIEEDEDDDPGSP----------CLEG-KECERFFCCIEDCQTGMWREGRV 424
```

```
Qy    474 CIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
          ||: |||:|||| ||  |  ||::||:  | |
Db    425 RIHISRLDSYSRVFFPTAFLLFNIVYWIAYLYL 457


RESULT   3
GAC3_MOUSE
ID   GAC3_MOUSE     STANDARD;      PRT;   467 AA.
AC   P27681;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C C57; TISSUE=BRAIN;
RX   MEDLINE; 91285135.
RA   WILSON-SHAW D., ROBINSON M., ALALJEV B., SIEGEL R.E., SIKELA J.M.;
RT   "A novel gamma subunit of the GABAA receptor identified using the
RT   polymerase chain reaction.";
RL   FEBS Lett. 284:211-215(1991).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X59300; CAA41988.1; -.
DR   PIR; S16915; S16915.
DR   MGD; MGI:95624; GABRG3.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN        18    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3
FT                                SUBUNIT.
FT   DOMAIN       18    254       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    255    277       PROBABLE.
FT   TRANSMEM    281    303       PROBABLE.
FT   TRANSMEM    315    337       PROBABLE.
FT   DOMAIN      338    443       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    444    467       PROBABLE.
FT   CARBOHYD    110    110       POTENTIAL.
FT   CARBOHYD    228    228       POTENTIAL.
FT   DISULFID    171    185       BY SIMILARITY.
SQ   SEQUENCE   467 AA;  54303 MW;  A332B008 CRC32;


  Query Match             40.8%;  Score 1097.5;  DB 1;  Length 467;
  Best Local Similarity   42.8%;  Pred. No. 2.3e-78;
  Matches  222;  Conservative   91;  Mismatches  141;  Indels   65;  Gaps    9;

Qy      1 MLSKVLPVLLGILLILQS-------RVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEE 53
            | :|:|     :|| | |       |||  : |:::  |::  |  |:||
Db      1 MAAKLL-----LLLCLFSGLHARSRRVE--EDENEDSPSNQKWVLAPKPQD--------- 45

Qy     54 TKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILD 113
                      :|: ||| :|  || |||| || ||||: |:| |||:||:| ::
Db     45 ---------------TDATLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSIN 89

Qy    114 MEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
          ||| ||| |:||| | || :| | ::| || |:|  :|||| |||||    | || |||
Db     90 MEYQIDIFFAQTWTDSRLRFNSTMKTLTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQ 149

Qy    174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLE 233
          ::||: |||:|||:|:||:| | | :  ||||:|:|||:|||: ||: ||||:|    :|
Db    150 LLRIWNDGKILYTLRLTINAECQLQLHNFPMDAHACPLTFSSYGYPKEEMIYRWRKNSVE 209

Qy    234 INEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTM 293
            :: ||:|:|||| |: | |||:||  ||::||||:| :||| ||   | |:|  :| :
Db    210 AADQKSWRLYQFDFMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVV 269

Qy    294 LSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFC 353
          ||||||||| :: ||||:||||:||||||| | :||: |||||:||:| :: :||:| |
Db    270 LSWVSFWIKKDATPARTTLGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFA 329

Qy    354 ALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTE 413
          ||:|:| ||:  |:  :    | :|  : :      ||      : |   :
Db    330 ALMEYATLNY--YSSCR---KPTIRKKKTSLLHPDSTRWIPDRISLQAPSNY-------- 377

Qy    414 GSDGEERPSCSAQQPPSPGSPEGPRSLC---SKLACCEWC---KRFKKYFCMVPDCEGST 467
                |    :|| |       |:    :  |   |   |  : :||   :|:  :
Db    377 --------SLLDMRPPPPVMITLNNSMYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGS 428

Qy    468 WQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
          |::||: | |  ||:|||| || :|  ||::||:  | |
Db    429 WRRGRIHIDVSELDSYSRVFFPTSFLLFNLVYWVGYLYL 467


RESULT   4
GAC2_CHICK
ID   GAC2_CHICK     STANDARD;      PRT;   474 AA.
AC   P21548;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COMMERCIAL RHODE ISLAND CROSS; TISSUE=BRAIN;
RX   MEDLINE; 91088318.
RA   GLENCORSE T.A., BATESON A.N., DARLISON M.G.;
RT   "Sequence of the chicken GABAA receptor gamma 2-subunit cDNA.";
RL   Nucleic Acids Res. 18:7157-7157(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
```

```
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X54944; CAA38704.1; -.
DR   PIR; S13086; S13086.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane; Phosphorylation.
FT   SIGNAL        1     38       POTENTIAL.
FT   CHAIN        39    474       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                                SUBUNIT.
FT   DOMAIN       39    272       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    273    295       PROBABLE.
FT   TRANSMEM    299    321       PROBABLE.
FT   TRANSMEM    333    355       PROBABLE.
FT   DOMAIN      356    450       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    451    474       PROBABLE.
FT   CARBOHYD     51     51       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    246    246       POTENTIAL.
FT   CARBOHYD    266    266       POTENTIAL.
FT   DISULFID    189    203       BY SIMILARITY.
FT   MOD_RES     411    411       PHOSPHORYLATION.
FT   DOMAIN      376    383       INSERTION, SIMILAR TO HUMAN GAMMA-2
FT                                SEQUENCE WHICH IS PROPOSED TO BE CAUSED
FT                                BY ALTERNATIVE SPLICING.
SQ   SEQUENCE   474 AA;  54969 MW;  F3975109 CRC32;

  Query Match             40.4%;  Score 1087;  DB 1;  Length 474;
  Best Local Similarity   43.7%;  Pred. No. 1.5e-77;
  Matches  197;  Conservative   90;  Mismatches  110;  Indels   54;  Gaps    6;

Qy      70 EASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDE 129
           : : ||| :|  ||:|||| || ||||:  :: |||:||:: ::|||||| |:|||||
Db      64 DVTLILNGLLEGYDNKLRPDIGVKPTVIHTDMYVNSIGPVNAINMEYTIDIFFAQTWYDR 123

Qy     130 RLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
           || :| | : | || |:| ::|||||||||||:   | || ||:|:||: ||:||||:|:
Db     124 RLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVLYTLRL 183

Qy     190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
           |||| | | :  ||||:||||| |||: ||  |:||:|:   :|: :  ||:|:|| |||
Db     184 TIDAECQLQLHNFPMDAHSCPLEFSSYGYPREEIIYQWKRSSVEVGDTRSWRLYQFSFTG 243

Qy     250 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 309
           : | ||:: |  ||::||:::||:||| ||   | |:| ::  :|||||||  :: |||
Db     244 LRNTTEVVKTTSGDYVVMSVYFNLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAVPAR 303

Qy     310 TSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYN-- 368
           ||||||:||||||| | :||: |:|||:||:| ::::||:| | ||:|:  |:: : |
Db     304 TSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVSNRK 363

Qy     368 ----QTKAHASPKLR-----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGS 415
               : |   :| ||      | |: |  : |   : |     |  :  : |
Db     364 PSKDKDKKKKNPLLRMFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------L 416

Qy     416 DGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCI 475
           ||::   |::                              :||   ||    |: ||: |
Db     417 DGKD---CAS-----------------------------FFCCFEDCRTGAWRHGRIHI 443

Qy     476 HVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
           : ::|:|:|: ||  |  ||::||:  | |
Db     444 RIAKMDSYARIFFPTAFCLFNLVYWVSYLYL 474


RESULT   5
GAC3_HUMAN
ID   GAC3_HUMAN     STANDARD;      PRT;   467 AA.
AC   Q99928;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=FETAL BRAIN;
RX   MEDLINE; 96360042.
RA   HADINGHAM K.L., WAFFORD K.A., THOMPSON S.A., PALMER K.J.,
RA   WHITING P.J.;
RT   "Expression and pharmacology of human GABAA receptors containing
RT   gamma 3 subunits.";
RL   Eur. J. Pharmacol. 291:301-309(1995).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S82769; AAB39369.1; -.
DR   MIM; 600233; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN        18    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3
FT                                SUBUNIT.
FT   DOMAIN       18    254       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    255    277       PROBABLE.
FT   TRANSMEM    281    303       PROBABLE.
FT   TRANSMEM    315    337       PROBABLE.
FT   DOMAIN      338    443       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    444    467       PROBABLE.
FT   CARBOHYD    110    110       POTENTIAL.
FT   CARBOHYD    228    228       POTENTIAL.
FT   DISULFID    171    185       BY SIMILARITY.
SQ   SEQUENCE   467 AA;  54284 MW;  EAB28EEC CRC32;

  Query Match             40.3%;  Score 1085.5;  DB 1;  Length 467;
  Best Local Similarity   43.1%;  Pred. No. 2e-77;
  Matches  223;  Conservative   80;  Mismatches  144;  Indels   71;  Gaps    9;

Qy       7 PVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETETGSRVG 66
           | || :|| | | :          | || |          ||      || :|
Db       3 PKLL-LLLCLFSGL---------HARSRKVEEDEYEDSSSNQKWVLAPKSQDT------- 46

Qy      67 KLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTW 126
             : : ||| :|  || |||| || ||||: |:| |||:||:| ::||| ||| |:|||
Db      46 ---DVTLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSINMEYQIDIFFAQTW 102

Qy     127 YDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYT 186
             | || :| | : | || |:|  :|||| ||||     | || |||::||: |||:|||
Db     103 TDSRLRFNSTMKILTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQLLRIWNDGKILYT 162

Qy     187 IRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFD 246
           :|:||:| | | :  |||| |||| ||| || |||:|    :|  :: ||:|:|||
```

```
Db    163 LRLTINAECQLQLHNFPMDEHSCPLIFSSYGYPKEEMIYRWRKNSVEAADQKSWRLYQFD 222

Qy    247 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 306
          | |: | |||:||  ||::||||:| :||| ||   | |:|  :| :|||||||| ::
Db    223 FMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFWIKKDAT 282

Qy    307 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 366
          ||||:||||:||||||| | :||: |||||:||:| :: :||:| | ||:|:| ||:  |
Db    283 PARTALGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEYATLNY--Y 340

Qy    367 NQTKAHASPK----LRHP--------RINSRAHARTRARSRACARQHQEAFVCQIVTTEG 414
          :  :   : |    | ||         ||: :| :
Db    341 SSCRKPTTTKKTTSLLHPDSSRWIPERISLQAPSNY---------------------- 377

Qy    415 SDGEERPSCSAQQPPSPGSPEGPRSLC---SKLACCEWC---KRFKKYFCMVPDCEGSTW 468
                |    :|| |       |:     :  |   |   | : :||   :|:  :|
Db    377 -------SLLDMRPPPPAMITLNNSVYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSW 429

Qy    469 QQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
          ::||: | :  ||:|||| || :|  ||::||:  | |
Db    430 RKGRIHIDILELDSYSRVFFPTSFLLFNLVYWVGYLYL 467


RESULT   6
GAC3_RAT
ID   GAC3_RAT       STANDARD;      PRT;   467 AA.
AC   P28473;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 92159063.
RA   HERB A., WISDEN W., LUEDDENS H., PUIA G., VICINI S., SEEBURG P.H.;
RT   "The third gamma subunit of the gamma-aminobutyric acid type A
RT   receptor family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:1433-1437(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZUR-SIV; TISSUE=BRAIN;
RX   MEDLINE; 92070559.
RA   KNOFLACH F., RHYNER T., VILLA M., KELLENBERGER S., DRESCHER U.,
RA   MALHERBE P., SIGEL E., MOEHLER H.;
RT   "The gamma 3-subunit of the GABAA-receptor confers sensitivity to
RT   benzodiazepine receptor ligands.";
RL   FEBS Lett. 293:191-194(1991).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M81142; AAA41181.1; -.
DR   EMBL; X63324; CAA44930.1; -.
DR   PIR; S19317; S19317.
DR   PIR; A40221; A40221.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN        18    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3
FT                                SUBUNIT.
FT   DOMAIN       18    254       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    255    277       PROBABLE.
FT   TRANSMEM    281    303       PROBABLE.
FT   TRANSMEM    315    337       PROBABLE.
FT   DOMAIN      338    443       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    444    467       PROBABLE.
FT   CARBOHYD    110    110       POTENTIAL.
FT   CARBOHYD    228    228       POTENTIAL.
FT   DISULFID    171    185       BY SIMILARITY.
FT   CONFLICT    416    416       S -> T (IN REF. 2).
SQ   SEQUENCE   467 AA;  54292 MW;  B7263D44 CRC32;


  Query Match           40.3%;  Score 1084.5;  DB 1;  Length 467;
  Best Local Similarity   42.8%;  Pred. No. 2.4e-77;
  Matches  222;  Conservative   90;  Mismatches  142;  Indels   65;  Gaps   10;

Qy      1 MLSKVLPVLLGILLILQS-------RVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEE 53
          | :|:|     :|| | |         |||  : :|::  |::  |  |
Db      1 MAAKLL-----LLLCLFSGLHARSRRVE--EDDSEDSPSNQKWVLAP------------- 41

Qy     54 TKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILD 113
           || :|          : : ||| :|  || |||| || ||||: |:| |||:||:| ::
Db     41 -KSQDT----------DVTLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSIN 89

Qy    114 MEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
          ||| ||| |:||| | || :| | : | || |:|  :||||| |||||    | || |||
Db     90 MEYQIDIFFAQTWTDSRLRFNSTMKILTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQ 149

Qy    174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLE 233
          ::||: |||:|||:|:||:| | | :  ||||:|:|||:|||: ||: ||||:|    :|
Db    150 LLRIWNDGKILYTLRLTINAECQLQLHNFPMDAHACPLTFSSYGYPKEEMIYRWRKNSVE 209

Qy    234 INEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTM 293
            :: ||:|:|||| |: | |||:||  ||::||||:| :||| ||   | |:|  :| :
Db    210 AADQKSWRLYQFDFMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVV 269

Qy    294 LSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFC 353
          |||||||| :: ||||:||||:||||||| | :||: |||||:||:| :: :|||:| |
Db    270 LSWVSFWIKKDATPARTTLGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFA 329

Qy    354 ALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTE 413
          ||:|:| ||:  |:  :    | :|  : :    ||      : |   :
Db    330 ALMEYATLNY--YSSCR---KPTIRKKKTSLLHPDSTRWIPDRISLQAPSNY-------- 377

Qy    414 GSDGEERPSCSAQQPPSPGSPEGPRSLC---SKLACCEWC---KRFKKYFCMVPDCEGST 467
                |    :|| |       |:     :  |   |   | : :||   :|:  :
Db    377 --------SLLDMRPPPPVMITLNNSMYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGS 428

Qy    468 WQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
          |::||: | |  ||:|||| || :|  ||::||:  | |
Db    429 WRRGRIHIDVSELDSYSRVFFPTSFLLFNLVYWVGYLYL 467


RESULT   7
GAC2_BOVIN
ID   GAC2_BOVIN     STANDARD;      PRT;   475 AA.
AC   P22300;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
```

```
GN   GABRG2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC   Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN CORTEX;
RX   MEDLINE; 91088632.
RA   WHITING P.J., MCKERNAN R.M., IVERSEN L.L.;
RT   "Another mechanism for creating diversity in gamma-aminobutyrate type
RT   A receptors: RNA splicing directs expression of two forms of gamma 2
RT   phosphorylation site.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:9966-9970(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: ALTERNATIVE RNA SPLICING DIRECTS EXPRESSION
CC       OF TWO FORMS OF GAMMA-2 SUBUNITS (2S AND 2L), ONE (2L) CONTAINS A
CC       PROTEIN KINASE C PHOSPHORYLATION SITE.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M55563; AAA30531.1; -.
DR   PIR; A39272; A39272.
DR   PIR; B39272; B39272.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane; Phosphorylation;
KW   Alternative splicing.
FT   SIGNAL        1     39       POTENTIAL.
FT   CHAIN        40    475       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                                SUBUNIT.
FT   DOMAIN       40    273       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    274    296       PROBABLE.
FT   TRANSMEM    300    322       PROBABLE.
FT   TRANSMEM    334    356       PROBABLE.
FT   DOMAIN      357    451       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    452    475       PROBABLE.
FT   CARBOHYD     52     52       POTENTIAL.
FT   CARBOHYD    129    129       POTENTIAL.
FT   CARBOHYD    247    247       POTENTIAL.
FT   DISULFID    190    204       BY SIMILARITY.
FT   MOD_RES     382    382       PHOSPHORYLATION (BY PKC) (PROBABLE).
FT   VARSPLIC    377    384       MISSING (IN ISOFORM GAMMA-2S).
FT   VARIANT     230    230       S -> G.
SQ   SEQUENCE   475 AA;  55264 MW;  EEBD5FCE CRC32;


  Query Match             40.2%;  Score 1082;  DB 1;  Length 475;
  Best Local Similarity   43.2%;  Pred. No. 3.8e-77;
  Matches  197;  Conservative   91;  Mismatches  112;  Indels   56;  Gaps    7;

Qy      67 KLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
           |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|||||| | |
Db      60 KVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFGQ 119

Qy     125 TWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVL 184
           |||| || :| | : | || |:| ::|||||||||||:   | || ||:|:||: ||:||

Db     120 TWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVL 179

Qy     185 YTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQ 244
           ||:|:|||| | | :  |||| ||||| ||| || |::|:|:   :|:::  ||:|:|
Db     180 YTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEVSDTRSWRLYQ 239

Qy     245 FDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTE 304
           | | |: | ||:: |  ||::|||::|::||| ||   | |:| ::  :|||||||  :
Db     240 FSFVGLRNTTEVVKTTSGDYVVMTVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKD 299

Qy     305 SAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL 364
           : |||||||||:||||||| | :||: |:|||:||:| ::::||:| | ||:|:  |::
Db     300 AVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYF 359

Qy     365 IYN------QTKAHASPKLR-----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIV 410
           : |      : |   :| ||      | |: |  : |   : |     |  :  : |
Db     360 VSNRKPSKDKDKKKKNPLLRMFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYEC--- 417

Qy     411 TTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQ 470
               ||::   |::                                :||   ||    |:
Db     417 ----LDGKD---CAS----------------------------FFCCFEDCRTGAWRH 439

Qy     471 GRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
           ||: | : ::|:|:|: ||  |  ||::||:  | |
Db     440 GRIHIRIAKMDSYARIFFPTAFCLFNLVYWVSYLYL 475


RESULT   8
GAC2_MOUSE
ID   GAC2_MOUSE     STANDARD;      PRT;   474 AA.
AC   P22723;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91108470.
RA   KOFUJI P., WANG J.B., MOSS S.J., HUGANIR R.L., BURT D.R.;
RT   "Generation of two forms of the gamma-aminobutyric acidA receptor
RT   gamma 2-subunit in mice by alternative splicing.";
RL   J. Neurochem. 56:713-715(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   SIKELA J.M., SHAW W.D., KHAN A.S., LIN L.-H., LEIDENHEIMER G.,
RA   SIEGEL R.E.;
RL   Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: ALTERNATIVE RNA SPLICING DIRECTS EXPRESSION
CC       OF TWO FORMS OF GAMMA2 SUBUNIT (2S AND 2L), ONE (2L) CONTAINS A
CC       PROTEIN KINASE C PHOSPHORYLATION SITE.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
```

```
CC   ----------------------------------------------------------------------
DR   EMBL; M86572; AAB59635.1; -.
DR   EMBL; M62374; AAA37653.1; -.
DR   PIR; JH0317; JH0317.
DR   PIR; JH0316; JH0316.
DR   MGD; MGI:95623; GABRG2.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane; Phosphorylation;
KW   Alternative splicing.
FT   SIGNAL       1     38       POTENTIAL.
FT   CHAIN       39    474       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                               SUBUNIT.
FT   DOMAIN       39    272       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    273    295       PROBABLE.
FT   TRANSMEM    299    321       PROBABLE.
FT   TRANSMEM    333    355       PROBABLE.
FT   DOMAIN      356    450       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    451    474       PROBABLE.
FT   CARBOHYD     51     51       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    246    246       POTENTIAL.
FT   DISULFID    189    203       BY SIMILARITY.
FT   MOD_RES     381    381       PHOSPHORYLATION (BY PKC) (PROBABLE).
FT   VARSPLIC    376    383       MISSING (IN ISOFORM GAMMA-2S).
FT   CONFLICT     49     49       T -> A (IN REF. 2).
FT   CONFLICT    414    414       Q -> E (IN REF. 2).
FT   CONFLICT    443    443       M -> I (IN REF. 2).
SQ   SEQUENCE   474 AA;  55145 MW;  A3049225 CRC32;


  Query Match             40.1%;  Score 1078;  DB 1;  Length 474;
  Best Local Similarity   42.3%;  Pred. No. 7.7e-77;
  Matches  197;  Conservative   94;  Mismatches  119;  Indels   56;  Gaps    7;

Qy      57 TETETGSRVGKLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDM 114
           |  :|     |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|
Db      49 TSNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINM 108

Qy     115 EYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQM 174
           |||||| |:||||| || :| | : | || |:| ::|||||||||||:   | || ||:|
Db     109 EYTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRM 168

Qy     175 VRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEI 234
           :||: ||:||||:|:|||| | | :  |||| ||||| ||||: ||  |::|:|:   :|:
Db     169 LRIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEV 228

Qy     235 NEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTML 294
             :  ||:|:|| | |: | ||:: |  ||::||:::|::||| ||   | |:| ::  :|
Db     229 GDTRSWRLYQFSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVL 288

Qy     295 SWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCA 354
           |||||||  :: |||||||||:|||||| | :||: |:|||:||:| ::::||:| | |
Db     289 SWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSA 348

Qy     355 LLEFAVLNFLIYN------QTKAHASPKLR-----HPRINSRAHARTRARSRAC---ARQ 400
           |:|:  |:: : |      : |   :| ||      | |: |  : |   : |     |
Db     349 LVEYGTLHYFVSNRKPSKDKDKKKKNPLLRMFSFKAPTIDIRPRSATIQMNNATHLQERD 408

Qy     401 HQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMV 460
             : : |        ||::   |::                          :||
Db     409 EEYGYQC-------LDGKD---CAS-----------------------------FFCCF 428

Qy     461 PDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
           ||    |: ||: : : ::|:|:|: ||  |  ||::||:  | |
Db     429 EDCRTGAWRHGRIHMRIAKMDSYARIFFPTAFCLFNLVYWVSYLYL 474


RESULT   9
GAC2_RAT
ID   GAC2_RAT       STANDARD;      PRT;   466 AA.
AC   P18508;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 90380375.
RA   SHIVERS B.D., KILLISCH I., SPRENGEL R., SONTHEIMER H., KOEHLER M.,
RA   SCHOFIELD P.R., SEEBURG P.H.;
RT   "Two novel GABAA receptor subunits exist in distinct neuronal
RT   subpopulations.";
RL   Neuron 3:327-337(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90331051.
RA   MALHERBE P., SIGEL E., BAUR R., PERSOHN E., RICHARDS J.G., MOHLER H.;
RT   "Functional characteristics and sites of gene expression of the alpha
RT   1, beta 1, gamma 2-isoform of the rat GABAA receptor.";
RL   J. Neurosci. 10:2330-2337(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L08497; AAC42036.1; -.
DR   PIR; A37164; A37164.
DR   PIR; JQ0077; JQ0077.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL       1     38       POTENTIAL.
FT   CHAIN       39    466       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                               SUBUNIT.
FT   DOMAIN       39    272       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    273    295       PROBABLE.
FT   TRANSMEM    299    321       PROBABLE.
FT   TRANSMEM    333    355       PROBABLE.
FT   DOMAIN      356    442       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    443    465       PROBABLE.
FT   CARBOHYD     51     51       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    246    246       POTENTIAL.
FT   DISULFID    189    203       BY SIMILARITY.
FT   CONFLICT     22     22       M -> I (IN REF. 2).
SQ   SEQUENCE   466 AA;  54077 MW;  EDDEFFEF CRC32;


  Query Match             40.0%;  Score 1077;  DB 1;  Length 466;
  Best Local Similarity   43.1%;  Pred. No. 9e-77;
  Matches  193;  Conservative   93;  Mismatches  114;  Indels   48;  Gaps    6;

Qy      67 KLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
```

```
          |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|||||||  |:|
Db     59 KVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFAQ 118

Qy    125 TWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVL 184
          |||| || :| | : | || |:| ::|||||||||||:   | || ||:|:||: ||:||
Db    119 TWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVL 178

Qy    185 YTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQ 244
          ||:|:|||| | | :  |||| ||||| ||||: ||  |::|:|:   :|: :  ||:|:|
Db    179 YTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQ 238

Qy    245 FDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTE 304
          | | |: | ||:: |  ||::||:::|::||| ||   | |:| ::  :|||||||  :
Db    239 FSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKD 298

Qy    305 SAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL 364
          : |||||||||:|||||| | :|| |:|||:||:| ::::||:| | ||:|:  |::
Db    299 AVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYF 358

Qy    365 IYNQTKAHASPKLRH---PRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGE 418
          : |:  :    | :    | |: |  : |   : |     |  :  : |        ||:
Db    359 VSNRKPSKDKDKKKKNPAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGK 411

Qy    419 ERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVY 478
          :   |::                              :||   ||    |: ||: | :
Db    412 D---CAS-----------------------------FFCCFEDCRTGAWRHGRIHIRIA 438

Qy    479 RLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
          ::|:|:|: ||  |  ||::||:  | |
Db    439 KMDSYARIFFPTAFCLFNLVYWVSYLYL 466


RESULT  10
GAC2_HUMAN
ID   GAC2_HUMAN     STANDARD;      PRT;   467 AA.
AC   P18507;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 89181956.
RA   PRITCHETT D.B., SONTHEIMER H., SHIVERS B.D., YMER S., KETTENMANN H.,
RA   SCHOFIELD P.R., SEEBURG P.H.;
RT   "Importance of a novel GABAA receptor subunit for benzodiazepine
RT   pharmacology.";
RL   Nature 338:582-585(1989).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X15376; CAA33437.1; -.
DR   PIR; S03905; S03905.
DR   MIM; 137164; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     39       POTENTIAL.
FT   CHAIN        40    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                                SUBUNIT.
FT   DOMAIN       40    273       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    274    296       PROBABLE.
FT   TRANSMEM    300    322       PROBABLE.
FT   TRANSMEM    334    356       PROBABLE.
FT   DOMAIN      357    443       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    444    466       PROBABLE.
FT   CARBOHYD     52     52       POTENTIAL.
FT   CARBOHYD    129    129       POTENTIAL.
FT   CARBOHYD    247    247       POTENTIAL.
FT   DISULFID    190    204       BY SIMILARITY.
SQ   SEQUENCE   467 AA;  54178 MW;  E78E8090 CRC32;


  Query Match             39.7%;  Score 1067;  DB 1;  Length 467;
  Best Local Similarity   42.6%;  Pred. No. 5.5e-76;
  Matches  191;  Conservative   94;  Mismatches  115;  Indels   48;  Gaps    6;

Qy     67 KLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
          |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|||||||  |:|
Db     60 KVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFAQ 119

Qy    125 TWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVL 184
          ||| || :| | : | || |:| ::|||||||||||:   | || ||:|:||: ||:||
Db    120 MWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVL 179

Qy    185 YTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQ 244
          |::|:|||| | | :  |||| ||||| |||: ||  |::|:|:   :|: :  ||:|:|
Db    180 YSLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQ 239

Qy    245 FDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTE 304
          | | |: | ||:: |  ||::||:::|::||| ||   | |:| ::  :|||||||  :
Db    240 FSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKD 299

Qy    305 SAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL 364
          : |||||||||:|||||| | :|| |:|||:||:| ::::||:| | ||:|:  |::
Db    300 AVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYF 359

Qy    365 IYNQTKAHASPKLRH---PRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGE 418
          : |:  :    | :    | |: |  : |   : |     |  :  : |        ||:
Db    360 VSNRKPSKDKDKKKKNPAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGK 412

Qy    419 ERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVY 478
          :   |::                              :||   ||    |: ||: | :
Db    413 D---CAS-----------------------------FFCCFEDCRTGAWRHGRIHIRIA 439

Qy    479 RLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
          ::|:|:|: ||  |  ||::||:  | |
Db    440 KMDSYARIFFPTAFCLFNLVYWVSYLYL 467


RESULT  11
GAC1_RAT
ID   GAC1_RAT       STANDARD;      PRT;   465 AA.
AC   P23574;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 91006020.
RA   YMER S., DRAGUHN A., WISDEN W., WERNER P., KEINAENEN K.,
RA   SCHOFIELD P.R., SPRENGEL R., PRITCHETT D.B., SEEBURG P.H.;
RT   "Structural and functional characterization of the gamma 1 subunit of
RT   GABAA/benzodiazepine receptors.";
RL   EMBO J. 9:3261-3267(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X57514; CAA40739.1; -.
DR   PIR; S12056; S12056.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36    465       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1
FT                                 SUBUNIT.
FT   DOMAIN       36    272       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    273    294       PROBABLE.
FT   TRANSMEM    299    320       PROBABLE.
FT   TRANSMEM    332    354       PROBABLE.
FT   DOMAIN      355    444       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    445    465       PROBABLE.
FT   CARBOHYD     50     50       POTENTIAL.
FT   CARBOHYD    127    127       POTENTIAL.
FT   CARBOHYD    245    245       POTENTIAL.
FT   DISULFID    188    202       BY SIMILARITY.
SQ   SEQUENCE   465 AA;  53550 MW;  963AF632 CRC32;


  Query Match             39.2%;  Score 1054;  DB 1;  Length 465;
  Best Local Similarity   43.1%;  Pred. No. 5.6e-75;
  Matches  193;  Conservative   91;  Mismatches  108;  Indels   56;  Gaps    5;

Qy      70 EASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDE 129
           : ::|||::|  ||:|||| || :|||:  :: |||:||:  ::||||||||||:|||:|
Db      63 DITQILNSLLQGYDNKLRPDIGVRPTVIETDVYVNSIGPVDPINMEYTIDIIFAQTWFDS 122

Qy     130 RLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
           || :| | : |:|| |:| ::||||||||||:::  | || ||:::||: ||:||||:|:
Db     123 RLKFNSTMKVLMLNSNMVGKIWIPDTFFRNSRKSDAHWITTPNRLLRIWSDGRVLYTLRL 182

Qy     190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
           ||:| | | :  |||| ||||| ||||: ||:||: |||:   :|: :   |:|:|| | |
Db     183 TINAECYLQLHNFPMDEHSCPLEFSSYGYPKNEIEYKWKKPSVEVADPKYWRLYQFAFVG 242

Qy     250 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 309
           : | |||  |  ||:::||||::||| ||   | |:|  :| :||||||||  :: |||
Db     243 LRNSTEISHTISGDYIIMTIFFDLSRRMGYFTIQTYIPCILTVVLSWVSFWINKDAVPAR 302

Qy     310 TSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYN-- 368
           |||||||:|||||| | :|: |:|||:||:| ::::||:| | ||:|:  |::   |
Db     303 TSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFAALMEYGTLHYFTSNNK 362

Qy     368 ---------QTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGE 418
                    ::|   || |        | :     :     | :: :  | :  || |
Db     363 GKTTRDRKLKSKTSVSPGL-------HAGSTLIPMNNISMPQGEDDYGYQCL--EGKD-- 412

Qy     419 ERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVY 478
             |:                                 :||   ||   :|::||: | :
Db     412 ----CAT-----------------------------FFCCFEDCRTGSWREGRIHIRIA 437

Qy     479 RLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
           ::|:|||: ||  |  ||::||:  | |
Db     438 KIDSYSRIFFPTAFALFNLVYWVGYLYL 465


RESULT  12
GAA6_CHICK
ID   GAA6_CHICK     STANDARD;      PRT;   465 AA.
AC   Q90845;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRA6.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EMBRYONIC BRAIN;
RX   MEDLINE; 96373714.
RA   BAHN S., HARVEY R.J., DARLISON M.G., WISDEN W.;
RT   "Conservation of gamma-aminobutyric acid type A receptor alpha 6
RT   subunit gene expression in cerebellar granule cells.";
RL   J. Neurochem. 66:1810-1818(1996).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X94343; CAA64069.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    465       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6
FT                                 SUBUNIT.
FT   DOMAIN       20    242       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    243    264       PROBABLE.
FT   TRANSMEM    269    290       PROBABLE.
FT   TRANSMEM    302    324       PROBABLE.
FT   DOMAIN      325    421       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    422    443       PROBABLE.
FT   CARBOHYD     31     31       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    141    141       POTENTIAL.
FT   DISULFID    156    170       BY SIMILARITY.
SQ   SEQUENCE   465 AA;  51717 MW;  B74B26D1 CRC32;
```

```
  Query Match             32.0%;  Score 861;  DB 1;  Length 465;
  Best Local Similarity   39.2%;  Pred. No. 6.5e-60;
  Matches  179;  Conservative   85;  Mismatches  125;  Indels   68;  Gaps    9;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           :|||: :|  ||::|||| |   | |  :| | | ||:| ::||||:|: | ||| ||||
Db      33 TRILDKLLDGYDNRLRPGFGGAVTEVKTDIYVTSFGPVSDVEMEYTMDVFFRQTWTDERL 92

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
           :    | | ||  :||::| |||||| |::  | :| ||:: || ::| :|||:|:||
Db      93 KFGGPTEILRLNNLMVSKIWTPDTFFRNGKKSIAHNMTTPNKLFRIMQNGTILYTMRLTI 152

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLEINEKNSWKLFQFDFT 248
           :| | : :: |||| |:||| | |::||::|:|| |:      :|: :::|  | |:|
Db     153 NADCPMRLVNFPMDGHACPLKFGSYAYPKSEIIYTWKKGPLHSVEVPQESS-SLLQYDLI 211

Qy     249 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 308
           | :  :| | :  |::::||::|:: |: ||   | | |  :| :|| |||||  || ||
Db     212 GQTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPA 271

Qy     309 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 368
           ||  |||:|||||||   :| : |:||| ||:|::||:|| | | ||:||| :|:    |
Db     272 RTVFGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQ 331

Qy     369 TKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFV-----CQI---VTTEGSDGEER 420
           |:       |  :|| |   | | |       |         | :   | :  |  ::
Db     332 TQ-------RAMRKAARAAALAAALSAATVPAEDEIVSHSDSNCNLKKRVNSVTSQADQS 384

Qy     421 P-----SCSAQQ-------PPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTW 468
           |     | || |       ||:| :|                          |   |::
Db     385 PEASIVSNSASQCQPVSAPPPAPPAP--------------------------PPVGGTS- 418

Qy     469 QQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
                   ::| |||::||| |  ||::||:| |:
Db     418 ----------KIDQYSRILFPVAFAGFNLVYWVVYLS 444


RESULT  13
GAA6_RAT
ID   GAA6_RAT       STANDARD;      PRT;   453 AA.
AC   P30191;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRA6 OR GABRA-6.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 90348963.
RA   LUEDDENS H., PRITCHETT D., KHLER M., KILLISCH I., KEINAENEN K.,
RA   MONYER H., SPRENGEL R., SEEBURG P.H.;
RT   "Cerebellar GABAA receptor selective for a behavioural alcohol
RT   antagonist.";
RL   Nature 346:648-651(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: ONLY FOUND IN CEREBELLAR GRANULE CELLS.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L08495; AAC42034.1; -.
DR   EMBL; X55742; CAA39273.1; -.
DR   PIR; S11087; S11087.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    453       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6
FT                                SUBUNIT.
FT   DOMAIN       20    242       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    243    264       PROBABLE.
FT   TRANSMEM    269    290       PROBABLE.
FT   TRANSMEM    301    324       PROBABLE.
FT   DOMAIN      325    419       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    420    441       PROBABLE.
FT   CARBOHYD     31     31       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    141    141       POTENTIAL.
FT   DISULFID    156    170       BY SIMILARITY.
SQ   SEQUENCE   453 AA;  51184 MW;  0ED8616E CRC32;


  Query Match             31.9%;  Score 858;  DB 1;  Length 453;
  Best Local Similarity   37.7%;  Pred. No. 1.1e-59;
  Matches  171;  Conservative   88;  Mismatches  132;  Indels   62;  Gaps    6;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           ||||: :|  ||::|||| |   | |  :| | | ||:| ::||||:|: | ||| ||||
Db      33 SRILDNLLEGYDNRLRPGFGGAVTEVKTDIYVTSFGPVSDVEMEYTMDVFFRQTWTDERL 92

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
           :    | | ||  :||::| |||||| |::  | :| ||:: |:  :| :|||:|:||
Db      93 KFKGPAEILSLNNLMVSKIWTPDTFFRNGKKSIAHNMTTPNKLFRLMHNGTILYTMRLTI 152

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLEINEKNSWKLFQFDFT 248
           :| | : :: |||| |:||| | |::||::|:|| |:    : :|: |::|  | |:|
Db     153 NADCPMRLVNFPMDGHACPLKFGSYAYPKSEIIYTWKKGPLYSVEVPEESS-SLLQYDLI 211

Qy     249 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 308
           | :  :| | :  |::::||::|:: |: ||   | | |  :| :|| |||||  || ||
Db     212 GQTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPA 271

Qy     309 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 368
           ||  |||:|||||||   :| : |:||| ||:|::||:|| | | ||:||| :|:    |
Db     272 RTVFGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQ 331

Qy     369 TKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGS------------ 416
           ::              :   |:| |:      :  |:   :||    |
Db     332 SQ------------KAERQAQTAAKPPVAKSKTTESLEAEIVVHSDSKYHLKKRISSLTL 379

Qy     416 ---DGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGR 472
                |     :: |  | :|  |  |                     :|   |::
Db     380 PIVPSSEASKVLSRTPILPSTPVTPPLL-------------------LPAIGGTS----- 416

Qy     473 LCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
                   ::| |||::||| |  ||::||:| |:
Db     416 ------KIDQYSRILFPVAFAGFNLVYWIVYLS 442


RESULT  14
GAA4_RAT
ID   GAA4_RAT       STANDARD;      PRT;   552 AA.
AC   P28471;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
```

```
GN   GABRA4.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92008629.
RA   WISDEN W., HERB A., WIELAND H., KEINAENEN K., LUEDDENS H.,
RA   SEEBURG P.H.;
RT   "Cloning, pharmacological characteristics and expression pattern of
RT   the rat GABAA receptor alpha 4 subunit.";
RL   FEBS Lett. 289:227-230(1991).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L08493; AAC42032.1; -.
DR   EMBL; S55933; AAB19902.1; -.
DR   PIR; S17551; S17551.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36    552       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4
FT                                 SUBUNIT.
FT   DOMAIN       36    258       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    259    280       PROBABLE.
FT   TRANSMEM    285    306       PROBABLE.
FT   TRANSMEM    318    340       PROBABLE.
FT   DOMAIN      341    521       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    522    541       PROBABLE.
FT   CARBOHYD     47     47       POTENTIAL.
FT   CARBOHYD    144    144       POTENTIAL.
FT   CARBOHYD    157    157       POTENTIAL.
FT   DISULFID    172    186       BY SIMILARITY.
SQ   SEQUENCE   552 AA;  60951 MW;  62956C8F CRC32;


  Query Match             31.8%;  Score 855.5;  DB 1;  Length 552;
  Best Local Similarity   34.3%;  Pred. No. 2.2e-59;
  Matches  198;  Conservative   87;  Mismatches  172;  Indels  121;  Gaps   12;

Qy       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
           : | |   || :| :     | |   ||:|
Db      12 LCSGVSLALLHVLCLATCLNESPGQNSKDE---------------------------- 42

Qy      61 TGSRVGKL-PE-ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTI 118
                || ||  :|||:::|  ||::|||| |   | |  :| | | ||:| ::||||:
Db      42 ------KLCPENFTRILDSLLDGYDNRLRPGFGGPVTEVKTDIYVTSFGPVSDVEMEYTM 95

Qy     119 DIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIY 178
           |: | ||| |:|| |:    | | ||  :|:::| ||||||| |::  | :| ||:: ||
Db      96 DVFFRQTWIDKRLKYDGPIEILRLNNMMVTKVWTPDTFFRNGKKSVSHNMTAPNKLFRIM 155

Qy     179 KDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEIN 235
           ::| :|||:|:|| | | : :: |||| |:||| | |::||::|||| |       :|:
Db     156 RNGTILYTMRLTISAECPMRLVDFPMDGHACPLKFGSYAYPKSEMIYTWTKGPEKSVEV- 215

Qy     236 EKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLS 295
           | |  | |:|  | :  :| | :  |:::|||::|:: |: ||   | |:|  :| :||
Db     215 PKESSSLVQYDLIGQTVSSETIKSITGEYIVMTVYFHLRRKMGYFMIQTYIPCIMTVILS 274

Qy     296 WVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCAL 355
             |||||  || |||| |||:|||||||   :| : |:||| ||:|::||:|| | | ||
Db     275 QVSFWINKESVPARTVFGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSAL 334

Qy     356 LEFAVLNFLIYNQ-----------TKAHASPKLRHPRINS---RAHARTRARSRACARQ 400
           :||| :|:    |              :  |:| |:     :     ||    | |  |
Db     335 IEFAAVNYFTNIQMQKAKKKISKPPPEVPAAPVLKEKHTETSLQNTHANLNMRKRTNALV 394

Qy     401 HQEAFV---------CQIVTTEGSDGEERPSCSAQQPPSP------------------- 432
           | |: |             |      |  |       |:|
Db     395 HSESDVNSRTEVGNHSSKTTAAQESSETTPKAHLASSPNPFSRANAAETISAAARGLSSA 454

Qy     432 --GSPEG---PRSLCSKLACCEWCKRFKKYFCMV------------------PDCEGST 467
             || |   |  | |  |   :  |  :   |                     |   |::
Db     455 ASPSPHGTLQPAPLRSASARPAFGARLGRIKTTVNTTGVPGNVSATPPPSAPPPSGSGTS 514

Qy     468 WQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
                     ::| |:|::|||||  ||::||:| |:
Db     515 -----------KIDKYARILFPVTFGAFNMVYWVVYLS 541


RESULT  15
GAA6_HUMAN
ID   GAA6_HUMAN     STANDARD;      PRT;   453 AA.
AC   Q16445;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRA6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=CEREBELLUM;
RX   MEDLINE; 96226062.
RA   HADINGHAM K.L., GARRETT E.M., WAFFORD K.A., BAIN C., HEAVENS R.P.,
RA   SIRINATHSINGHJI D.J., WHITING P.J.;
RT   "Cloning of cDNAs encoding the human gamma-aminobutyric acid type A
RT   receptor alpha 6 subunit and characterization of the pharmacology of
RT   alpha 6-containing receptors.";
RL   Mol. Pharmacol. 49:253-259(1996).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S81944; AAB36480.1; -.
DR   MIM; 137143; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    453       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6
FT                                 SUBUNIT.
```

```
FT   DOMAIN       20    242       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    243    264       PROBABLE.
FT   TRANSMEM    269    290       PROBABLE.
FT   TRANSMEM    301    324       PROBABLE.
FT   DOMAIN      325    419       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    420    441       PROBABLE.
FT   CARBOHYD     31     31       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    141    141       POTENTIAL.
FT   DISULFID    156    170       BY SIMILARITY.
SQ   SEQUENCE   453 AA;  51034 MW;  4FE3C480 CRC32;


  Query Match           31.6%;  Score 851;  DB 1;  Length 453;
  Best Local Similarity 37.8%;  Pred. No. 3.8e-59;
  Matches  179;  Conservative   86;  Mismatches  128;  Indels   80;  Gaps   10;

Qy      65 VGKL--------PEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEY 116
           :|||           ||||: :|  ||::|||| |   | |  :| | | ||:| ::|||
Db      18 LGKLEVEGNFYSENVSRILDNLLEGYDNRLRPGFGGAVTEVKTDIYVTSFGPVSDVEMEY  77

Qy     117 TIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVR 176
           |:|: | ||| |||| :    | | ||  :||::| |||||| |::  | :| ||:: |
Db      78 TMDVFFRQTWTDERLKFGGPTEILSLNNLMVSKIWTPDTFFRNGKKSIAHNMTTPNKLFR 137

Qy     177 IYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLE 233
           | ::| :|||:|:||:| | : :: |||| |:||| | |::||::|:|| |:    : :|
Db     138 IMQNGTILYTMRLTINADCPMRLVNFPMDGHACPLKFGSYAYPKSEIIYTWKKGPLYSVE 197

Qy     234 INEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTM 293
           : |::|  | |:|  | :  :| | :  |::::||::|:: |: ||   | | |  :| :
Db     198 VPEESS-SLLQYDLIGQTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVI 256

Qy     294 LSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFC 353
           || ||||| || ||||  |||:|||||||   :| : |:||| ||:|::||:|| | |
Db     257 LSQVSFWINKESVPARTVFGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFS 316

Qy     354 ALLEFAVLNFLIYNQTK------AHASPK--------------LRHPRINSRAHARTRA 392
           ||:||| :|:    ||:        |:|                : ||  :|: | : |
Db     317 ALIEFAAVNYFTNLQTQKAKRKAQFAAPPTVTISKATEPLEAEIVLHP--DSKYHLKKRI 374

Qy     393 RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKR 452
           | :          ||::      |      : |    :|  |  |
Db     375 TSLS----------LPIVSS-----SEANKVLTRAPILQSTPVTPPPL------------ 408

Qy     453 FKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
                 |   | |           ::| |||::||| |  ||::||:| |:
Db     408 --------PPAFGGT----------SKIDQYSRILFPVAFAGFNLVYWVVYLS 442


Search completed: March 11, 2000, 06:26:39
Job time: 42 sec
```

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:18:26 ; Search time 41.51 Seconds
(without alignments)
845.171 Million cell updates/sec

Title: US-09-030-832-42
Perfect score: 2691
Sequence: 1 MLSKVLPVLLGILLILQSRV.....VFPVTFFFFNVLYWLVCLNL 506

Scoring table: BLOSUM62

Searched: 225878 seqs, 69334122 residues

Database : SPTREMBL_12:*

Word size : 0

Number of hits that pass the threshold : 225878
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2688	99.9	506	4	O15346	O15346 homo sapien
2	2676.5	99.5	505	4	Q99520	Q99520 homo sapien
3	1515.5	56.3	384	11	O55209	O55209 rattus norv
4	849.5	31.6	438	13	Q90288	Q90288 carassius a
5	671	24.9	453	13	O57430	O57430 fugu rubrip
6	662.5	24.6	686	5	Q24352	Q24352 drosophila
7	662	24.6	286	11	O54736	O54736 mus musculu
8	649	24.1	512	4	Q16323	Q16323 homo sapien
9	648	24.1	499	5	O17555	O17555 caenorhabdi
10	640.5	23.8	479	13	Q9YGQ5	Q9ygq5 morone amer
11	635	23.6	545	5	O18276	O18276 caenorhabdi
12	633.5	23.5	449	4	O75816	O75816 homo sapien
13	630	23.4	444	13	O93430	O93430 brachydanio
14	628.5	23.4	472	5	Q25035	Q25035 haemonchus
15	622	23.1	476	13	Q9YGQ4	Q9ygq4 morone amer
16	617	22.9	466	13	Q9YGQ3	Q9ygq3 morone amer
17	610.5	22.7	496	5	O18468	O18468 heliothis v
18	610.5	22.7	494	5	Q9XZW0	Q9xzw0 heliothis v
19	609.5	22.6	473	13	O42157	O42157 morone amer
20	607	22.6	430	13	Q90590	Q90590 gallus gall
21	599	22.3	478	5	P92023	P92023 caenorhabdi
22	598	22.2	606	5	Q24561	Q24561 drosophila
23	595.5	22.1	481	5	O18471	O18471 heliothis v
24	594	22.1	478	5	O17548	O17548 caenorhabdi
25	594	22.1	533	5	Q16896	Q16896 aedes aegyp
26	589	21.9	657	5	O17547	O17547 caenorhabdi
27	586.5	21.8	550	5	O17145	O17145 lucilia cup
28	583	21.7	601	5	P92138	P92138 drosophila
29	581	21.6	475	5	Q9Y0I4	Q9y0i4 caenorhabdi
30	580	21.6	416	5	Q17367	Q17367 caenorhabdi
31	576.5	21.4	487	5	Q9Y0I6	Q9y0i6 caenorhabdi
32	575	21.4	487	5	Q9Y0I5	Q9y0i5 caenorhabdi
33	574	21.3	448	5	Q9Y0I2	Q9y0i2 caenorhabdi
34	572.5	21.3	506	5	Q9Y0I3	Q9y0i3 caenorhabdi
35	561	20.8	461	5	Q17327	Q17327 caenorhabdi
36	560	20.8	495	5	O17793	O17793 caenorhabdi
37	555.5	20.6	456	5	Q94900	Q94900 drosophila
38	550	20.4	430	5	Q17369	Q17369 caenorhabdi
39	549.5	20.4	434	5	Q17328	Q17328 caenorhabdi
40	547.5	20.3	453	5	O77295	O77295 drosophila
41	546.5	20.3	452	5	O76773	O76773 lucilia cup
42	542	20.1	654	5	O01436	O01436 caenorhabdi
43	541.5	20.1	432	5	P91730	P91730 haemonchus
44	536.5	19.9	438	5	O46124	O46124 haemonchus
45	536	19.9	442	5	Q19358	Q19358 caenorhabdi

ALIGNMENTS

```
RESULT  1
O15346
ID   O15346      PRELIMINARY;      PRT;   506 AA.
AC   O15346;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GABA RECEPTOR EPSILON SUBUNIT.
GN   GABRE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 97480709.
RA   WILKE K., GAUL R., KLAUCK S.M., POUSTKA A.;
RT   "A gene in human chromosome band Xq28 (GABRE) defines a putative new
RT   subunit class of the GABAA neurotransmitter receptor.";
RL   Genomics 45:1-10(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   HANNA M.C., HALES T.G., KIRKNESS E.F.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Y09765; CAA70904.1; -.
DR   EMBL; U92283; AAB94645.1; -.
DR   EMBL; U92281; AAB94645.1; JOINED.
DR   EMBL; U92282; AAB94645.1; JOINED.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00253; GABAARECEPTR.
SQ   SEQUENCE   506 AA;  57971 MW;  95B5B1C4 CRC32;

  Query Match             99.9%;  Score 2688;  DB 4;  Length 506;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-221;
  Matches  505;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60

Qy      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
           ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEISVNSLGPLSILDMEYTIDI 120

Qy     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
```

```
Qy    181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240

Qy    241 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300

Qy    301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360

Qy    361 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 420

Qy    421 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 480

Qy    481 DNYSRVVFPVTFFFFNVLYWLVCLNL 506
          |||||||||||||||||||||||||||
Db    481 DNYSRVVFPVTFFFFNVLYWLVCLNL 506
```

```
RESULT   2
Q99520
ID   Q99520      PRELIMINARY;      PRT;   505 AA.
AC   Q99520;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   PUTATIVE GABA-GATED CHLORIDE CHANNEL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97238072.
RA   GARRET M., BASCLES L., BOUE-GRABOT E., SARTOR P., CHARRON G.,
RA   BLOCH B., MARGOLSKEE R.F.;
RT   "An mRNA encoding a putative GABA-gated chloride channel is expressed
RT   in the human cardiac conduction system.";
RL   J. Neurochem. 68:1382-1389(1997).
DR   EMBL; Y07637; CAA68914.1; -.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00253; GABAARECEPTR.
SQ   SEQUENCE   505 AA;  57856 MW;  1E6B104C CRC32;
```

Sequence Comparison D

```
  Query Match             99.5%;  Score 2676.5;  DB 4;  Length 505;
  Best Local Similarity   99.8%;  Pred. No. 1.8e-220;
  Matches  505;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy      1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60

Qy     61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120

Qy    121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180

Qy    181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240

Qy    241 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
```

```
Db    241 KLFQFDFTGVSNKTEIITTP-GDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 299

Qy    301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 359

Qy    361 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 419

Qy    421 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 479

Qy    481 DNYSRVVFPVTFFFFNVLYWLVCLNL 506
          |||||||||||||||||||||||||||
Db    480 DNYSRVVFPVTFFFFNVLYWLVCLNL 505
```

```
RESULT   3
O55209
ID   O55209      PRELIMINARY;      PRT;   384 AA.
AC   O55209;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   GABA-A RECEPTOR EPSILON SUBUNIT (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   HANNA M.C., HALES T.G., KIRKNESS E.F.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U92284; AAB93879.1; -.
DR   PFAM; PF00065; neur_chan; 2.
FT   NON_TER      1      1
SQ   SEQUENCE   384 AA;  45465 MW;  E5D0E1B9 CRC32;
```

```
  Query Match             56.3%;  Score 1515.5;  DB 11;  Length 384;
  Best Local Similarity   72.1%;  Pred. No. 1.6e-121;
  Matches  282;  Conservative   41;  Mismatches   55;  Indels   13;  Gaps    4;

Qy    122 FSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDG 181
          | |||||||||||||||:|:|:|||||||||||||||||||| |::||:|||| |:|||
Db      1 FYQTWYDERLCYNDTFETLILHGNVVSQLWIPDTFFRNSKRTQEYDITIPNQMALIHKDG 60

Qy    182 KVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWK 241
          |||||:|||||| |||||| |||||||||||||||| |:||||||||||||:|: ||:||
Db     61 KVLYTVRMTIDARCSLHMLNFPMDSHSCPLSFSSFSYDEHEMIYKWENFKLKIDAKNTWK 120

Qy    242 LFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWI 301
          | :||||||:||||||:|||||||||| |||||||||:: ||||:|||||||||||||||
Db    121 LLEFDFTGVNNKTEIISTPVGDFMVMTFFFNVSRRFGIVFQNYIPSSVTTMLSWVSFWI 180

Qy    302 KTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVL 361
          | |:| || |:|::||||| ||||||||||||||:|||||||||||| ||| |||| ||
Db    181 KIEAAAARASVGVSSVLTMATLGTFSRKNFPRVSYLTALDFYIAICFVLCFCTLLEFTVL 240

Qy    362 NFLIYNQTKAHASPKLRHPRINSRAH------ARTRARSRACARQHQEAFVCQIVTTEGS 415
          ||| ||  :  |||      |||||:|| ||| || |||:||| |
Db    241 NFLTYNNIERQASPKFYQFPTNSRANARTRARARTRARARARQQQEVFVCEIVTYE-E 299

Qy    416 DGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCI 475
          : ||      | |    |: |   | :   |   :  :|||||| |||::||:||:||
Db    300 NAEE----GYQWSPRSRRPQCPWRRCGRSYVC--FRVLRKYFCMVPGCEGNSWQRGRICI 353

Qy    476 HVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
          ||||||||||:||:|||||||:||::||||
Db    354 HVYRLDNYSRVLFPITFFFFNVVYWVICLNL 384
```

```
RESULT   4
Q90288
ID   Q90288      PRELIMINARY;      PRT;   438 AA.
AC   Q90288;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   NEUROTRANSMITTER RECEPTOR ALPHA SUBUNIT PRECURSOR.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC   Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC   Cyprinoidea; Cyprinidae; Cyprininae; Carassius.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 96373714.
RA   BAHN S., HARVEY R.J., DARLISON M.G., WISDEN W.;
RT   "Conservation of gamma-aminobutyric acid type A receptor alpha 6
RT   subunit gene expression in cerebellar granule cells.";
RL   J. Neurochem. 66:1810-1818(1996).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; X94342; CAA64068.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
DR   PRINTS; PR01079; GABAARALPHA.
KW   Signal; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW   Transmembrane.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    483       NEUROTRANSMITTER RECEPTOR ALPHA SUBUNIT.
SQ   SEQUENCE   438 AA;  49982 MW;  ED9DBE5C CRC32;


  Query Match             31.6%;  Score 849.5;  DB 13;  Length 438;
  Best Local Similarity   39.6%;  Pred. No. 1.4e-64;
  Matches  179;  Conservative   85;  Mismatches  135;  Indels   53;  Gaps   10;

Qy      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
           | :||   |    :|||: :|  ||::|||| |    | |  :| | | ||:| ::||||:|: 
Db      22 TETRV-YLDNITRILDRLLDGYDNRLRPGFGGPVTEVKTDIFVTSFGPVSDVEMEYTMDV 80

Qy     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
           | ||| |:|| :    | | ||  :||::| |||||||  ||:  | :| ||:: || :: 
Db      81 FFRQTWIDDRLKFEGPIEILRLNNLMVSKIWTPDTFFRNGKRSISHNMTTPNKLFRIMQN 140

Qy     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLEINEK 237
           | :|||:|:||:| | : :: |||| ||||| | |::|| :|::| |:    | :|: ::
Db     141 GTILYTMRLTINAECPMRLINFPMDGHSCPLKFGSYAYPMSEIVYTWKKGPLFSVEVPQE 200

Qy     238 NSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWV 297
           :|  | |:|  | :  :| : :  |:::|||::|:: |: |:   | |:|  :| :|: |
Db     201 SS-SLLQYDLIGQTVSSERLKSNTGEYIVMTVYFHLQRKMGFFLIQTYIPCIMTVILAQV 259

Qy     298 SFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLE 357
           ||||  || ||||  |||:|||||||   :| : |:||| ||:|::||:|| | | ||:| 
Db     260 SFWIDKESVPARTVFGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIE 319

Qy     358 FAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDG 417
           || :|:    |                    |:   |  | |||                 |||
Db     320 FAAVNYFSTLQ----------------ANKELRRASMACAAVR------------SDG 349

Qy     418 EERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHV 477
           |      |  ||     |   : ::  :  :|| :     ||      |||     :
Db     350 E-----LVTNPLDPGGVLKKR--LNSVSQRDAPERFSR--APQPDLH----QQGSTVPAI 396

Qy     478 YRL-----DNYSRVVFPVTFFFFNVLYWLVCL 504
             |     | |||::||::|  ||::||:| |
Db     397 NTLTTSIIDKYSRILFPLSFGAFNLVYWIVYL 428


RESULT   5
```

```
O57430
ID   O57430      PRELIMINARY;      PRT;   453 AA.
AC   O57430;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GAMMA-AMINOBUTYRIC ACID RECEPTOR BETA SUBUNIT (FRAGMENT).
GN   GABAB RECEPTOR.
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC   Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC   Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   RIBOLDI TUNNICLIFFE G.R., NYAKATURA G., PLATZER M., ELGAR G.S.,
RA   BRENNER S., ROSENTHAL A.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; AF016494; AAB94045.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
FT   NON_TER       1      1
SQ   SEQUENCE   453 AA;  52409 MW;  39C0992B CRC32;


  Query Match             24.9%;  Score 671;  DB 13;  Length 453;
  Best Local Similarity   30.1%;  Pred. No. 2.5e-49;
  Matches  140;  Conservative   88;  Mismatches  171;  Indels   66;  Gaps    5;

Qy      94 PTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIP 153
             | :| : | : |:  :| ::|:||| : | |:| |:|| | :   :| |:  |  |||:| 
Db       2 PVIVGMSINIASIDSISEVNMDYTITMYFQQSWRDKRLAYGELKLNLTLDNRVADQLWLP 61

Qy     154 DTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSF 213
           ||:| | |::  | :|: |:|:|:: || ||| :|:|  | | : : |:|:|  :| | 
Db      62 DTYFLNDKKSFLHGVTVKNRMIRLHPDGTVLYGLRITTTAACMMDLRRYPLDEQNCTLEI 121

Qy     214 SSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNV 273
             |: |  ::::: |:     :   :  :| ||   |:   :  :   | :  ::: | : 
Db     122 ESYGYTTDDIVFFWQGGDTAVTGVDKLELPQFSIVGIRLVSREVRFTTGSYPRLSLSFRI 181

Qy     274 SRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPR 333
           |  ||   | |:|| : |:|||||||  ::: || :||:|:|||||: |  |:  |: 
Db     182 KRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALGVTTVLTMTTINTHLRETLPK 241

Qy     334 VSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRAR 393
           : |: |:| |:  |||| | ||||:| :|:: :   :  | |    |:    : | |
Db     242 IPYVKAIDVYLMGCFVFVFLALLEYAFVNYVFFG--RGPAQQKKLSERVGKSNNERMRYE 299

Qy     394 SRACARQHQEAFVCQ----------------------------IVTTEGSDGEERPS-- 423
           :    |   :  |                            ::||   : |  ||
Db     300 EKRLREQDSISVPFQTNTFRSFTQRRNLYLEEQRKVGVDPYGNILLTTLEMNNEVMPSDV 359

Qy     423 ---------------CSAQQPPSPGSPEG-------PRSLCSKLACCEWCKRFKKYFCMV 460
                          |  |   |  |           ||     | |   :|  |    :
Db     360 GSSVSDSRNSVMSFDSSGVQFRKPMVPRDGFSHHSLDRSAMRSRANCRLRRRSSKLKLKI 419

Qy     461 PDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
           |:                |  :| :|||:||:|| |||::|||  :|
Db     420 PNLS-----------DVSTIDKWSRVIFPITFGFFNLIYWLYYVN 453


RESULT   6
Q24352
ID   Q24352      PRELIMINARY;      PRT;   686 AA.
AC   Q24352;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GLYCINE RECEPTOR PRECURSOR.
GN   GRD.
```

```
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERLIN K; TISSUE=HEAD;
RX   MEDLINE; 94246427.
RA   HARVEY R.J., SCHMITT B., HERMANS-BORGMEYER I., GUNDELFINGER E.D.,
RA   BETZ H., DARLISON M.G.;
RT   "Sequence of a Drosophila ligand-gated ion-channel polypeptide with an
RT   unusual amino-terminal extracellular domain.";
RL   J. Neurochem. 62:2480-2483(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; X78349; CAA55144.1; -.
DR   FLYBASE; FBgn0001134; Grd.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 3.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
KW   Signal.
FT   SIGNAL        1     72       POTENTIAL.
FT   CHAIN        73    686       GLYCINE RECEPTOR.
SQ   SEQUENCE   686 AA;  76557 MW;  D70F536E CRC32;

  Query Match             24.6%;  Score 662.5;  DB 5;  Length 686;
  Best Local Similarity   26.5%;  Pred. No. 2.4e-48;
  Matches  156;  Conservative   81;  Mismatches  161;  Indels  191;  Gaps    8;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           | :|: :|  ||: :||  |  |  : |:| | |:||:| :|| |::|  | |:| |:|| 
Db     110 SELLDNLLRGYDNSIRPDFGGPPATIEVDIMVRSMGPISEVDMTYSMDCYFRQSWVDKRL 169

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
             :    ::| |: ::::::| |||:| | |::: | || ||: ||||::|:|||: |:||
Db     170 AFEGAQDTLALSVSMLARIWKPDTYFYNGKQSYLHTITTPNKFVRIYQNGRVLYSSRLTI 229

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDF---- 248
            ||| :::  ||||   ||| | || |  :::|||:|   :  :      || |||
Db     230 KAGCPMNLADFPMDIQKCPLKFGSFGYTTSDVIYRWNKERPPVAIAEDMKLSQFDLVDCP 289

Qy     248 ------------------------------------------------------------ 248

Db     290 AGNLTDIVYKAAAPRPQRRPFNNKDPPRPTSKVMTTFAGPAAKNQHVRGTGLKLDKGAFG 349

Qy     248 ------------TGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLS 295
                       ||:|    : |    :: :: : |:: |  |    | | |  :  :||
Db     350 TGRDATGGSGSTTGLSGTITLETNHPSEYSMLMVNFHLQRHMGNFLIQVYGPCCLLVVLS 409

Qy     296 WVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCAL 355
           |||||:  |:   | |||||:|||| ||  :| : |:||| |||||:: : | | |  :
Db     410 WVSFWLNREATADRVSLGITTVLTMTFLGLEARTDLPKVSYPTALDFFVFLSFGFIFATI 469

Qy     356 LEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGS 415
           |:|||:                        | |:  |  |       |: : : :|
Db     470 LQFAVV------------------------HYYTKYGSGEC------YFIIEELDSESG 498

Qy     416 DGEERP-------------------SCSAQQPPSP-------GSPEGPRS------LCS 442
           : |  |                    |:   || |          ||:
Db     499 ESETEPLTSDFRGSTESKIYEVIPLSMCAISMPPPPTRLGMLTSRNRRPRNRRHGLWSMK 558

Qy     443 KLACCEWCKRFKKYFCMVPDCEGSTWQQ----------------------------GR 472
           |   :| :| |       : |     |                             ||
Db     559 LLGLFDWRRRRKPPRADSDEDEDDEQTQLRANEAPTTSAAAAAAQAAAQAARISPPTGGR 618

Qy     473 LCIHVYR--------------------LDNYSRVVFPVTFFFFNVLYW 500
             :  ||                    :|  ||:|||: |   || ||
Db     619 RRMSYYRREEMEARRKGKRTPQYNSVSKIDRASRIVFPLLFILINVFYW 667
```

```
RESULT   7
O54736
ID   O54736      PRELIMINARY;      PRT;   286 AA.
AC   O54736;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GAMMA-AMINOBUTYRIC ACID A RECPTOR, SUBUNIT ALPHA 6 (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=BRAIN, CEREBELLUM;
RX   MEDLINE; 97404410.
RA   BAHN S., JONES A., WISDEN W.;
RT   "Directing gene expression to cerebellar granule cells using gamma-
RT   aminobutyric acid type A receptor alpha6 subunit transgenes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:9417-9421(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=BRAIN, CEREBELLUM;
RX   MEDLINE; 96355730.
RA   JONES A., BAHN S., GRANT A.L., KOHLER M., WISDEN W.;
RT   "Characterization of a cerebellar granule cell-specific gene encoding
RT   the gamma-aminobutyric acid type A receptor alpha 6 subunit.";
RL   J. Neurochem. 67:907-916(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=BRAIN, CEREBELLUM;
RX   MEDLINE; 97160644.
RA   JONES A., KORPI E.R., MCKERNAN R.M., PELZ R., NUSSER Z., MAKELA R.,
RA   MELLOR J.R., POLLARD S., BAHN S., STEPHENSON F.A., RANDALL A.D.,
RA   SIEGHART W., SOMOGYI P., SMITH A.J., WISDEN W.;
RT   "Ligand-gated ion channel subunit partnerships: GABAA receptor alpha6
RT   subunit gene inactivation inhibits delta subunit expression.";
RL   J. Neurosci. 17:1350-1362(1997).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=BRAIN, CEREBELLUM;
RX   MEDLINE; 96373714.
RA   BAHN S., HARVEY R.J., DARLISON M.G., WISDEN W.;
RT   "Conservation of gamma-aminobutyric acid type A receptor alpha 6
RT   subunit gene expression in cerebellar granule cells.";
RL   J. Neurochem. 66:1810-1818(1996).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; AJ222970; CAA11024.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
FT   NON_TER     286    286
SQ   SEQUENCE   286 AA;  32983 MW;  4C3C2E4E CRC32;

  Query Match             24.6%;  Score 662;  DB 11;  Length 286;
  Best Local Similarity   47.2%;  Pred. No. 8e-49;
  Matches  120;  Conservative   56;  Mismatches   74;  Indels    4;  Gaps    2;

Qy      73 RILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERLC 132
           |||: :|  ||::|||| |   | |  :| | | ||:| ::|||:|: | ||| ||||
Db      34 RILDNLLEGYDNRLRPGFGGAVTEVKTDIYVTSFGPVSDVEMEYTMDVFFRQTWTDERLK 93

Qy     133 YNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTID 192
             :    | | ||  :||::| ||||||| |::  | :| ||:: |: ::| :|||:|:||:
Db      94 FKGPAEILSLNNLMVSKIWTPDTFFRNGKKSIAHNMTTPNKLFRLMQNGTILYTMRLTIN 153

Qy     193 AGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLEINEKNSWKLFQFDFTG 249
           | | : :: |||| |:||| | |::||: |:|| |:    : :|: |::|  | |:|  |
Db     154 ADCPMRLVNFPMDGHACPLKFGSYAYPKTEIIYTWKKGPLYSVEVPEESS-SLLQYDLIG 212

Qy     250 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 309
             :  :| | :  |::::||::|:: |: ||   | | |  :| :|| |||||  || |||
```

```
Db    213 QTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPAR 272

Qy    310 TSLGITSVLTMTTL 323
          |  |||:|||||||
Db    273 TVFGITTVLTMTTL 286


RESULT   8
Q16323
ID   Q16323      PRELIMINARY;      PRT;   512 AA.
AC   Q16323;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GABAA RECEPTOR BETA 2 SUBUNIT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95223118.
RA   MCKINLEY D.D., LENNON D.J., CARTER D.B.;
RT   "Cloning, sequence analysis and expression of two forms of mRNA coding
RT   for the human beta 2 subunit of the GABAA receptor.";
RL   Brain Res. Mol. Brain Res. 28:175-179(1995).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; S77553; AAB33982.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
DR   PRINTS; PR01160; GABAARBETA.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   512 AA;  59150 MW;  FF0E2B52 CRC32;


  Query Match             24.1%;  Score 649;  DB 4;  Length 512;
  Best Local Similarity   30.2%;  Pred. No. 2.3e-47;
  Matches  147;  Conservative   87;  Mismatches  184;  Indels   68;  Gaps    8;

Qy     75 LNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERLCYN 134
          :: :|  || :|||  |  |  | : | : |:  :| ::|:||: : | | | |:|| ||
Db     40 VDRLLKGYDIRLRPDFGGPPVAVGMNIDIASIDMVSEVNMDYTLTMYFQQAWRDKRLSYN 99

Qy    135 DTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAG 194
              :| |:  |  |||:|||:| | |::  | :|: |:|:|:: || ||| :|:|  |
Db    100 VIPLNLTLDNRVADQLWVPDTYFLNDKKSFVHGVTVKNRMIRLHPDGTVLYGLRITTTAA 159

Qy    195 CSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKT 254
          | : : |:|:|  :| |   |: |  ::: : |      :     :| ||       |
Db    160 CMMDLRRYPLDEQNCTLEIESYGYTTDDIEFYWRGDDNAVTGVTKIELPQFSIVDYKLIT 219

Qy    255 EIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGI 314
          : :    | :  ::: | : |  ||   | |:|| : |:|||||||  ::: || :|||
Db    220 KKVVFSTGSYPRLSLSFKLKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALGI 279

Qy    315 TSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYN---QTKA 371
          |:|||||: |  |:  |:: |: |:| |:  |||| | ||||:|::|:: :    | :
Db    280 TTVLTMTTINTHLRETLPKIPYVKAIDMYLMGCFVFVFMALLEYALVNYIFFGRGPQRQK 339

Qy    372 HASPK-----------------------------LRHPRINSRAHARTRAR--SRACAR 399
           |: |                             |  |  |     ||     |
Db    340 KAAEKAASANNEKMRLDVNKIFYKDIKQNGTQYRSLWDPTGNLSPTRRTTNYDFSLYTMD 399

Qy    400 QHQEAFVC------QIVTTEGSDGEERP-------SCSAQQPPSPGSPEG-------PRS 439
           |:   :       :: |:|   |  |         |: |   | |           |
Db    400 PHENILLSTLEIKNEMATSEAVMGLGDPRSTMLAYDASSIQYRKAGLPRHSFGRNALERH 459

Qy    440 LCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLY 499
          :  | :     :|  :   :||             |  :| :||: ||| | |||::|
Db    460 VAQKKSRLR--RRASQLKITIPD-----------LTDVNAIDRWSRIFFPVVFSFFNIVY 506
```

```
Qy    500 WLVCLN 505
           ||  :|
Db    507 WLYYVN 512


RESULT   9
O17555
ID   O17555      PRELIMINARY;      PRT;   499 AA.
AC   O17555; O18279;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   ZC482.5 PROTEIN.
GN   ZC482.5.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC   Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   MCMURRAY A.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94150718.
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA   GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA   JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA   LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA   THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA   WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; Z93397; CAB07722.1; -.
DR   EMBL; Z93372; CAB07722.1; JOINED.
DR   EMBL; Z93372; CAB07549.1; -.
DR   EMBL; Z93397; CAB07549.1; JOINED.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   499 AA;  57553 MW;  34743390 CRC32;


  Query Match             24.1%;  Score 648;  DB 5;  Length 499;
  Best Local Similarity   29.3%;  Pred. No. 2.7e-47;
  Matches  161;  Conservative   97;  Mismatches  173;  Indels  118;  Gaps   17;

Qy      5 VLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETETGSR 64
            ::|:   | ||      :      :   |||   |         || |   |
Db      6 IIPI---IALIHGHHSQAVIDMKRQRLSSRSTTY--------NQTLIRYT---------- 45

Qy     65 VGKLPEASRILNTILSNYDHKLRP-GIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFS 123
                :::|:||| | |   ||       |  | |:|:: |:||:|  :||:::|  |
Db     45 -------TKVLDTILLNQDKNFRPVNPDNSPLQVEVDISIRSMGPVSEQNMEFSLDCYFR 97

Qy    124 QTWYDERLCY---NDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
          | | | || :   | :   : |   ::  :|||||: || :::: | :|:|| : |:  |
Db     98 QKWLDRRLAFTPINPSKPEIPLASKMLKDIWIPDTYIRNGRKSYLHTLTVPNILFRVRSD 157

Qy    181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
          |:|  : |:|| : | : : :|||: :|||:   |  |   :::|||:: :|:    |:
Db    158 GQVHVSQRLTIRSRCQMFLKKFPMDTQACPIEVGSLGYFSKDVVYKWKDVELDAKMGNT- 217

Qy    241 KLFQFDFTGVSNKTEIITTPVGDF-------MVMTIFFNVSRRFGYVAFQNYVPSSVTTM 293
           | |:    :| |:|     | ||        |: ::| : |: ||   | | | ::  :
```

```
Db    217 -LSQYQVLSLS-KSE---RNVSDFRFSDRNISVLNVYFKLQRQQGYYILQIYTPCTLVVV 271

Qy    294 LSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFC 353
          :|||||||  |::|||| |||| :||:|:|:|   | : |:||: |||| ||  |||| |
Db    272 MSWVSFWINKEASPARVSLGIMTVLSMSTIGFGLRTDLPKVSHSTALDVYILTCFVFLFA 331

Qy    354 ALLEFAVLNF--LIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVT 411
          |::|:||:|:  ::| : : |    |                          |   : |: |
Db    332 AMVEYAVINYAQIVYIRKQIHDLKGL----------------------EQNTAMGQMFT 368

Qy    412 TEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKR--FKKYFCMVPDCEGST-- 468
            |  |  |       :    |      ::|    |:|:  ||       | :|:|
Db    369 A-GLMGARRRDTIQVDDLTVEKEE------ARLKAVPWWKKLCFK-------DEQGNTSS 414

Qy    468 -WQ----------------------------QGRLCIHVYRLDNYSRVVFPVTFFFFNV 497
           ||                          |    | ::||:|:: ||  :  |||
Db    415 EWQLEKKINFEKNSPVFYRMAVKAAIAKKTLRNGDPAEVVNKIDNFSKLAFPTLYIIFNV 474

Qy    498 LYWLVCLNL 506
           ||:  |:|
Db    475 FYWVAYLHL 483
```

RESULT 10
Q9YGQ5
ID Q9YGQ5 PRELIMINARY; PRT; 479 AA.
AC Q9YGQ5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-2A SUBUNIT PRECURSOR.
OS Morone americana (white perch).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC Perciformes; Percoidei; Moronidae; Morone.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RETINA;
RX MEDLINE; 99022091.
RA QIAN H., DOWLING J.E., RIPPS H.;
RT "Molecular and pharmacological properties of GABA-rho subunits from
RT white perch retina.";
RL J. Neurobiol. 37:305-320(1998).
DR EMBL; AF101034; AAD17893.1; -.
KW Receptor.
SQ SEQUENCE 479 AA; 55381 MW; 0CEFE4A0 CRC32;

Query Match 23.8%; Score 640.5; DB 13; Length 479;
Best Local Similarity 29.8%; Pred. No. 1.1e-46;
Matches 157; Conservative 108; Mismatches 184; Indels 77; Gaps 13;

```
Qy      2 LSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETET 61
            ::| | :|| :::| : |  | :                          :   | : ||:
Db      4 MTKPLILLLCLVVIGECRKHGHR------------------------VRRWTGTVETQK 38

Qy     62 -GSRVGKLP---EASRILNT----ILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILD 113
           |: : | |     || : |     : ::|  :|| |     | |:: | ||  :| :|
Db     39 HGTSLAKKPPDVTKSRKMKTEHLLKVDDHDFTMRPAFGGPAIPVGVDVQVESLDSISEVD 98

Qy    114 MEYTIDIIFSQTWYDERLCY-NDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPN 172
          |::|: :     | |||| : : | :|:  :| :| ::|:|| || :|||:  |: |  |
Db     99 MDFTMTLYLRHYWKDERLSFTSSTNKSMTFDGRLVKKIWVPDVFFVHSKRSFIHDTTTDN 158

Qy    173 QMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKL 232
           |:|:: || |||:::|:|: | |::   |||:|| :| |   |:::| : :::  |::
Db    159 IMLRVFPDGHVLYSLRVTVTAACNMDFSRFPLDSQTCSLELESYAYTDEDLMLYWKSGDE 218

Qy    233 EINEKNSWKLFQFDFTGVSNKTEI-ITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVT 291
            ::  :   | ||        : :   :  | :  : | | : |   :    | | |:::
Db    219 SLSTDDRISLSQFLIQKFHTTSRLAFYSSTGWYNRLYINFTLRRHIFFFLLQTYFPATLM 278

Qy    292 TMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFC 351
```

```
          |||||||||   : ||| |||||:||||:|: |    : |||||| |:| |: : |||
Db    279 VMLSWVSFWIDRRAVPARVSLGITTVLTMSTIITGVNASMPRVSYIKAVDIYLWVSFVFV 338

Qy    352 FCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVT 411
          | ::||:| :|:|   | :     |:|          | |::|  |          | |
Db    339 FLSVLEYAAVNYLSTVQDRRER--KMRE---------RARSQSLPC--------TCGISQ 379

Qy    412 T------EGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDC-- 464
          |      :|:  |   :  |      |  ||  |  |:::         :|   ||  |
Db    380 TRTMTMLDGTYSEADTNSLAGYTEEPMVPERSRKSCTEV--------LEKPEHMVVICVS 431

Qy    464 -EGSTWQQGR------LCIHVYRLDNYSRVVFPVTFFFFNVLYWLV 502
           | :| :: :      :  : : :| |||::|| :: |||::|| |
Db    432 SESTTTKKKKSLRAINIIQNTHAIDKYSRMIFPGSYIFFNLIYWSV 477
```

RESULT 11
O18276
ID O18276 PRELIMINARY; PRT; 545 AA.
AC O18276;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE ZC482.1 PROTEIN.
GN ZC482.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA MCMURRAY A.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; Z93397; CAB07719.1; -.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR PFAM; PF00065; neur_chan; 2.
DR PRINTS; PR00252; NRIONCHANNEL.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ SEQUENCE 545 AA; 61601 MW; 26207FDB CRC32;

Query Match 23.6%; Score 635; DB 5; Length 545;
Best Local Similarity 28.9%; Pred. No. 3.9e-46;
Matches 153; Conservative 86; Mismatches 185; Indels 106; Gaps 10;

```
Qy     71 ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDER 130
          || :|: :| :|| :|||| |    ::|::| : |   :| :||:||: :   | | |||
Db     16 ASSLLSDLLLDYDIRLRPGFGGDALLLTMDIIIASFDSISEVDMDYTLTMYLHQYWTDER 75

Qy    131 LCYND--TFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIR 188
          | :::    : : |:|     :|:|||||  | | :: ||:|  |:|:||  |||| | :|
Db     76 LRWSNEIPIDEMTLSGEFSQNIWVPDTFLANDKHSYLHEVTERNKMLRINVDGKVAYGMR 135

Qy    189 MTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFT 248
          :|    ||:::  ||:|| :| :   |: |  :|:: || |: | ::       : ||  |
Db    136 LTSTLSCSMNLRNFPLDSQNCTVEIESYGYTTSEVLMKW-NYPLAVHGVEQADVPQFTIT 194
```

```
Qy    249 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 308
Db    195 GFHTEDSIVSTATGSYQRLSLVFQLRRSVGYFIFQTYLPCVLIVMLSWVSFWINHEATSA 254

Qy    309 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYI---------------------- 345
Db    255 RVALGITTVLTMTTISTGVRQSLPRISYVKSIDIYLFPTLTNQRQAPPTSKPISDARLRS 314

Qy    345 --------------------AICFVFCFCALLEFAVLNFLIYNQTKAH----------- 373
Db    315 LVEERAVLSADWSEFGIFILQVMCFVFVFAALLEYAAVNYSYWGRERGKGGGGNEWPVNG 374

Qy    373 ASPKLRHPRIN-----------------SRAHARTRARSRACARQHQEAFVCQIVTTEG 414
Db    375 ANKEDRESAVNVQKWVPSGLMDGVPQPQDRRVEALEEAMSTSNTAAQNNNFESTSKPKKR 434

Qy    415 SDGEERPSCSA-----QQPPSPGSP-------EGPRSLCSKLACCEWCK-----RFKKYF 457
Db    435 SSSPIPPLCRAGNTISEESESPDYPRYSTTSLKGARPHASLNHKTHHLKGRSSARAKRRM 494

Qy    458 CM------VPDCEGSTWQQGRLCIHVYR------LDNYSRVVFPVTFFFF 495
Db    495 TLARMNVSMKQSISGIGRRARKVIPTIRVRDVNLIDKYSRVVFPVCFIVF 544
```

RESULT 12
O75816
ID O75816 PRELIMINARY; PRT; 449 AA.
AC O75816;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE GLYCINE RECEPTOR ALPHA 3 SUBUNIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98344067.
RA NIKOLIC Z., LAUBE B., WEBER R.G., LICHTER P., KIOSCHIS P., POUSTKA A.,
RA MULHARDT C., BECKER C.M.;
RT "The human glycine receptor subunit alpha3. Glra3 gene structure,
RT chromosomal localization, and functional characterization of
RT alternative transcripts.";
RL J. Biol. Chem. 273:19708-19714(1998).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; U93917; AAC39917.1; -.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR PFAM; PF00065; neur_chan; 2.
DR PRINTS; PR00252; NRIONCHANNEL.
DR PRINTS; PR00253; GABAARECEPTR.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ SEQUENCE 449 AA; 51963 MW; 3170F74B CRC32;

Query Match 23.5%; Score 633.5; DB 4; Length 449;
Best Local Similarity 30.2%; Pred. No. 4e-46;
Matches 143; Conservative 90; Mismatches 169; Indels 71; Gaps 10;

```
Qy     46 ENQLLSEETKSTETETGSRVGKLPEASRILNTIL---SNYDHKLRPGIGEKPTVVTVEIA 102
Db     18 EAALLLSLVATKETDSARSRSAPMSPSDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIF 77

Qy    103 VNSLGPLSILDMEYTIDIIFSQTWYDERLCYND-TFESLVLNGNVVSQLWIPDTFFRNSK 161
Db     78 INSFGSIAETTMDYRVNIFLRQKWNDPRLAYSEYPDDSLDLDPSMLDSIWKPDLFFANEK 137

Qy    162 RTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPEN 221
Db    138 GANFHEVTTDNKLLRIFKNGNVLYSIRLTLTLSCPMDLKNFPMDVQTCIMQLESFGYTMN 197

Qy    222 EMIYKWENFKLEINEKNSWKLFQF---DFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFG 278
Db    198 DLIFEWQD-EAPVQVAEGLTLPQFLLKEEKDLRYCTKHYNT--GKFTCIEVRFHLERQMG 254

Qy    279 YVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYIT 338
Db    255 YYLIQMYIPSLLIVILSWVSFWINMDAAPARVALGITTVLTMTTQSSGSRASLPKVSYVK 314

Qy    339 ALDFYIAICFVFCFCALLEFAVLNF--------LIYNQTKAHASPKLRHPRINSRAHART 390
Db    315 AIDIWMAVCLLFVFSALLEYAAVNFVSRQHKELLRFRRKRKNKDDEVRESRFSFTAYGM- 374

Qy    391 RARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWC 450
Db    374 ----------------------------GPCLQAKDGMTPKGPNHPVQVMPK------- 398

Qy    451 KRFKKYFCMVPDCEGSTWQQGRLCI-HVYRLDNYSRVVFPVTFFFFNVLYWLV 502
Db    398 ---------SPD------EMRKVFIDRAKKIDTISRACFPLAFLIFNIFYWVI 435
```

RESULT 13
O93430
ID O93430 PRELIMINARY; PRT; 444 AA.
AC O93430;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE GLYCINE RECEPTOR, ALPHA2 SUBUNIT PRECURSOR.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinoidea; Cyprinidae; Rasborinae; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA DAVID-WATINE B., GOBLET C., DE SAINT JAN D., FUCILE S., DEVIGNOT V.,
RA BREGESTOVSKI P., KORN H.;
RT "A novel alpha subunit of the glycine receptor from zebrafish: primary
RT structure and functional expression.";
RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED ION
CC   CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHLORIDE
CC   CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF
CC   NEURONAL FIRING).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- DOMAIN: THE N-TERMINAL DOMAIN CARRIES STRUCTURAL DETERMINANTS
CC   ESSENTIAL FOR AGONIST AND ANTAGONIST BINDING. TM2 IS THOUGHT TO
CC   FORM THE INNERT WALL OF THE CHLORIDE CHANNEL. THE CYTOPLASMIC LOOP
CC   MAY BE AN IMPORTANT DETERMINANT OF CHANNEL INACTIVATION KINETICS.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; AJ005812; CAA06711.1; -.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR PFAM; PF00065; neur_chan; 2.
DR PRINTS; PR00252; NRIONCHANNEL.
DR PRINTS; PR00253; GABAARECEPTR.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 444 GLYCINE RECEPTOR, ALPHA2 SUBUNIT.
FT DOMAIN 26 242 EXTRACELLULAR (PROBABLE).
FT TRANSMEM 248 268 PROBABLE.
FT TRANSMEM 277 294 PROBABLE.
FT TRANSMEM 311 331 PROBABLE.
FT DOMAIN 343 346 POLY-ARG.
FT DOMAIN 332 415 CYTOPLASMIC (PROBABLE).
FT DOMAIN 381 384 POLY-ASN.
FT TRANSMEM 416 436 PROBABLE.
FT DISULFID 162 176 BY SIMILARITY.
FT DISULFID 222 233 BY SIMILARITY.
SQ SEQUENCE 444 AA; 50765 MW; 3405DED8 CRC32;

```
  Query Match             23.4%;  Score 630;  DB 13;  Length 444;
  Best Local Similarity   30.3%;  Pred. No. 7.8e-46;
  Matches  141;  Conservative   69;  Mismatches  134;  Indels  122;  Gaps    9;

Qy      79 LSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERLCYND-TF 137
           :| || ::||     |  ||  | :|| | ::   |:| ::|   | | | || |::
Db      45 VSGYDARIRPNFKGPPVNVTCNIFINSFGSIAETTMDYRVNIFLRQQWNDPRLAYSEYPD 104

Qy     138 ESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSL 197
           :|| |: :::  :| || || | |  : ||:|  |:::|| |:| |||:||:|:   | :
Db     105 DSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRISKNGNVLYSIRITLVLACPM 164

Qy     198 HMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEII 257
           :  |||| :| :   || |  |::|::|                 | |     : :
Db     165 DLKNFPMDVQTCIMQLESFGYTMNDLIFEW-----------------DEKGAVQVADGL 206

Qy     258 TTP-----------------VGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSF 299
           | |                 | |  :   |:: |: ||   | |:|| :  :||||||
Db     207 TLPQFILKEEKDLRYCTKHYNTGKFTCIEARFHLERQMGYYLIQMYIPSLLIVILSWVSF 266

Qy     300 WIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFA 359
           ||  ::|||| ||||:|||||| : || : |:|||: |:| ::|:| :| | ||||:|
Db     267 WINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFSALLEYA 326

Qy     360 VLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQ-----IVTTEG 414
           :|||:                          ||||:|    |     :   |
Db     327 AVNFI---------------------------------ARQHKELLRFQRRRRHLKEDEA 353

Qy     415 SDGE-------ERPSC------------SAQQPPSPGSPEGPRSLCSKLACCEWCKRFKK 455
             ||        |:|            :  | |  ||           :  :  :|
Db     354 GDGRFSFAAYGMGPACLQAKDGMAIKGNNNNAPTSTNPPE-----------KTVEEMRK 401

Qy     456 YFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWL 501
           |                    |:|  ||| ||: |  ||: ||:
Db     402 LFIS----------------RAKRIDTVSRVAFPLVFLIFNIFYWI 431


RESULT  14
Q25035
ID   Q25035      PRELIMINARY;      PRT;   472 AA.
AC   Q25035;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GABA A/GLYCINE RECEPTOR SUBUNIT.
GN   HG1.
OS   Haemonchus contortus.
OC   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Strongylida;
OC   Trichostrongyloidea; Trichostrongylidae; Haemonchinae; Haemonchus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95041083.
RA   LAUGHTON D.L., AMAR M., THOMAS P., TOWNER P., HARRIS P., LUNT G.C.,
RA   WOLSTENHOLME A.J.;
RT   "Cloning of a putative inhibitory amino acid receptor subunit from the
RT   parasitic nematode Haemonchus contortus.";
RL   Recept. Channels 2:155-163(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; X73584; CAA51991.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
FT   VARIANT     231    231       G -> D.
FT   VARIANT     329    329       S -> A.
SQ   SEQUENCE   472 AA;  54732 MW;  7B8A2213 CRC32;


  Query Match             23.4%;  Score 628.5;  DB 5;  Length 472;
  Best Local Similarity   31.0%;  Pred. No. 1.1e-45;
  Matches  143;  Conservative   93;  Mismatches  153;  Indels   73;  Gaps   11;

Qy      72 SRILNTILSNYDHKLRP-GIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDER 130
           :::|||| | | | ||       |  | ::|:| |:||:|  |||:::|  | | | | |
Db      37 TKLLNTILLNQDKKFRPTNPDSSPLNVEIDISVRSMGPISEQDMEFSLDCYFRQKWLDRR 96

Qy     131 LCY---NDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTI 187
           | :   |     : |   ::  :|:|||: || :::: | :|:|| : |:  ||:|  :
Db      97 LAFTPINPDKPVMPLASKMLKDIWVPDTYIRNGRKSYLHTLTVPNILFRVRSDGQVHVSQ 156

Qy     188 RMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDF 247
           |:||   | : : :|||| :||:   |  |  |:::| |::  :|:: |    | |:
Db     157 RLTIKTKCLMFLKKFPMDVQACPIEIGSLGYFSNDVVYYWKD--VELDAKMGNMLSQYKI 214

Qy     248 TGV-------SNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300
           |:       |:  ||      :  |: ::| : |: ||   | | | ::  ::||||||
Db     215 LGLFKSEHNFSDHREI----GRNISVLKVYFKLQRQQGYYVLQIYTPCTLLVVMSWVSFW 270

Qy     301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360
           |  |::||| :||| :||:|:|||   | : |:||: |||| ||  || | | |::|::|
Db     271 INKEASPARVALGIMTVLSMSTLGFGLRTDLPKVSHSTALDIYIILSCFGFVFAAMVEYSV 330

Qy     361 LNF--LIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGE 418
           :|:  ::| : : |     |     ::||  : |  :          :|    |:      : |
Db     331 INYAQIVYIRKQVHDLKGLE----SNRAMEKMRLFTAGLMGARRETI--QVDDLVLDEEE 384

Qy     419 ERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIH-- 477
           : |  |                        | : |: ||   |           |: :
Db     385 DLPWYS---------------------CFFRKKTKKQSSMF----------YRMAVKAA 412

Qy     477 -------------VYRLDNYSRVVFPVTFFFFNVLYWLVCL 504
                         | |:|: |:|:|| :  ||:|||:  |
Db     413 KARRKLKMKDPAKVVNRVDDVSKVIFPSLYVLFNILYWVAFL 454


RESULT  15
Q9YGQ4
ID   Q9YGQ4      PRELIMINARY;      PRT;   476 AA.
AC   Q9YGQ4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-1A SUBUNIT PRECURSOR.
OS   Morone americana (white perch).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC   Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC   Perciformes; Percoidei; Moronidae; Morone.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=RETINA;
RX   MEDLINE; 99022091.
RA   QIAN H., DOWLING J.E., RIPPS H.;
RT   "Molecular and pharmacological properties of GABA-rho subunits from
RT   white perch retina.";
RL   J. Neurobiol. 37:305-320(1998).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; AF101035; AAD17894.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW   Transmembrane.
SQ   SEQUENCE   476 AA;  54703 MW;  945F8375 CRC32;


  Query Match             23.1%;  Score 622;  DB 13;  Length 476;
  Best Local Similarity   29.3%;  Pred. No. 4.1e-45;
  Matches  153;  Conservative   93;  Mismatches  194;  Indels   82;  Gaps   13;

Qy       8 VLLGILLILQ---SRVEGPQTE--SKNEASSRDVVYGPQPQPLENQLLSEETKSTETETG 62
           ||  : | :|     |||  |       : : ||   |        :|: |   | :   |
Db       8 VLFCVWLAVQLEDGPVEGSQAGDLQTEQVAKRDQNGG----GWRSQIRSPIYKQSPDMTK 63

Qy      63 SRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIF 122
           | : |  :  ||      ::|  :||  |  |  | |:: | ||  :| :||::|: :
```

```
Db      64 SLMTKSEQLLRI-----DDHDFTMRPAFGGPPIPVGVDVQVESLDTISEVDMDFTMTLYL 118

Qy     123 SQTWYDERLCYNDT-FESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDG 181
           | |||| :  |  :|:  :  :| ::|:|| || :|||:  |: |  | |:|:| ||
Db     119 RHYWKDERLSFPSTNNQSMTFDSRLVKKIWVPDMFFVHSKRSFIHDTTTDNVMLRVYPDG 178

Qy     182 KVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWK 241
            |||::|:|: | |:: : |||:|: :| |   |::| ::::  |:     :|  :
Db     179 NVLYSLRVTVTAMCNMDLSRFPLDTQTCSLEIESYAYTDDDLMLSWKKGNESLNTDDRIS 238

Qy     242 LFQFDFTGVSNKTEI-ITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300
           | ||       |::   :  | :  : | | : | | :   | | |::: ||||||||
Db     239 LSQFLIQKFHTTTKLAFYSSTGWYNRLYIHFTLRRTFFFFLLQTYFPATLMVMLSWVSFW 298

Qy     301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360
           |   : |||  ||||:||||:|: |    : |||||| |:| |: : ||| | :::|:|
Db     299 IDRRAVPARVPLGITTVLTMSTIITGVNASMPRVSYIKAVDIYLWVSFVFVFLSVIEYAA 358

Qy     361 LNFLIYNQTKAHASPKLRH----------------PRINSRAHARTRARSRACARQH-- 402
           :|:|  :  :    |||                  |:|                ::
Db     359 VNYL--STVQERKERKLRERLPCTCGIGNPDEMMIDPQITGYGSMDINTTGNYGMPENGG 416

Qy     402 -QEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMV 460
            ||  : |:   :       |  : |  || |                       |
Db     417 RQERMLAQVALND-------PQIAGQVKPSRG----------------------YV--- 444

Qy     461 PDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLV 502
           : |      |  : :| |||||||  :  ||::|| :
Db     444 -----NIW------IDTHAIDKYSRVVFPGAYILFNIIYWSI 474
```

Search completed: March 11, 2000, 06:18:28
Job time: 56 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 10, 2000, 06:28:42 ; Search time 3678.19 Seconds
(without alignments)
-6944.969 Million cell updates/sec

Title: US-09-030-832-1
Perfect score: 6146
Sequence: 1 GTCTTATAATTGCTAAGCAC.....TCACCATCATCTGAAATGGG 6146

Scoring table: IDENTITY_NUC

Searched: 4799332 seqs, -2078174120 residues

Database : Pending_Patents_NA:*

Word size : 0

Number of hits that pass the threshold : 9598654

1: /cgn2_6/ptodata/2/pna/PCTUS9_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US081A_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US081B_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US081C_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US081D_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US082A_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US082B_COMB.seq:*
10: /cgn2_6/ptodata/2/pna/US082C_COMB.seq:*
11: /cgn2_6/ptodata/2/pna/US083A_COMB.seq:*
12: /cgn2_6/ptodata/2/pna/US083B_COMB.seq:*
13: /cgn2_6/ptodata/2/pna/US084A_COMB.seq:*
14: /cgn2_6/ptodata/2/pna/US084B_COMB.seq:*
15: /cgn2_6/ptodata/2/pna/US084C_COMB.seq:*
16: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*
17: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*
18: /cgn2_6/ptodata/2/pna/US087A_COMB.seq:*
19: /cgn2_6/ptodata/2/pna/US087B_COMB.seq:*
20: /cgn2_6/ptodata/2/pna/US087C_COMB.seq:*
21: /cgn2_6/ptodata/2/pna/US088A_COMB.seq:*
22: /cgn2_6/ptodata/2/pna/US088B_COMB.seq:*
23: /cgn2_6/ptodata/2/pna/US088C_COMB.seq:*
24: /cgn2_6/ptodata/2/pna/US088D_COMB.seq:*
25: /cgn2_6/ptodata/2/pna/US089A_COMB.seq:*
26: /cgn2_6/ptodata/2/pna/US089B_COMB.seq:*
27: /cgn2_6/ptodata/2/pna/US089C_COMB.seq:*
28: /cgn2_6/ptodata/2/pna/US089D_COMB.seq:*
29: /cgn2_6/ptodata/2/pna/US089E_COMB.seq:*
30: /cgn2_6/ptodata/2/pna/US089F_COMB.seq:*
31: /cgn2_6/ptodata/2/pna/US089G_COMB.seq:*
32: /cgn2_6/ptodata/2/pna/US089H_COMB.seq:*
33: /cgn2_6/ptodata/2/pna/US089I_COMB.seq:*
34: /cgn2_6/ptodata/2/pna/US090A_COMB.seq:*
35: /cgn2_6/ptodata/2/pna/US090B_COMB.seq:*
36: /cgn2_6/ptodata/2/pna/US090C_COMB.seq:*
37: /cgn2_6/ptodata/2/pna/US090D_COMB.seq:*
38: /cgn2_6/ptodata/2/pna/US090E_COMB.seq:*
39: /cgn2_6/ptodata/2/pna/US091A_COMB.seq:*
40: /cgn2_6/ptodata/2/pna/US091B_COMB.seq:*
41: /cgn2_6/ptodata/2/pna/US091C_COMB.seq:*
42: /cgn2_6/ptodata/2/pna/US092A_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US092B_COMB.seq:*
44: /cgn2_6/ptodata/2/pna/US092C_COMB.seq:*
45: /cgn2_6/ptodata/2/pna/US092D_COMB.seq:*
46: /cgn2_6/ptodata/2/pna/US092E_COMB.seq:*
47: /cgn2_6/ptodata/2/pna/US093A_COMB.seq:*
48: /cgn2_6/ptodata/2/pna/US093B_COMB.seq:*
49: /cgn2_6/ptodata/2/pna/US093C_COMB.seq:*
50: /cgn2_6/ptodata/2/pna/US093D_COMB.seq:*
51: /cgn2_6/ptodata/2/pna/US093E_COMB.seq:*
52: /cgn2_6/ptodata/2/pna/US093F_COMB.seq:*
53: /cgn2_6/ptodata/2/pna/US094A_COMB.seq:*
54: /cgn2_6/ptodata/2/pna/US094B_COMB.seq:*
55: /cgn2_6/ptodata/2/pna/US6000_COMB.seq:*
56: /cgn2_6/ptodata/2/pna/US6001A_COMB.seq:*
57: /cgn2_6/ptodata/2/pna/US6001B_COMB.seq:*
58: /cgn2_6/ptodata/2/pna/US6002A_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6002B_COMB.seq:*
60: /cgn2_6/ptodata/2/pna/US6002C_COMB.seq:*
61: /cgn2_6/ptodata/2/pna/US6003A_COMB.seq:*
62: /cgn2_6/ptodata/2/pna/US6003B_COMB.seq:*
63: /cgn2_6/ptodata/2/pna/US6004A_COMB.seq:*
64: /cgn2_6/ptodata/2/pna/US6004B_COMB.seq:*
65: /cgn2_6/ptodata/2/pna/US6004C_COMB.seq:*
66: /cgn2_6/ptodata/2/pna/US6005_COMB.seq:*
67: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
68: /cgn2_6/ptodata/2/pna/US6007_COMB.seq:*
69: /cgn2_6/ptodata/2/pna/US6008A_COMB.seq:*
70: /cgn2_6/ptodata/2/pna/US6008B_COMB.seq:*
71: /cgn2_6/ptodata/2/pna/US6008C_COMB.seq:*
72: /cgn2_6/ptodata/2/pna/US6009A_COMB.seq:*
73: /cgn2_6/ptodata/2/pna/US6009B_COMB.seq:*
74: /cgn2_6/ptodata/2/pna/US6010A_COMB.seq:*
75: /cgn2_6/ptodata/2/pna/US6010B_COMB.seq:*
76: /cgn2_6/ptodata/2/pna/US6011A_COMB.seq:*
77: /cgn2_6/ptodata/2/pna/US6011B_COMB.seq:*
78: /cgn2_6/ptodata/2/pna/US6012A_COMB.seq:*
79: /cgn2_6/ptodata/2/pna/US6012B_COMB.seq:*
80: /cgn2_6/ptodata/2/pna/US6013A_COMB.seq:*
81: /cgn2_6/ptodata/2/pna/US6013B_COMB.seq:*
82: /cgn2_6/ptodata/2/pna/US6014A_COMB.seq:*
83: /cgn2_6/ptodata/2/pna/US6014B_COMB.seq:*
84: /cgn2_6/ptodata/2/pna/US6014C_COMB.seq:*
85: /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*
86: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:*
87: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:*
88: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
89: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
90: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
91: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
92: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6146	100.0	6146	24	US-08-888-012-1 ABN 5	Sequence 1, Appli
2	6146	100.0	6146	35	US-09-030-832-1 CIP of 5	Sequence 1, Appli
3	5542.2	90.2	9631	24	US-08-888-012-5	Sequence 5, Appli
4	5542.2	90.2	9631	35	US-09-030-832-5	Sequence 5, Appli
5	2284	37.2	3154	35	US-09-030-832-41	Sequence 41, Appl
6	2228.4	36.3	3268	87	US-60-172-373-15901	Sequence 15901, A
7	654.4	10.6	7479	24	US-08-888-012-6	Sequence 6, Appli
8	654.4	10.6	7479	35	US-09-030-832-6	Sequence 6, Appli
c 9	445.8	7.3	523	86	US-60-160-190-439	Sequence 439, App
10	401	6.5	599	86	US-60-168-603-89	Sequence 89, Appl
11	398.8	6.5	467	44	US-09-277-227-869	Sequence 869, App
12	397.6	6.5	406	45	US-09-287-618-34164	Sequence 34164, A
13	392.4	6.4	406	48	US-09-332-782-13902	Sequence 13902, A
14	381	6.2	382	51	US-09-362-510-41441	Sequence 41441, A
15	377.4	6.1	380	53	US-09-431-517-25013	Sequence 25013, A
16	376.6	6.1	385	50	US-09-359-067-19805	Sequence 19805, A
17	373.8	6.1	545	42	US-09-205-070-26466	Sequence 26466, A
18	373.8	6.1	544	47	US-09-306-609-1014	Sequence 1014, Ap
19	373.8	6.1	545	49	US-09-340-623-26466	Sequence 26466, A
20	351.8	5.7	393	45	US-09-287-618-31313	Sequence 31313, A

21	315	5.1	346	7	US-08-196-363-6942	Sequence 6942, Ap
22	315	5.1	346	7	US-08-196-363A-6942	Sequence 6942, Ap
23	301.4	4.9	303	7	US-08-196-363-16523	Sequence 16523, A
24	301.4	4.9	303	7	US-08-196-363A-16523	Sequence 16523, A
25	301.4	4.9	303	35	US-09-030-832-43	Sequence 43, Appl
26	292	4.8	293	24	US-08-878-504-506	Sequence 506, App
27	292	4.8	293	58	US-60-020-310-506	Sequence 506, App
28	271	4.4	272	36	US-09-044-001-1760	Sequence 1760, Ap
29	271	4.4	272	63	US-60-041-239-1760	Sequence 1760, Ap
30	268	4.4	268	29	US-08-951-198-2954	Sequence 2954, Ap
31	268	4.4	268	34	US-09-016-434-339	Sequence 339, App
32	268	4.4	268	60	US-60-027-249-2914	Sequence 2914, Ap
33	268	4.4	268	86	US-60-164-285-3990	Sequence 3990, Ap
34	267	4.3	267	31	US-08-974-756-1195	Sequence 1195, Ap
35	267	4.3	279	37	US-09-074-999-1497	Sequence 1497, Ap
36	267	4.3	279	65	US-60-048-431-1497	Sequence 1497, Ap
37	255.4	4.2	257	36	US-09-049-497-1561	Sequence 1561, Ap
38	255.4	4.2	257	63	US-60-042-121-1561	Sequence 1561, Ap
39	252	4.1	252	35	US-09-021-702-858	Sequence 858, App
40	252	4.1	252	63	US-60-041-220-858	Sequence 858, App
41	247	4.0	295	22	US-08-839-968-1086	Sequence 1086, Ap
42	247	4.0	295	29	US-08-951-198-1086	Sequence 1086, Ap
43	246	4.0	247	21	US-08-810-325-955	Sequence 955, App
44	245	4.0	247	36	US-09-049-497-1749	Sequence 1749, Ap
45	245	4.0	247	63	US-60-042-121-1749	Sequence 1749, Ap

ALIGNMENTS

```
RESULT   1
US-08-888-012-1
; Sequence 1, Application US/08888012
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  ET2: An Alternative Transcript of the GABA-A
;    TITLE OF INVENTION:  Receptor n Subunit
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,012
;      FILING DATE:  Herewith
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950000/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6146 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3872..4597
US-08-888-012-1
```

Query Match 100.0%; Score 6146; DB 24; Length 6146;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 GTCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTAT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GTCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTAT 60

Qy      61 GTCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GTCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAA 120

Qy     121 GTAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGCTGGCTTTTTCATGCAGACCCTTCAG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GTAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGCTGGCTTTTTCATGCAGACCCTTCAG 180

Qy     181 TTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTCGTGTGAGTT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTCGTGTGAGTT 240

Qy     241 CTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTCCATTGTAGTGGGA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTCCATTGTAGTGGGA 300

Qy     301 GGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTCTGGAGGAAGTTA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTCTGGAGGAAGTTA 360

Qy     361 CAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAGTCTGAAAAGCAC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAGTCTGAAAAGCAC 420

Qy     421 AGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGCCACTGGTTTTCT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGCCACTGGTTTTCT 480

Qy     481 GACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTACACTTCAGCTCCC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTACACTTCAGCTCCC 540

Qy     541 AATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAGGAGCCAAGGGAC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAGGAGCCAAGGGAC 600

Qy     601 CTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACATCCTGACCAAGTT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACATCCTGACCAAGTT 660

Qy     661 CAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAGCCAGTCACCCAA 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAGCCAGTCACCCAA 720

Qy     721 CCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAGGCAGAAAATCTG 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAGGCAGAAAATCTG 780

Qy     781 CTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATGCTCATGTGGCTA 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATGCTCATGTGGCTA 840

Qy     841 GAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCTTAAAAATACTTG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCTTAAAAATACTTG 900

Qy     901 CCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTTGGGAGCCTTGCT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 CCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTTGGGAGCCTTGCT 960

Qy     961 CTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAGCTTTTCCCGGAT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAGCTTTTCCCGGAT 1020
```

```
Qy   1021 AGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGGCTTTCAAGTCAC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGGCTTTCAAGTCAC 1080

Qy   1081 TAGTGGTTCCGTTTAGTAGATGATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTACA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TAGTGGTTCCGTTTAGTAGATGATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTACA 1140

Qy   1141 AAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAGACCTCCTT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAGACCTCCTT 1200

Qy   1201 GGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTGGAGACTAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTGGAGACTAG 1260

Qy   1261 TTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTCTCAAACTC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTCTCAAACTC 1320

Qy   1321 TTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCTCGGCGATT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 TTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCTCGGCGATT 1380

Qy   1381 AAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGATCCAGAGA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGATCCAGAGA 1440

Qy   1441 ATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGGCTTGCCCT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGGCTTGCCCT 1500

Qy   1501 TCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAGGAATTCACTGTCTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAGGAATTCACTGTCTT 1560

Qy   1561 ACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAACTCTCCCTGTTCTT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAACTCTCCCTGTTCTT 1620

Qy   1621 CTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTTTTTCCTTGGAACTG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTTTTTCCTTGGAACTG 1680

Qy   1681 TCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTAAACGATCAACATCAT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTAAACGATCAACATCAT 1740

Qy   1741 CATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTAGTTTATTTTTCTTCC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTAGTTTATTTTTCTTCC 1800

Qy   1801 CTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGTCCTCTGGACATGGTC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGTCCTCTGGACATGGTC 1860

Qy   1861 TATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCTGGTCAAAGAGGATAA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCTGGTCAAAGAGGATAA 1920

Qy   1921 GAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTGGTTCATCAGCCCCAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 GAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTGGTTCATCAGCCCCAG 1980

Qy   1981 ATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGAAGAAAGTGTGTGTTA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGAAGAAAGTGTGTGTTA 2040

Qy   2041 GCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGAGCGGAGAAGGTTCTT 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGAGCGGAGAAGGTTCTT 2100

Qy   2101 TTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAATAATAAATCTTCGTG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAATAATAAATCTTCGTG 2160

Qy   2161 CAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGGGTATAACTAATTAGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 CAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGGGTATAACTAATTAGA 2220

Qy   2221 AGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTGATAAATACATTCTGG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTGATAAATACATTCTGG 2280

Qy   2281 CCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGAGTTCTATCCCAAAGC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGAGTTCTATCCCAAAGC 2340

Qy   2341 TATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTTGCCTTCTTCCAGAAG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTTGCCTTCTTCCAGAAG 2400

Qy   2401 AATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGAGTACGAAAGGCTGCT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 AATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGAGTACGAAAGGCTGCT 2460

Qy   2461 CTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGATCCACTTTCCAAAATA 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGATCCACTTTCCAAAATA 2520

Qy   2521 GGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAGCTGTTGCCTGACAGGA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 GGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAGCTGTTGCCTGACAGGA 2580

Qy   2581 GCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAGCTTGGATGGGCAGGGGC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 GCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAGCTTGGATGGGCAGGGGC 2640

Qy   2641 TAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAAAAGACGACCTAATTATA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 TAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAAAAGACGACCTAATTATA 2700

Qy   2701 GGCCTAGGAATTTTACAGTATTGCAACTGCAATGTGATGCTGAAAGTGGAAAATGATGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GGCCTAGGAATTTTACAGTATTGCAACTGCAATGTGATGCTGAAAGTGGAAAATGATGTC 2760

Qy   2761 CTGGGCTCAGAGAAAAGCCCACACCAGCCTGGGAGTCATGATAGCAGCAGAGTGCTTGGG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 CTGGGCTCAGAGAAAAGCCCACACCAGCCTGGGAGTCATGATAGCAGCAGAGTGCTTGGG 2820

Qy   2821 GAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCTACAAAAGAAGATGCCAACTAGAGAT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCTACAAAAGAAGATGCCAACTAGAGAT 2880

Qy   2881 ATAGGTTGTCATCAGGTCCCGGAGGAGCCATGACCGTCTAGCTGAGAGCCATGACCAAGG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 ATAGGTTGTCATCAGGTCCCGGAGGAGCCATGACCGTCTAGCTGAGAGCCATGACCAAGG 2940

Qy   2941 ACACAATGTCCAAGTGACTGTGAGGACCTCAGTCTGCCCTGTGGATGTGTATGCCACAGA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 ACACAATGTCCAAGTGACTGTGAGGACCTCAGTCTGCCCTGTGGATGTGTATGCCACAGA 3000

Qy   3001 CCTGACTTCTGGAGGGCTGACTGAAATGTTCATTTTAAGCTTTTTCTTCTCTTTCCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCTGACTTCTGGAGGGCTGACTGAAATGTTCATTTTAAGCTTTTTCTTCTCTTTCCCTGA 3060

Qy   3061 AACACTCAGTTTGGGTTAGGGGTCATAGACTAAGACCAAAGAGTCCAGGGTTAGAATCTT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AACACTCAGTTTGGGTTAGGGGTCATAGACTAAGACCAAAGAGTCCAGGGTTAGAATCTT 3120

Qy   3121 GGTGTAAAATTGCAGGCCATCTCAGGAAATCTGTGAGCAGATGGGATTGGCTTTGGGTAA 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGTGTAAAATTGCAGGCCATCTCAGGAAATCTGTGAGCAGATGGGATTGGCTTTGGGTAA 3180

Qy   3181 GGTGCGTGTGGAAAATGTCAGTGGGAGCCGGGTCATGGTGGGCCTTTAGCATCAGATTCC 3240
```

```
Db   3181 GGTGCGTGTGGAAAATGTCAGTGGGAGCCGGGTCATGGTGGGCCTTTAGCATCAGATTCC 3240
Qy   3241 AGAGTGCAGATAGTCTGTATAGCTCATGTGAAACAGGGAGCCACCAAAACTTTGGGGAGC 3300
Db   3241 AGAGTGCAGATAGTCTGTATAGCTCATGTGAAACAGGGAGCCACCAAAACTTTGGGGAGC 3300
Qy   3301 AGGCTAGTGCCGGTTTTGACCACCTGTGGAGCAGTGCTCACTCACGAAGGCATTTTGCCA 3360
Db   3301 AGGCTAGTGCCGGTTTTGACCACCTGTGGAGCAGTGCTCACTCACGAAGGCATTTTGCCA 3360
Qy   3361 TCACATGAATGTGCAGAAAGGAGGCCAAAAGCATTCTGTGCTTCTCCACCACAGCACAGA 3420
Db   3361 TCACATGAATGTGCAGAAAGGAGGCCAAAAGCATTCTGTGCTTCTCCACCACAGCACAGA 3420
Qy   3421 CTTCCCTAGTCTCATTTGCTGAGAGTAGACATTCTGAGGGCCAGCAGTGCAGGTGTGATG 3480
Db   3421 CTTCCCTAGTCTCATTTGCTGAGAGTAGACATTCTGAGGGCCAGCAGTGCAGGTGTGATG 3480
Qy   3481 TGCCTCAGAGGGTATGAAGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGAT 3540
Db   3481 TGCCTCAGAGGGTATGAAGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGAT 3540
Qy   3541 ATCTAGAAGGCTAATTGATTTTTTCACTTTCACCTGACTCTCTTGCCAACCTGCAGAGAC 3600
Db   3541 ATCTAGAAGGCTAATTGATTTTTTCACTTTCACCTGACTCTCTTGCCAACCTGCAGAGAC 3600
Qy   3601 AGACATTGGGTGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCTT 3660
Db   3601 AGACATTGGGTGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCTT 3660
Qy   3661 AGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCTTCTGGTCCTA 3720
Db   3661 AGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCTTCTGGTCCTA 3720
Qy   3721 TTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGTGAGCTGAAAA 3780
Db   3721 TTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGTGAGCTGAAAA 3780
Qy   3781 ATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCACTGTAATGCA 3840
Db   3781 ATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCACTGTAATGCA 3840
Qy   3841 GTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAG 3900
Db   3841 GTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAG 3900
Qy   3901 CAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCT 3960
Db   3901 CAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCT 3960
Qy   3961 CTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGAT 4020
Db   3961 CTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGAT 4020
Qy   4021 CACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTTCTCGTAAGAATTTCCCGCGTGT 4080
Db   4021 CACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTTCTCGTAAGAATTTCCCGCGTGT 4080
Qy   4081 CTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGC 4140
Db   4081 CTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGC 4140
Qy   4141 TCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTC 4200
Db   4141 TCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTC 4200
Qy   4201 TCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTC 4260
Db   4201 TCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTC 4260
Qy   4261 CCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGG 4320
Db   4261 CCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGG 4320
Qy   4321 AAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCC 4380
Db   4321 AAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCC 4380
Qy   4381 TGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAA 4440
Db   4381 TGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAA 4440
Qy   4441 GAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTG 4500
Db   4441 GAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTG 4500
Qy   4501 CATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTT 4560
Db   4501 CATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTT 4560
Qy   4561 CTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTG 4620
Db   4561 CTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTG 4620
Qy   4621 GGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAG 4680
Db   4621 GGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAG 4680
Qy   4681 CAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTG 4740
Db   4681 CAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTG 4740
Qy   4741 CAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAG 4800
Db   4741 CAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAG 4800
Qy   4801 CAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTG 4860
Db   4801 CAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTG 4860
Qy   4861 ATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGT 4920
Db   4861 ATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGT 4920
Qy   4921 ACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTGCATTTTTCCA 4980
Db   4921 ACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTGCATTTTTCCA 4980
Qy   4981 GAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGC 5040
Db   4981 GAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGC 5040
Qy   5041 ACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACA 5100
Db   5041 ACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACA 5100
Qy   5101 GGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCT 5160
Db   5101 GGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCT 5160
Qy   5161 ACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCA 5220
Db   5161 ACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCA 5220
Qy   5221 GCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTC 5280
Db   5221 GCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTC 5280
Qy   5281 CTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGTATC 5340
Db   5281 CTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGTATC 5340
Qy   5341 TATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTC 5400
Db   5341 TATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTC 5400
```

```
Qy   5401 TTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGG 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5401 TTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGG 5460

Qy   5461 CACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGG 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 CACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGG 5520

Qy   5521 CATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCT 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCT 5580

Qy   5581 TGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCACAAT 5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 TGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCACAAT 5640

Qy   5641 CAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGAC 5700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 CAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGAC 5700

Qy   5701 AAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTA 5760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701 AAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTA 5760

Qy   5761 TCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACT 5820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 TCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACT 5820

Qy   5821 GGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCA 5880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 GGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCA 5880

Qy   5881 GTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGG 5940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5881 GTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGG 5940

Qy   5941 CGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAAT 6000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5941 CGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAAT 6000

Qy   6001 CTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATG 6060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6001 CTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATG 6060

Qy   6061 CTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTAC 6120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6061 CTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTAC 6120

Qy   6121 TTTTTGTCACCATCATCTGAAATGGG 6146
          |||||||||||||||||||||||||
Db   6121 TTTTTGTCACCATCATCTGAAATGGG 6146


RESULT   2
US-09-030-832-1
; Sequence 1, Application US/09030832
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/030,832
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/888,012
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950001/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6146 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3872..4597
US-09-030-832-1


  Query Match             100.0%;  Score 6146;  DB 35;  Length 6146;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 6146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GTCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTAT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTAT 60

Qy     61 GTCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAA 120

Qy    121 GTAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGCTGGCTTTTTCATGCAGACCCTTCAG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GTAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGCTGGCTTTTTCATGCAGACCCTTCAG 180

Qy    181 TTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTCGTGTGAGTT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTCGTGTGAGTT 240

Qy    241 CTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTCCATTGTAGTGGGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTCCATTGTAGTGGGA 300

Qy    301 GGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTCTGGAGGAAGTTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTCTGGAGGAAGTTA 360

Qy    361 CAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAGTCTGAAAAGCAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAGTCTGAAAAGCAC 420

Qy    421 AGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGCCACTGGTTTTCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGCCACTGGTTTTCT 480

Qy    481 GACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTACACTTCAGCTCCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTACACTTCAGCTCCC 540

Qy    541 AATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAGGAGCCAAGGGAC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAGGAGCCAAGGGAC 600
```

```
Qy    601 CTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACATCCTGACCAAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACATCCTGACCAAGTT 660

Qy    661 CAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAGCCAGTCACCCAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAGCCAGTCACCCAA 720

Qy    721 CCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAGGCAGAAAATCTG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAGGCAGAAAATCTG 780

Qy    781 CTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATGCTCATGTGGCTA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATGCTCATGTGGCTA 840

Qy    841 GAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCTTAAAAATACTTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCTTAAAAATACTTG 900

Qy    901 CCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTTGGGAGCCTTGCT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTTGGGAGCCTTGCT 960

Qy    961 CTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAGCTTTTCCCGGAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAGCTTTTCCCGGAT 1020

Qy   1021 AGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGGCTTTCAAGTCAC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGGCTTTCAAGTCAC 1080

Qy   1081 TAGTGGTTCCGTTTAGTAGATGATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTACA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TAGTGGTTCCGTTTAGTAGATGATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTACA 1140

Qy   1141 AAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAGACCTCCTT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAGACCTCCTT 1200

Qy   1201 GGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTGGAGACTAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTGGAGACTAG 1260

Qy   1261 TTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTCTCAAACTC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTCTCAAACTC 1320

Qy   1321 TTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCTCGGCGATT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 TTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCTCGGCGATT 1380

Qy   1381 AAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGATCCAGAGA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGATCCAGAGA 1440

Qy   1441 ATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGGCTTGCCCT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGGCTTGCCCT 1500

Qy   1501 TCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAGGAATTCACTGTCTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAGGAATTCACTGTCTT 1560

Qy   1561 ACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAACTCTCCCTGTTCTT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAACTCTCCCTGTTCTT 1620

Qy   1621 CTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTTTTTCCTTGGAACTG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTTTTTCCTTGGAACTG 1680

Qy   1681 TCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTAAACGATCAACATCAT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTAAACGATCAACATCAT 1740

Qy   1741 CATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTAGTTTATTTTTCTTCC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTAGTTTATTTTTCTTCC 1800

Qy   1801 CTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGTCCTCTGGACATGGTC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGTCCTCTGGACATGGTC 1860

Qy   1861 TATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCTGGTCAAAGAGGATAA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCTGGTCAAAGAGGATAA 1920

Qy   1921 GAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTGGTTCATCAGCCCCAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 GAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTGGTTCATCAGCCCCAG 1980

Qy   1981 ATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGAAGAAAGTGTGTGTTA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGAAGAAAGTGTGTGTTA 2040

Qy   2041 GCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGAGCGGAGAAGGTTCTT 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGAGCGGAGAAGGTTCTT 2100

Qy   2101 TTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAATAATAAATCTTCGTG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAATAATAAATCTTCGTG 2160

Qy   2161 CAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGGGTATAACTAATTAGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 CAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGGGTATAACTAATTAGA 2220

Qy   2221 AGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTGATAAATACATTCTGG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTGATAAATACATTCTGG 2280

Qy   2281 CCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGAGTTCTATCCCAAAGC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGAGTTCTATCCCAAAGC 2340

Qy   2341 TATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTTGCCTTCTTCCAGAAG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTTGCCTTCTTCCAGAAG 2400

Qy   2401 AATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGAGTACGAAAGGCTGCT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 AATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGAGTACGAAAGGCTGCT 2460

Qy   2461 CTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGATCCACTTTCCAAAATA 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGATCCACTTTCCAAAATA 2520

Qy   2521 GGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAGCTGTTGCCTGACAGGA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 GGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAGCTGTTGCCTGACAGGA 2580

Qy   2581 GCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAGCTTGGATGGGCAGGGGC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 GCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAGCTTGGATGGGCAGGGGC 2640

Qy   2641 TAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAAAAGACGACCTAATTATA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 TAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAAAAGACGACCTAATTATA 2700

Qy   2701 GGCCTAGGAATTTTACAGTATTGCAACTGCAATGTGATGCTGAAAGTGGAAAATGATGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GGCCTAGGAATTTTACAGTATTGCAACTGCAATGTGATGCTGAAAGTGGAAAATGATGTC 2760

Qy   2761 CTGGGCTCAGAGAAAAGCCCACACCAGCCTGGGAGTCATGATAGCAGCAGAGTGCTTGGG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   2761 CTGGGCTCAGAGAAAAGCCCACACCAGCCTGGGAGTCATGATAGCAGCAGAGTGCTTGGG 2820
Qy   2821 GAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCTACAAAAGAAGATGCCAACTAGAGAT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCTACAAAAGAAGATGCCAACTAGAGAT 2880
Qy   2881 ATAGGTTGTCATCAGGTCCCGGAGGAGCCATGACCGTCTAGCTGAGAGCCATGACCAAGG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 ATAGGTTGTCATCAGGTCCCGGAGGAGCCATGACCGTCTAGCTGAGAGCCATGACCAAGG 2940
Qy   2941 ACACAATGTCCAAGTGACTGTGAGGACCTCAGTCTGCCCTGTGGATGTGTATGCCACAGA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 ACACAATGTCCAAGTGACTGTGAGGACCTCAGTCTGCCCTGTGGATGTGTATGCCACAGA 3000
Qy   3001 CCTGACTTCTGGAGGGCTGACTGAAATGTTCATTTTAAGCTTTTTCTTCTCTTTCCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCTGACTTCTGGAGGGCTGACTGAAATGTTCATTTTAAGCTTTTTCTTCTCTTTCCCTGA 3060
Qy   3061 AACACTCAGTTTGGGTTAGGGGTCATAGACTAAGACCAAAGAGTCCAGGGTTAGAATCTT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AACACTCAGTTTGGGTTAGGGGTCATAGACTAAGACCAAAGAGTCCAGGGTTAGAATCTT 3120
Qy   3121 GGTGTAAAATTGCAGGCCATCTCAGGAAATCTGTGAGCAGATGGGATTGGCTTTGGGTAA 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGTGTAAAATTGCAGGCCATCTCAGGAAATCTGTGAGCAGATGGGATTGGCTTTGGGTAA 3180
Qy   3181 GGTGCGTGTGGAAAATGTCAGTGGGAGCCGGGTCATGGTGGGCCTTTAGCATCAGATTCC 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 GGTGCGTGTGGAAAATGTCAGTGGGAGCCGGGTCATGGTGGGCCTTTAGCATCAGATTCC 3240
Qy   3241 AGAGTGCAGATAGTCTGTATAGCTCATGTGAAACAGGGAGCCACCAAAACTTTGGGGAGC 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 AGAGTGCAGATAGTCTGTATAGCTCATGTGAAACAGGGAGCCACCAAAACTTTGGGGAGC 3300
Qy   3301 AGGCTAGTGCCGGTTTTGACCACCTGTGGAGCAGTGCTCACTCACGAAGGCATTTTGCCA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 AGGCTAGTGCCGGTTTTGACCACCTGTGGAGCAGTGCTCACTCACGAAGGCATTTTGCCA 3360
Qy   3361 TCACATGAATGTGCAGAAAGGAGGCCAAAAGCATTCTGTGCTTCTCCACCACAGCACAGA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TCACATGAATGTGCAGAAAGGAGGCCAAAAGCATTCTGTGCTTCTCCACCACAGCACAGA 3420
Qy   3421 CTTCCCTAGTCTCATTTGCTGAGAGTAGACATTCTGAGGGCCAGCAGTGCAGGTGTGATG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 CTTCCCTAGTCTCATTTGCTGAGAGTAGACATTCTGAGGGCCAGCAGTGCAGGTGTGATG 3480
Qy   3481 TGCCTCAGAGGGTATGAAGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGAT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 TGCCTCAGAGGGTATGAAGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGAT 3540
Qy   3541 ATCTAGAAGGCTAATTGATTTTTTCACTTTCACCTGACTCTCTTGCCAACCTGCAGAGAC 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ATCTAGAAGGCTAATTGATTTTTTCACTTTCACCTGACTCTCTTGCCAACCTGCAGAGAC 3600
Qy   3601 AGACATTGGGTGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCTT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 AGACATTGGGTGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCTT 3660
Qy   3661 AGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCTTCTGGTCCTA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 AGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCTTCTGGTCCTA 3720
Qy   3721 TTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGTGAGCTGAAAA 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGTGAGCTGAAAA 3780
Qy   3781 ATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCACTGTAATGCA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 ATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCACTGTAATGCA 3840
Qy   3841 GTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAG 3900
```

```
Qy   3901 CAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 CAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCT 3960
Qy   3961 CTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGAT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGAT 4020
Qy   4021 CACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 CACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGT 4080
Qy   4081 CTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGC 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 CTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGC 4140
Qy   4141 TCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTC 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 TCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTC 4200
Qy   4201 TCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTC 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 TCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTC 4260
Qy   4261 CCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGG 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 CCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGG 4320
Qy   4321 AAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCC 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 AAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCC 4380
Qy   4381 TGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAA 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 TGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAA 4440
Qy   4441 GAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTG 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 GAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTG 4500
Qy   4501 CATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTT 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 CATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTT 4560
Qy   4561 CTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTG 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 CTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTG 4620
Qy   4621 GGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAG 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 GGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAG 4680
Qy   4681 CAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTG 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 CAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTG 4740
Qy   4741 CAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAG 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 CAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAG 4800
Qy   4801 CAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTG 4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 CAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTG 4860
Qy   4861 ATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 ATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGT 4920
Qy   4921 ACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTGCATTTTTCCA 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 ACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTGCATTTTTCCA 4980
```

```
Qy   4981 GAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 GAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGC 5040

Qy   5041 ACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACA 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 ACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACA 5100

Qy   5101 GGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCT 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 GGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCT 5160

Qy   5161 ACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCA 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 ACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCA 5220

Qy   5221 GCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTC 5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 GCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTC 5280

Qy   5281 CTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGTATC 5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5281 CTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGTATC 5340

Qy   5341 TATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTC 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTC 5400

Qy   5401 TTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGG 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5401 TTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGG 5460

Qy   5461 CACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGG 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 CACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGG 5520

Qy   5521 CATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCT 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCT 5580

Qy   5581 TGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCACAAT 5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 TGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCACAAT 5640

Qy   5641 CAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGAC 5700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 CAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGAC 5700

Qy   5701 AAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTA 5760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701 AAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTA 5760

Qy   5761 TCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACT 5820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 TCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACT 5820

Qy   5821 GGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCA 5880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 GGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCA 5880

Qy   5881 GTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGG 5940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5881 GTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGG 5940

Qy   5941 CGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAAT 6000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5941 CGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAAT 6000

Qy   6001 CTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATG 6060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6001 CTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATG 6060

Qy   6061 CTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTAC 6120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6061 CTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTAC 6120

Qy   6121 TTTTTGTCACCATCATCTGAAATGGG 6146
          |||||||||||||||||||||||||
Db   6121 TTTTTGTCACCATCATCTGAAATGGG 6146
```

```
RESULT   3
US-08-888-012-5
; Sequence 5, Application US/08888012
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  ET2: An Alternative Transcript of the GABA-A
;    TITLE OF INVENTION:  Receptor n Subunit
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,012
;      FILING DATE:  Herewith
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950000/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9631 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-888-012-5


  Query Match           90.2%;  Score 5542.2;  DB 24;  Length 9631;
  Best Local Similarity  93.4%;  Pred. No. 0;
  Matches 5987;  Conservative    0;  Mismatches    3;  Indels  423;  Gaps    2;

Qy      1 GTCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTAT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3219 GTCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTAT 3278

Qy     61 GTCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3279 GTCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAA 3338

Qy    121 GTAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGCTGGCTTTTTCATGCAGACCCTTCAG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3339 GTAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGCTGGCTTTTTCATGCAGACCCTTCAG 3398

Qy    181 TTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTCGTGTGAGTT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3399 TTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTCGTGTGAGTT 3458

Qy    241 CTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTCCATTGTAGTGGGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3459 CTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTCCATTGTAGTGGGA 3518
```

```
Qy    301 GGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTCTGGAGGAAGTTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3519 GGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTCTGGAGGAAGTTA 3578

Qy    361 CAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAGTCTGAAAAGCAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3579 CAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAGTCTGAAAAGCAC 3638

Qy    421 AGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGCCACTGGTTTTCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3639 AGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGCCACTGGTTTTCT 3698

Qy    481 GACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTACACTTCAGCTCCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3699 GACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTACACTTCAGCTCCC 3758

Qy    541 AATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAGGAGCCAAGGGAC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3759 AATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAGGAGCCAAGGGAC 3818

Qy    601 CTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACATCCTGACCAAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3819 CTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACATCCTGACCAAGTT 3878

Qy    661 CAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAGCCAGTCACCCAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3879 CAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAGCCAGTCACCCAA 3938

Qy    721 CCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAGGCAGAAAATCTG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3939 CCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAGGCAGAAAATCTG 3998

Qy    781 CTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATGCTCATGTGGCTA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3999 CTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATGCTCATGTGGCTA 4058

Qy    841 GAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCTTAAAAATACTTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4059 GAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCTTAAAAATACTTG 4118

Qy    901 CCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTTGGGAGCCTTGCT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4119 CCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTTGGGAGCCTTGCT 4178

Qy    961 CTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAGCTTTTCCCGGAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4179 CTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAGCTTTTCCCGGAT 4238

Qy   1021 AGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGGCTTTCAAGTCAC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4239 AGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGGCTTTCAAGTCAC 4298

Qy   1081 TAGTGGTTCCGTTTAGTAGATGATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTACA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4299 TAGTGGTTCCGTTTAGTAGATGATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTACA 4358

Qy   1141 AAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAGACCTCCTT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4359 AAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAGACCTCCTT 4418

Qy   1201 GGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTGGAGACTAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4419 GGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTGGAGACTAG 4478

Qy   1261 TTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTCTCAAACTC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4479 TTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTCTCAAACTC 4538

Qy   1321 TTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCTCGGCGATT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4539 TTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCTCGGCGATT 4598

Qy   1381 AAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGATCCAGAGA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4599 AAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGATCCAGAGA 4658

Qy   1441 ATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGGCTTGCCCT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4659 ATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGGCTTGCCCT 4718

Qy   1501 TCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAGGAATTCACTGTCTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4719 TCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAGGAATTCACTGTCTT 4778

Qy   1561 ACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAACTCTCCCTGTTCTT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4779 ACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAACTCTCCCTGTTCTT 4838

Qy   1621 CTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTTTTTCCTTGGAACTG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4839 CTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTTTTTCCTTGGAACTG 4898

Qy   1681 TCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTAAACGATCAACATCAT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4899 TCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTAAACGATCAACATCAT 4958

Qy   1741 CATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTAGTTTATTTTTCTTCC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4959 CATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTAGTTTATTTTTCTTCC 5018

Qy   1801 CTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGTCCTCTGGACATGGTC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5019 CTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGTCCTCTGGACATGGTC 5078

Qy   1861 TATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCTGGTCAAAGAGGATAA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5079 TATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCTGGTCAAAGAGGATAA 5138

Qy   1921 GAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTGGTTCATCAGCCCCAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5139 GAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTGGTTCATCAGCCCCAG 5198

Qy   1981 ATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGAAGAAAGTGTGTGTTA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5199 ATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGAAGAAAGTGTGTGTTA 5258

Qy   2041 GCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGAGCGGAGAAGGTTCTT 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5259 GCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGAGCGGAGAAGGTTCTT 5318

Qy   2101 TTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAATAATAAATCTTCGTG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5319 TTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAATAATAAATCTTCGTG 5378

Qy   2161 CAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGGGTATAACTAATTAGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5379 CAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGGGTATAACTAATTAGA 5438

Qy   2221 AGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTGATAAATACATTCTGG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5439 AGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTGATAAATACATTCTGG 5498

Qy   2281 CCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGAGTTCTATCCCAAAGC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5499 CCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGAGTTCTATCCCAAAGC 5558

Qy   2341 TATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTTGCCTTCTTCCAGAAG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5559 TATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTTGCCTTCTTCCAGAAG 5618

Qy   2401 AATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGAGTACGAAAGGCTGCT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5619 AATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGAGTACGAAAGGCTGCT 5678

Qy   2461 CTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGATCCACTTTCCAAAATA 2520
```

```
Db   5679 CTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGATCCACTTTCCAAAATA 5738
Qy   2521 GGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAGCTGTTGCCTGACAGGA 2580
Db   5739 GGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAGCTGTTGCCTGACAGGA 5798
Qy   2581 GCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAGCTTGGATGGGCAGGGGC 2640
Db   5799 GCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAGCTTGGATGGGCAGGGGC 5858
Qy   2641 TAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAAAAGACGACCTAATTATA 2700
Db   5859 TAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAAAAGACGACCTAATTATA 5918
Qy   2701 GGCCTAGGAATTTTACAGTATTGCAACTGCAATGTGATGCTGAAAGTGGAAAATGATGTC 2760
Db   5919 GGCCTAGGAATTTTACAGTATTGCAACTGCAATGTGATGCTGAAAGTGGAAAATGATGTC 5978
Qy   2761 CTGGGCTCAGAGAAAAGCCCACACCAGCCTGGGAGTCATGATAGCAGCAGAGTGCTTGGG 2820
Db   5979 CTGGGCTCAGAGAAAAGCCCACACCAGCCTGGGAGTCATGATAGCAGCAGAGTGCTTGGG 6038
Qy   2821 GAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCTACAAAAGAAGATGCCAACTAGAGAT 2880
Db   6039 GAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCTACAAAAGAAGATGCCAACTAGAGAT 6098
Qy   2881 ATAGGTTGTCATCAGGTCCCGGAGGAGCCATGACCGTCTAGCTGAGAGCCATGACCAAGG 2940
Db   6099 ATAGGTTGTCATCAGGTCCCGGAGGAGCCATGACCGTCTAGCTGAGAGCCATGACCAAGG 6158
Qy   2941 ACACAATGTCCAAGTGACTGTGAGGACCTCAGTCTGCCCTGTGGATGTGTATGCCACAGA 3000
Db   6159 ACACAATGTCCAAGTGACTGTGAGGACCTCAGTCTGCCCTGTGGATGTGTATGCCACAGA 6218
Qy   3001 CCTGACTTCTGGAGGGCTGACTGAAATGTTCATTTTAAGCTTTTTCTTCTCTTTCCCTGA 3060
Db   6219 CCTGACTTCTGGAGGGCTGACTGAAATGTTCATTTTAAGCTTTTTCTTCTCTTTCCCTGA 6278
Qy   3061 AACACTCAGTTTGGGTTAGGGGTCATAGACTAAGACCAAAGAGTCCAGGGTTAGAATCTT 3120
Db   6279 AACACTCAGTTTGGGTTAGGGGTCATAGACTAAGACCAAAGAGTCCAGGGTTAGAATCTT 6338
Qy   3121 GGTGTAAAATTGCAGGCCATCTCAGGAAATCTGTGAGCAGATGGGATTGGCTTTGGGTAA 3180
Db   6339 GGTGTAAAATTGCAGGCCATCTCAGGAAATCTGTGAGCAGATGGGATTGGCTTTGGGTAA 6398
Qy   3181 GGTGCGTGTGGAAAATGTCAGTGGGAGCCGGGTCATGGTGGGCCTTTAGCATCAGATTCC 3240
Db   6399 GGTGCGTGTGGAAAATGTCAGTGGGAGCCGGGTCATGGTGGGCCTTTAGCATCAGATTCC 6458
Qy   3241 AGAGTGCAGATAGTCTGTATAGCTCATGTGAAACAGGGAGCCACCAAAACTTTGGGGAGC 3300
Db   6459 AGAGTGCAGATAGTCTGTATAGCTCATGTGAAACAGGGAGCCACCAAAACTTTGGGGAGC 6518
Qy   3301 AGGCTAGTGCCGGTTTTGACCACCTGTGGAGCAGTGCTCACTCACGAAGGCATTTTGCCA 3360
Db   6519 AGGCTAGTGCCGGTTTTGACCACCTGTGGAGCAGTGCTCACTCACGAAGGCATTTTGCCA 6578
Qy   3361 TCACATGAATGTGCAGAAAGGAGGCCAAAAGCATTCTGTGCTTCTCCACCACAGCACAGA 3420
Db   6579 TCACATGAATGTGCAGAAAGGAGGCCAAAAGCATTCTGTGCTTCTCCACCACAGCACAGA 6638
Qy   3421 CTTCCCTAGTCTCATTTGCTGAGAGTAGACATTCTGAGGGCCAGCAGTGCAGGTGTGATG 3480
Db   6639 CTTCCCTAGTCTCATTTGCTGAGAGTAGACATTCTGAGGGCCAGCAGTGCAGGTGTGATG 6698
Qy   3481 TGCCTCAGAGGGTATGAAGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGAT 3540
Db   6699 TGCCTCAGAGGGTATGAAGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGAT 6758
Qy   3541 ATCTAGAAGGCTAATTGATTTTTTCACTTTCACCTGACTCTCTTGCCAACCTGCAGAGAC 3600
Db   6759 ATCTAGAAGGCTAATTGATTTTTTCACTTTCACCTGACTCTCTTGCCAACCTGCAGAGAC 6818
Qy   3601 AGACATTGGGTGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCTT 3660
Db   6819 AGACATTGGGTGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCTT 6878
Qy   3661 AGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCTTCTGGTCCTA 3720
Db   6879 AGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCTTCTGGTCCTA 6938
Qy   3721 TTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGTGAGCTGAAAA 3780
Db   6939 TTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGTGAGCTGAAAA 6998
Qy   3781 ATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCACTGTAATGCA 3840
Db   6999 ATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCACTGTAATGCA 7058
Qy   3841 GTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAG 3900
Db   7059 GTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAG 7118
Qy   3901 CAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCT 3960
Db   7119 CAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCT 7178
Qy   3961 CTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCT------ 4015
Db   7179 CTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGTAA 7238
Qy   4015 ------------------------------------------------------------ 4015
Db   7239 GAGGAGAAACAGGTATACGCATAGGCACATGGCTGGGAGTTGGCTGGGCCAGGGCAGAGT 7298
Qy   4015 ------------------------------------------------------------ 4015
Db   7299 TGCCTTGTCATGGAGTCTTTTAACCAATGTCGCACATAGGTCAGGAGCTGAGCCCATCAC 7358
Qy   4015 --------------AGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCT 4060
Db   7359 TCTTGTGCTCTTGCAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCT 7418
Qy   4061 CGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGC 4120
Db   7419 CGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGC 7478
Qy   4121 TTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAAC 4180
Db   7479 TTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAAC 7538
Qy   4181 CAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCAT---------------------- 4217
Db   7539 CAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATGTATGAGCTGGGTATGGGAGTGGT 7598
Qy   4217 ------------------------------------------------------------ 4217
Db   7599 GGCAAGGCTTTGGAGTGTAGAGACATGCTAGCAAGGGTACTGGGGTTATGGCACATGGGT 7658
Qy   4217 ------------------------------------------------------------ 4217
Db   7659 GGTCAGCTTGCTGAGTGATGGAATGTTACCCAGGGTGGTGGCGGGGTTGAATCAACTTCC 7718
Qy   4217 ------------------------------------------------------------ 4217
Db   7719 TGATGTAATGGTGAGAAGTTGGAGGAGAGAAGCCAAGATATGGTGTGCCAAAGACAGTTT 7778
Qy   4217 ------------------------------------------------------------ 4217
Db   7779 CCAGAAAATCCGGAGGCAGCACTTAGACTTGGGTTATCTTCCCTTGACTTTTCCCCACTT 7838
Qy   4217 -------------------CCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACG 4257
Db   7839 CTTTCCTTGTCCATTTTAGCCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACG 7898
```

```
Qy   4258 TTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGA 4317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7899 TTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGA 7958

Qy   4318 GGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAG 4377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7959 GGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAG 8018

Qy   4378 CCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTT 4437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8019 CCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTT 8078

Qy   4438 TAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCT 4497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8079 TAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCT 8138

Qy   4498 CTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTT 4557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8139 CTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTT 8198

Qy   4558 CTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCT 4617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8199 CTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCT 8258

Qy   4618 GTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGA 4677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8259 GTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGA 8318

Qy   4678 AAGCAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGC 4737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8319 AAGCAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGC 8378

Qy   4738 TTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCT 4797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8379 TTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCT 8438

Qy   4798 CAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCC 4857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8439 CAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCC 8498

Qy   4858 GTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTA 4917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8499 GTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTA 8558

Qy   4918 AGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTGCATTTTT 4977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8559 AGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTGCATTTTT 8618

Qy   4978 CCAGAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAG 5037
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   8619 CCAGAAGCCCACTATTGCCTTTGCAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAG 8678

Qy   5038 TGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATA 5097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8679 TGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATA 8738

Qy   5098 ACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCT 5157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8739 ACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCT 8798

Qy   5158 GCTACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGG 5217
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   8799 GCTACCCCTTTCTCTGCAGTTAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGG 8858

Qy   5218 GCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCT 5277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8859 GCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCT 8918

Qy   5278 CTCCTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGT 5337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8919 CTCCTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGT 8978

Qy   5338 ATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTT 5397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8979 ATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTT 9038

Qy   5398 CTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCC 5457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9039 CTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCC 9098

Qy   5458 AGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAAC 5517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9099 AGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAAC 9158

Qy   5518 AGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTT 5577
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9159 AGGCATTGCTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTT 9218

Qy   5578 GCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCAC 5637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9219 GCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCAC 9278

Qy   5638 AATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTT 5697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9279 AATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTT 9338

Qy   5698 GACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTC 5757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9339 GACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTC 9398

Qy   5758 TTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTC 5817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9399 TTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTC 9458

Qy   5818 ACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGC 5877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9459 ACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGC 9518

Qy   5878 TCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAA 5937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9519 TCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAA 9578

Qy   5938 TGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCC 5990
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9579 TGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCC 9631
```

```
RESULT   4
US-09-030-832-5
; Sequence 5, Application US/09030832
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/030,832
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/888,012
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950001/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9631 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-030-832-5
```

Query Match 90.2%; Score 5542.2; DB 35; Length 9631;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 5987; Conservative 0; Mismatches 3; Indels 423; Gaps 2;

```
Qy       1 GTCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTAT 60
Db    3219 GTCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTAT 3278

Qy      61 GTCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAA 120
Db    3279 GTCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAA 3338

Qy     121 GTAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGCTGGCTTTTTCATGCAGACCCTTCAG 180
Db    3339 GTAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGCTGGCTTTTTCATGCAGACCCTTCAG 3398

Qy     181 TTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTCGTGTGAGTT 240
Db    3399 TTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTCGTGTGAGTT 3458

Qy     241 CTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTCCATTGTAGTGGGA 300
Db    3459 CTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTCCATTGTAGTGGGA 3518

Qy     301 GGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTCTGGAGGAAGTTA 360
Db    3519 GGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTCTGGAGGAAGTTA 3578

Qy     361 CAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAGTCTGAAAAGCAC 420
Db    3579 CAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAGTCTGAAAAGCAC 3638

Qy     421 AGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGCCACTGGTTTTCT 480
Db    3639 AGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGCCACTGGTTTTCT 3698

Qy     481 GACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTACACTTCAGCTCCC 540
Db    3699 GACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTACACTTCAGCTCCC 3758

Qy     541 AATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAGGAGCCAAGGGAC 600
Db    3759 AATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAGGAGCCAAGGGAC 3818

Qy     601 CTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACATCCTGACCAAGTT 660
Db    3819 CTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACATCCTGACCAAGTT 3878

Qy     661 CAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAGCCAGTCACCCAA 720
Db    3879 CAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAGCCAGTCACCCAA 3938

Qy     721 CCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAGGCAGAAAATCTG 780
Db    3939 CCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAGGCAGAAAATCTG 3998

Qy     781 CTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATGCTCATGTGGCTA 840
Db    3999 CTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATGCTCATGTGGCTA 4058

Qy     841 GAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCTTAAAAATACTTG 900
Db    4059 GAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCTTAAAAATACTTG 4118

Qy     901 CCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTTGGGAGCCTTGCT 960
Db    4119 CCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTTGGGAGCCTTGCT 4178

Qy     961 CTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAGCTTTTCCCGGAT 1020
Db    4179 CTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAGCTTTTCCCGGAT 4238

Qy    1021 AGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGGCTTTCAAGTCAC 1080
Db    4239 AGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGGCTTTCAAGTCAC 4298

Qy    1081 TAGTGGTTCCGTTTAGTAGATGATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTACA 1140
Db    4299 TAGTGGTTCCGTTTAGTAGATGATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTACA 4358

Qy    1141 AAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAGACCTCCTT 1200
Db    4359 AAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAGACCTCCTT 4418

Qy    1201 GGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTGGAGACTAG 1260
Db    4419 GGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTGGAGACTAG 4478

Qy    1261 TTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTCTCAAACTC 1320
Db    4479 TTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTCTCAAACTC 4538

Qy    1321 TTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCTCGGCGATT 1380
Db    4539 TTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCTCGGCGATT 4598

Qy    1381 AAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGATCCAGAGA 1440
Db    4599 AAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGATCCAGAGA 4658

Qy    1441 ATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGGCTTGCCCT 1500
Db    4659 ATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGGCTTGCCCT 4718

Qy    1501 TCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAGGAATTCACTGTCTT 1560
Db    4719 TCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAGGAATTCACTGTCTT 4778

Qy    1561 ACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAACTCTCCCTGTTCTT 1620
Db    4779 ACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAACTCTCCCTGTTCTT 4838

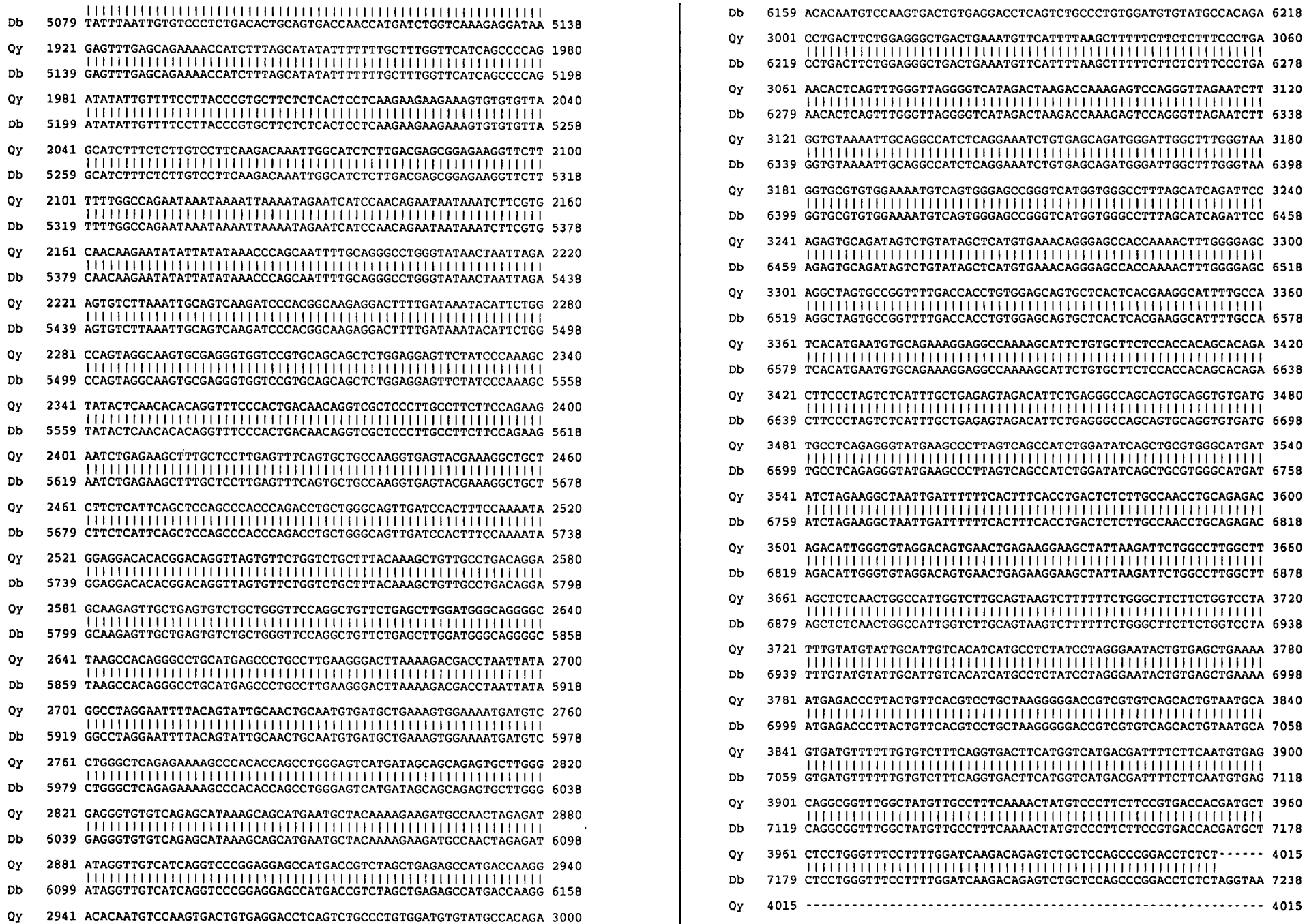
Qy    1621 CTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTTTTTCCTTGGAACTG 1680
Db    4839 CTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTTTTTCCTTGGAACTG 4898

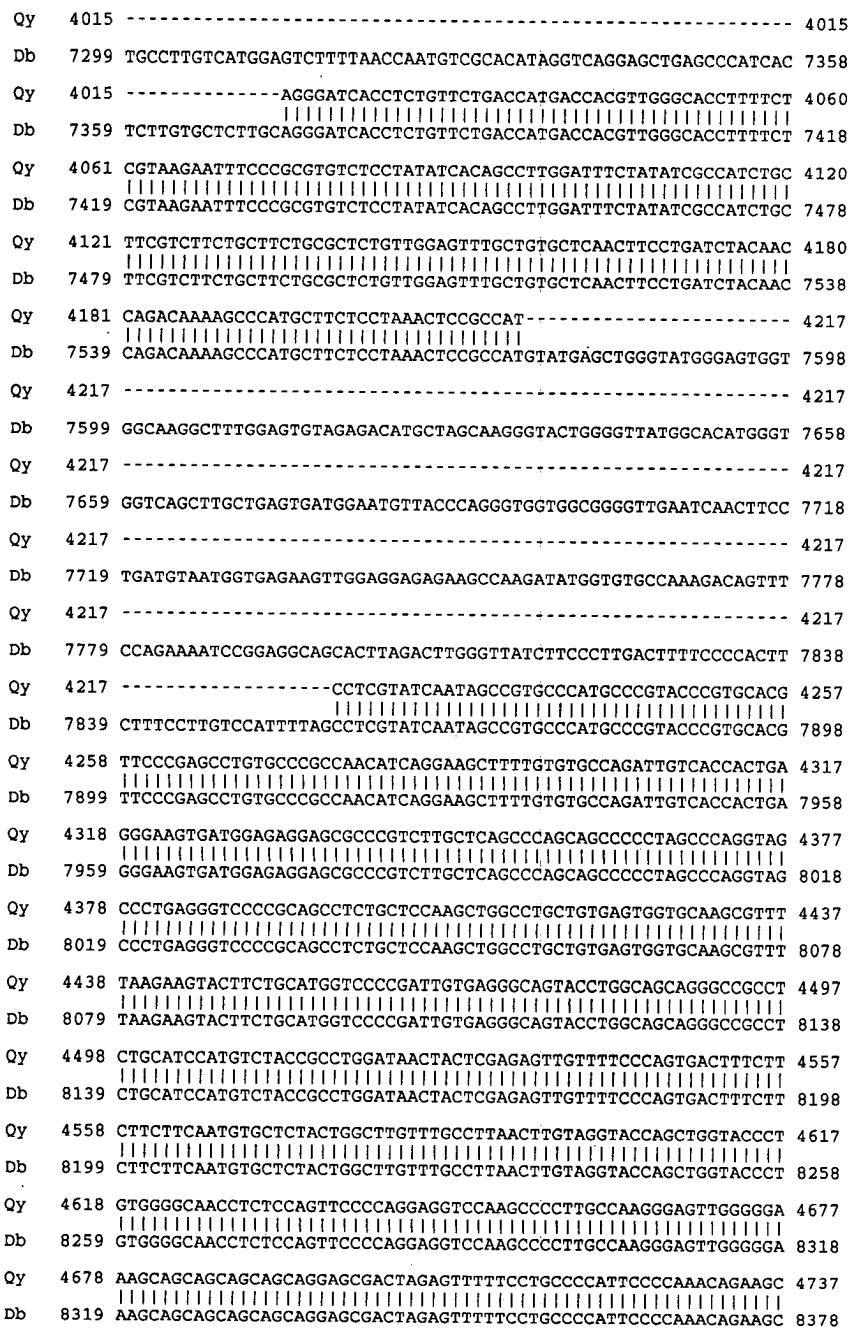
Qy    1681 TCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTAAACGATCAACATCAT 1740
Db    4899 TCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTAAACGATCAACATCAT 4958

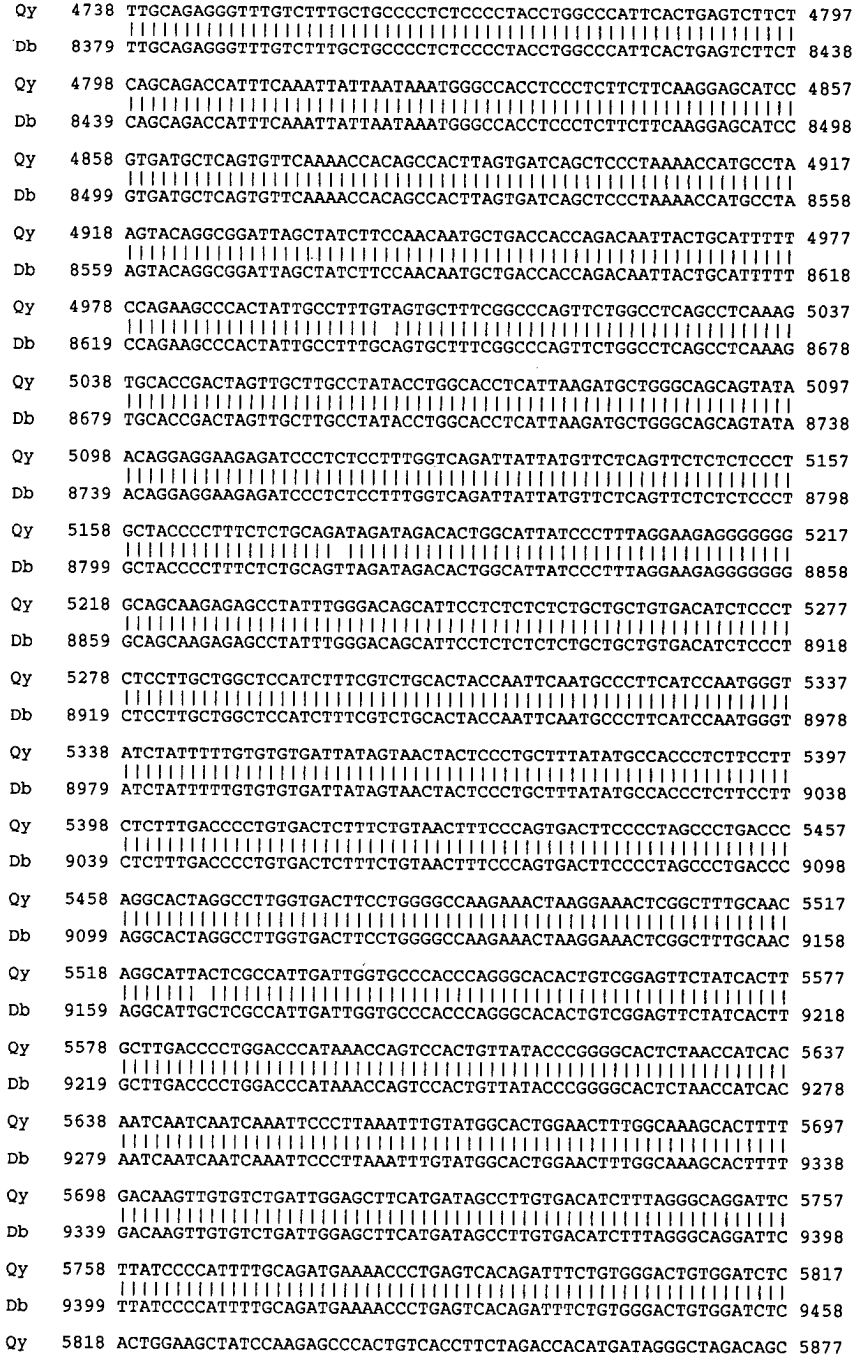
Qy    1741 CATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTAGTTTATTTTTCTTCC 1800
Db    4959 CATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTAGTTTATTTTTCTTCC 5018

Qy    1801 CTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGTCCTCTGGACATGGTC 1860
Db    5019 CTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGTCCTCTGGACATGGTC 5078

Qy    1861 TATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCTGGTCAAAGAGGATAA 1920
```


Db 5079 TATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCTGGTCAAAGAGGATAA 5138
Qy 1921 GAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTGGTTCATCAGCCCCAG 1980
Db 5139 GAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTGGTTCATCAGCCCCAG 5198
Qy 1981 ATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGAAGAAAGTGTGTGTTA 2040
Db 5199 ATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGAAGAAAGTGTGTGTTA 5258
Qy 2041 GCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGAGCGGAGAAGGTTCTT 2100
Db 5259 GCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGAGCGGAGAAGGTTCTT 5318
Qy 2101 TTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAATAATAAATCTTCGTG 2160
Db 5319 TTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAATAATAAATCTTCGTG 5378
Qy 2161 CAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGGGTATAACTAATTAGA 2220
Db 5379 CAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGGGTATAACTAATTAGA 5438
Qy 2221 AGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTGATAAATACATTCTGG 2280
Db 5439 AGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTGATAAATACATTCTGG 5498
Qy 2281 CCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGAGTTCTATCCCAAAGC 2340
Db 5499 CCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGAGTTCTATCCCAAAGC 5558
Qy 2341 TATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTTGCCTTCTTCCAGAAG 2400
Db 5559 TATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTTGCCTTCTTCCAGAAG 5618
Qy 2401 AATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGAGTACGAAAGGCTGCT 2460
Db 5619 AATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGAGTACGAAAGGCTGCT 5678
Qy 2461 CTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGATCCACTTTCCAAAATA 2520
Db 5679 CTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGATCCACTTTCCAAAATA 5738
Qy 2521 GGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAGCTGTTGCCTGACAGGA 2580
Db 5739 GGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAGCTGTTGCCTGACAGGA 5798
Qy 2581 GCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAGCTTGGATGGGCAGGGGC 2640
Db 5799 GCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAGCTTGGATGGGCAGGGGC 5858
Qy 2641 TAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAAAAGACGACCTAATTATA 2700
Db 5859 TAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAAAAGACGACCTAATTATA 5918
Qy 2701 GGCCTAGGAATTTTACAGTATTGCAACTGCAATGTGATGCTGAAAGTGGAAAATGATGTC 2760
Db 5919 GGCCTAGGAATTTTACAGTATTGCAACTGCAATGTGATGCTGAAAGTGGAAAATGATGTC 5978
Qy 2761 CTGGGCTCAGAGAAAAGCCCACACCAGCCTGGGAGTCATGATAGCAGCAGAGTGCTTGGG 2820
Db 5979 CTGGGCTCAGAGAAAAGCCCACACCAGCCTGGGAGTCATGATAGCAGCAGAGTGCTTGGG 6038
Qy 2821 GAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCTACAAAAGAAGATGCCAACTAGAGAT 2880
Db 6039 GAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCTACAAAAGAAGATGCCAACTAGAGAT 6098
Qy 2881 ATAGGTTGTCATCAGGTCCCGGAGGAGCCATGACCGTCTAGCTGAGAGCCATGACCAAGG 2940
Db 6099 ATAGGTTGTCATCAGGTCCCGGAGGAGCCATGACCGTCTAGCTGAGAGCCATGACCAAGG 6158
Qy 2941 ACACAATGTCCAAGTGACTGTGAGGACCTCAGTCTGCCCTGTGGATGTGTATGCCACAGA 3000
Db 6159 ACACAATGTCCAAGTGACTGTGAGGACCTCAGTCTGCCCTGTGGATGTGTATGCCACAGA 6218
Qy 3001 CCTGACTTCTGGAGGGCTGACTGAAATGTTCATTTTAAGCTTTTTCTTCTCTTTCCCTGA 3060
Db 6219 CCTGACTTCTGGAGGGCTGACTGAAATGTTCATTTTAAGCTTTTTCTTCTCTTTCCCTGA 6278
Qy 3061 AACACTCAGTTTGGGTTAGGGGTCATAGACTAAGACCAAAGAGTCCAGGGTTAGAATCTT 3120
Db 6279 AACACTCAGTTTGGGTTAGGGGTCATAGACTAAGACCAAAGAGTCCAGGGTTAGAATCTT 6338
Qy 3121 GGTGTAAAATTGCAGGCCATCTCAGGAAATCTGTGAGCAGATGGGATTGGCTTTGGGTAA 3180
Db 6339 GGTGTAAAATTGCAGGCCATCTCAGGAAATCTGTGAGCAGATGGGATTGGCTTTGGGTAA 6398
Qy 3181 GGTGCGTGTGGAAAATGTCAGTGGGAGCCGGGTCATGGTGGGCCTTTAGCATCAGATTCC 3240
Db 6399 GGTGCGTGTGGAAAATGTCAGTGGGAGCCGGGTCATGGTGGGCCTTTAGCATCAGATTCC 6458
Qy 3241 AGAGTGCAGATAGTCTGTATAGCTCATGTGAAACAGGGAGCCACCAAAACTTTGGGGAGC 3300
Db 6459 AGAGTGCAGATAGTCTGTATAGCTCATGTGAAACAGGGAGCCACCAAAACTTTGGGGAGC 6518
Qy 3301 AGGCTAGTGCCGGTTTTGACCACCTGTGGAGCAGTGCTCACTCACGAAGGCATTTTGCCA 3360
Db 6519 AGGCTAGTGCCGGTTTTGACCACCTGTGGAGCAGTGCTCACTCACGAAGGCATTTTGCCA 6578
Qy 3361 TCACATGAATGTGCAGAAAGGAGGCCAAAAGCATTCTGTGCTTCTCCACCACAGCACAGA 3420
Db 6579 TCACATGAATGTGCAGAAAGGAGGCCAAAAGCATTCTGTGCTTCTCCACCACAGCACAGA 6638
Qy 3421 CTTCCCTAGTCTCATTTGCTGAGAGTAGACATTCTGAGGGCCAGCAGTGCAGGTGTGATG 3480
Db 6639 CTTCCCTAGTCTCATTTGCTGAGAGTAGACATTCTGAGGGCCAGCAGTGCAGGTGTGATG 6698
Qy 3481 TGCCTCAGAGGGTATGAAGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGAT 3540
Db 6699 TGCCTCAGAGGGTATGAAGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGAT 6758
Qy 3541 ATCTAGAAGGCTAATTGATTTTTTCACTTTCACCTGACTCTCTTGCCAACCTGCAGAGAC 3600
Db 6759 ATCTAGAAGGCTAATTGATTTTTTCACTTTCACCTGACTCTCTTGCCAACCTGCAGAGAC 6818
Qy 3601 AGACATTGGGTGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCTT 3660
Db 6819 AGACATTGGGTGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCTT 6878
Qy 3661 AGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCTTCTGGTCCTA 3720
Db 6879 AGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCTTCTGGTCCTA 6938
Qy 3721 TTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGTGAGCTGAAAA 3780
Db 6939 TTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGTGAGCTGAAAA 6998
Qy 3781 ATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCACTGTAATGCA 3840
Db 6999 ATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCACTGTAATGCA 7058
Qy 3841 GTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAG 3900
Db 7059 GTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAG 7118
Qy 3901 CAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCT 3960
Db 7119 CAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCT 7178
Qy 3961 CTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCT------ 4015
Db 7179 CTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGTAA 7238
Qy 4015 ---------- 4015
Db 7239 GAGGAGAAACAGGTATACGCATAGGCACATGGCTGGGAGTTGGCTGGGCCAGGGCAGAGT 7298


Qy 4015 ---------- 4015
Db 7299 TGCCTTGTCATGGAGTCTTTTAACCAATGTCGCACATAGGTCAGGAGCTGAGCCCATCAC 7358
Qy 4015 ----------AGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCT 4060
Db 7359 TCTTGTGCTCTTGCAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCT 7418
Qy 4061 CGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGC 4120
Db 7419 CGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGC 7478
Qy 4121 TTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAAC 4180
Db 7479 TTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAAC 7538
Qy 4181 CAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCAT---------- 4217
Db 7539 CAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATGTATGAGCTGGGTATGGGAGTGGT 7598
Qy 4217 ---------- 4217
Db 7599 GGCAAGGCTTTGGAGTGTAGAGACATGCTAGCAAGGGTACTGGGGTTATGGCACATGGGT 7658
Qy 4217 ---------- 4217
Db 7659 GGTCAGCTTGCTGAGTGATGGAATGTTACCCAGGGTGGTGGCGGGGTTGAATCAACTTCC 7718
Qy 4217 ---------- 4217
Db 7719 TGATGTAATGGTGAGAAGTTGGAGGAGAGAAGCCAAGATATGGTGTGCCAAAGACAGTTT 7778
Qy 4217 ---------- 4217
Db 7779 CCAGAAAATCCGGAGGCAGCACTTAGACTTGGGTTATCTTCCCTTGACTTTTCCCCACTT 7838
Qy 4217 ----------CCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACG 4257
Db 7839 CTTTCCTTGTCCATTTTAGCCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACG 7898
Qy 4258 TTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGA 4317
Db 7899 TTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGA 7958
Qy 4318 GGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAG 4377
Db 7959 GGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAG 8018
Qy 4378 CCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTT 4437
Db 8019 CCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTT 8078
Qy 4438 TAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCT 4497
Db 8079 TAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCT 8138
Qy 4498 CTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTT 4557
Db 8139 CTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTT 8198
Qy 4558 CTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCT 4617
Db 8199 CTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCT 8258
Qy 4618 GTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGA 4677
Db 8259 GTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGA 8318
Qy 4678 AAGCAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGC 4737
Db 8319 AAGCAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGC 8378


Qy 4738 TTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCT 4797
Db 8379 TTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCT 8438
Qy 4798 CAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCC 4857
Db 8439 CAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCC 8498
Qy 4858 GTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTA 4917
Db 8499 GTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTA 8558
Qy 4918 AGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTGCATTTTT 4977
Db 8559 AGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTGCATTTTT 8618
Qy 4978 CCAGAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAG 5037
Db 8619 CCAGAAGCCCACTATTGCCTTTGCAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAG 8678
Qy 5038 TGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATA 5097
Db 8679 TGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATA 8738
Qy 5098 ACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCT 5157
Db 8739 ACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCT 8798
Qy 5158 GCTACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGG 5217
Db 8799 GCTACCCCTTTCTCTGCAGTTAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGG 8858
Qy 5218 GCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCT 5277
Db 8859 GCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCT 8918
Qy 5278 CTCCTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGT 5337
Db 8919 CTCCTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGT 8978
Qy 5338 ATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTT 5397
Db 8979 ATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTT 9038
Qy 5398 CTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCC 5457
Db 9039 CTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCC 9098
Qy 5458 AGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAAC 5517
Db 9099 AGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAAC 9158
Qy 5518 AGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTT 5577
Db 9159 AGGCATTGCTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTT 9218
Qy 5578 GCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCAC 5637
Db 9219 GCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCAC 9278
Qy 5638 AATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTT 5697
Db 9279 AATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTT 9338
Qy 5698 GACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTC 5757
Db 9339 GACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTC 9398
Qy 5758 TTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTC 5817
Db 9399 TTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTC 9458
Qy 5818 ACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGC 5877

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9459 ACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGC 9518

Qy   5878 TCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAA 5937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9519 TCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAA 9578

Qy   5938 TGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCC 5990
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9579 TGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCC 9631


RESULT   5
US-09-030-832-41
; Sequence 41, Application US/09030832
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/030,832
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/888,012
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950001/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3154 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  41..1558
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  41..94
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  95..1558
US-09-030-832-41


  Query Match             37.2%;  Score 2284;  DB 35;  Length 3154;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2284;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3863 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 3922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    824 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 883

Qy   3923 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 3982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    884 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 943

Qy   3983 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 4042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    944 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 1003

Qy   4043 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGAT 4102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1004 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGAT 1063

Qy   4103 TTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTC 4162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1064 TTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTC 1123

Qy   4163 AACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGT 4222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1124 AACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGT 1183

Qy   4223 ATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACAT 4282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1184 ATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACAT 1243

Qy   4283 CAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCG 4342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1244 CAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCG 1303

Qy   4343 TCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGC 4402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1304 TCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGC 1363

Qy   4403 TCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCC 4462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1364 TCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCC 1423

Qy   4463 GATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGAT 4522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1424 GATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGAT 1483

Qy   4523 AACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTT 4582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1484 AACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTT 1543

Qy   4583 GTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCA 4642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1544 GTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCA 1603

Qy   4643 GGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGCGAC 4702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1604 GGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGCGAC 1663

Qy   4703 TAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCC 4762
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1664 TAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCC 1723

Qy   4763 CCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAAT 4822
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1724 CCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAAT 1783

Qy   4823 AAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACA 4882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1784 AAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACA 1843

Qy   4883 GCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCC 4942
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1844 GCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCC 1903

Qy   4943 AACAATGCTGACCACCAGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTA 5002
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1904 AACAATGCTGACCACCAGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTA 1963
```

```
Qy   5003 GTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATA 5062
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1964 GTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATA 2023

Qy   5063 CCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTT 5122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2024 CCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTT 2083

Qy   5123 TGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGAT 5182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2084 TGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGAT 2143

Qy   5183 AGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACA 5242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2144 AGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACA 2203

Qy   5243 GCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTC 5302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2204 GCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTC 2263

Qy   5303 TGCACTACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGT 5362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2264 TGCACTACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGT 2323

Qy   5363 AACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCT 5422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2324 AACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCT 2383

Qy   5423 GTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCT 5482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2384 GTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCT 2443

Qy   5483 GGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTG 5542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2444 GGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTG 2503

Qy   5543 CCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCA 5602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2504 CCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCA 2563

Qy   5603 GTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAA 5662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2564 GTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAA 2623

Qy   5663 TTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTT 5722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2624 TTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTT 2683

Qy   5723 CATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAAC 5782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2684 CATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAAC 2743

Qy   5783 CCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACT 5842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2744 CCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACT 2803

Qy   5843 GTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGT 5902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2804 GTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGT 2863

Qy   5903 CACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTT 5962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2864 CACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTT 2923

Qy   5963 CTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCA 6022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2924 CTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCA 2983

Qy   6023 GTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTA 6082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2984 GTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTA 3043

Qy   6083 ATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAA 6142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3044 ATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAA 3103

Qy   6143 TGGG 6146
          ||||
Db   3104 TGGG 3107
```

RESULT 6
US-60-172-373-15901
; Sequence 15901, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polym
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 15901
; LENGTH: 3268
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 331742.2
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3257, 3265
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-15901

Query Match 36.3%; Score 2228.4; DB 87; Length 3268;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2283; Conservative 0; Mismatches 1; Indels 14; Gaps 4;

```
Qy   3863 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 3922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    919 ggtgacttcatggtcatgacgattttcttcaatgtgagcaggcggtttggctatgttgcc 978

Qy   3923 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 3982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    979 tttcaaaactatgtcccttcttccgtgaccacgatgctctcctgggtttccttttggatc 1038

Qy   3983 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 4042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 aagacagagtctgctccagcccggacctctctagggatcacctctgttctgaccatgacc 1098

Qy   4043 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGAT 4102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1099 acgttgggcacctttttctcgtaagaatttcccgcgtgtctcctatatcacagccttggat 1158

Qy   4103 TTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTC 4162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 ttctatatcgccatctgcttcgtcttctgcttctgcgctctgttggagtttgctgtgctc 1218

Qy   4163 AACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCAT------ 4217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1219 aacttcctgatctacaaccagacaaaagcccatgcttctcctaaactccgccatgtatga 1278

Qy   4217 -----CCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTG 4271
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1279 gctggcctcgtatcaatagccgtgcccatgcccgtacccgtgcacgttcccgagcctgtg 1338

Qy   4272 CCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAG 4331
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1339 cccgccaacatcaggaagcttttgtgtgccagattgtcaccactgagggaagtgatggag 1398

Qy   4332 AGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCC 4391
```

```
Db   1399 aggagcgcccgtcttgctcagcccagcagccccctagcccaggtagccctgagggtcccc 1458

Qy   4392 GCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCT 4451

Db   1459 gcagcctctgctccaagctggcctgctgtgagtggtgcaagcgttttaagaagtacttct 1518

Qy   4452 GCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCT 4511

Db   1519 gcatggtccccgattgtgagggcagtacctggcagcagggccgcctctgcatccatgtct 1578

Qy   4512 ACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGC 4571

Db   1579 accgcctggataactactcgagagttgttttcccagtgactttcttcttcttcaatgtgc 1638

Qy   4572 TCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCT 4631

Db   1639 tctactggcttgtttgccttaacttgtaggtaccagctggtaccctgtggggcaacctct 1698

Qy   4632 CCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCA 4691

Db   1699 ccagttccccaggaggtccaagccccttgccaagggagttgggggaaagcagcagcagca 1758

Qy   4692 GCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTG 4751

Db   1759 gcaggagcgactagagtttttcctgccccattccccaaacagaagcttgcagagggtttg 1818

Qy   4752 TCTTTGCTGCCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAGCAGACCATTTC 4811

Db   1819 tctttgctgcccctctccccctacctggcccattcactgagttttctcagcagaccatttc 1878

Qy   4812 AAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGT 4871

Db   1879 aaattattaataaatgggccacctccctcttcttcaaggagcatccgtgatgctcagtgt 1938

Qy   4872 TCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGGATT 4931

Db   1939 tcaaaaccacagccacttagtgatcagctccctaaaaccatgcctaagtacaggcggatt 1998

Qy   4932 AGCTATCTTCCAACAATGCTGACCACCAGACAATTACTGCATTTTTCCAGAAGCCCACTA 4991

Db   1999 agctatcttccaacaatgctgaccaccagacaattactgcatttttccagaagcccacta 2058

Qy   4992 TTGCCTTTGTAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTT 5051

Db   2059 ttgcctttgtagtgctttcggcccagttctggcctcagcctcaaagtgcaccgactagtt 2118

Qy   5052 GCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGA 5111

Db   2119 gcttgcctatacctggcacctcattaagatgctgggcagcagtataacaggaggaagaga 2178

Qy   5112 TCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTC 5171

Db   2179 tccctctcctttggtcagattattatgttctcagttctctctccctgctacccctttctc 2238

Qy   5172 TGCAGATAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCC 5231

Db   2239 tgcagatagatagacactggcattatccctttaggaagaggggggggcagcaagagagcc 2298

Qy   5232 TATTTGGGACAGCATTCCTCTCTCTCTGCT-GCTGTGACATCTCCCTCTCCTTGCTGGCT 5290

Db   2299 tatttgggacagcattcctctctctctgctggctgtgacatctccctctccttgctggct 2358

Qy   5291 CCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTG 5350

Db   2359 ccatctttcgtctgcactaccaattcaatgcccttcatccaatgggtatctatttttgtg 2418

Qy   5351 TGTGATTATAGTAACTACT-CCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCC 5409

Db   2419 tgtgattatagtaactactgccctgctttatatgccaccctcttccttctctttgacccc 2478

Qy   5410 TGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGGCACTAGGCC 5469

Db   2479 tgtgactctttctgtaactttcccagtgacttcccctagccctgacccaggcactaggcc 2538

Qy   5470 TTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACA-GGCATTACTC 5528

Db   2539 ttggtgacttcctggggccaagaaactaaggaaactcggctttgcaacagggcattactc 2598

Qy   5529 GCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCT 5588

Db   2599 gccattgattggtgcccacccagggcacactgtcggagttctatcacttgcttgaccccct 2658

Qy   5589 GGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAAT 5648

Db   2659 ggacccataaaccagtccactgttatacccggggcactctaaccatcacaatcaatcaat 2718

Qy   5649 CAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTG 5708

Db   2719 caaattcccttaaatttgtatggcactggaactttggcaaagcacttttgacaagttgtg 2778

Qy   5709 TCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATT 5768

Db   2779 tctgattggagcttcatgatagccttgtgacatctttagggcaggattcttatccccatt 2838

Qy   5769 TTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTA 5828

Db   2839 ttgcagatgaaaaccctgagtcacagatttctgtgggactgtggatctcactggaagcta 2898

Qy   5829 TCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCA 5888

Db   2899 tccaagagcccactgtcaccttctagaccacatgatagggctagacagctcagttcacca 2958

Qy   5889 TGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCT 5948

Db   2959 tgattctcttctgtcacctctgctggcacaccagtggcaaggcccagaatggcgacctct 3018

Qy   5949 CTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTG 6008

Db   3019 ctttagctcaatttctgggcctgaggtgctcagactgcccccaagatcaaatctctcctg 3078

Qy   6009 GCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGA 6068

Db   3079 gctgtagtaacccagtggaatgaatttggacatgccccaatgcttctatatgctaagtga 3138

Qy   6069 AATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTC 6128

Db   3139 aatctgtgtctgtaatttgttgggggggtggatagggtggggtctccatctacttttgtc 3198

Qy   6129 ACCATCATCTGAAATGGG 6146

Db   3199 accatcatctgaaatggg 3216
```

```
RESULT   7
US-08-888-012-6
; Sequence 6, Application US/08888012
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  ET2: An Alternative Transcript of the GABA-A
;    TITLE OF INVENTION:  Receptor n Subunit
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
```

```
;       APPLICATION NUMBER:  US/08/888,012
;       FILING DATE:  Herewith
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Steffe, Eric K.
;       REGISTRATION NUMBER:  36,688
;       REFERENCE/DOCKET NUMBER:  1488.0950000/EKS/SGW
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 371-2600
;       TELEFAX:  (202) 371-2540
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  7479 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-888-012-6


  Query Match           10.6%;  Score 654.4;  DB 24;  Length 7479;
  Best Local Similarity  57.7%;  Pred. No. 1.9e-193;
  Matches 2515;  Conservative    0;  Mismatches 1341;  Indels  506;  Gaps   55;

Qy       2 TCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTATG 61
           ||| |||  |||||| ||||||||||||||||||||||||||||||||||  || |||||
Db    2402 TCTCATATATGCTAAACACTTACAACTGTTTGCAGAGGAAACTGAGACTTCATAGCTATG 2461

Qy      62 TCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAAG 121
           ||||||||||||||||||||||||||||||||||||||||||| ||||||  |    ||||||
Db    2462 TCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCCCCTTGAAGGACGGGGTAAG 2521

Qy     122 TAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGC-------TGGCTTTTTCATGCAGACC 174
           ||||||  |  | ||   |  || | ||||  | |       ||  ||||  ||
Db    2522 TAGATATATGTTTGTAACCTTCAGTATGTTAATCTACCTTTTGAGTTTTAGATCTTTTGT 2581

Qy     175 CTTCAGTTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTC-GT 233
            || | ||||    ||| | | |||||    || ||  || |||||||  ||  ||| ||
Db    2582 ATTTAATTTCTTTCTTATATCACTGACTAACTTAGACAACATTGGGGAGGGGTACTCTGT 2641

Qy     234 GTGAGTTCTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTC-----C 288
           |||| ||  ||| | || ||||||   ||   ||||||| ||||||| ||   |
Db    2642 GTGATTTTACCAAATCCTGAACCAGGTCAAGTTGGTTGAGTGGGAAGGAAGACCACCCTA 2701

Qy     289 ATTGTAGTGGGAGGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTC 348
             | ||   || |||||  |||||||   |||| | |||||  || || | |   ||||
Db    2702 GCAGGAGGTAGAAGTGGAAACTAGAGTGACAATGGCGGCTAG--TAGGGATTGAGGAGTC 2759

Qy     349 TGGAGGAAGTTACAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAG 408
           || ||   |||||  ||| | || ||||| | | | |     ||||||||||||| |||
Db    2760 TGCAGATGGTTAC-TCAGGTGCAATGGCTACAGTAAT----ATTATCTTAAAGGAGCAAC 2814

Qy     409 TCTGAAAAGCACAGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGC 468
           | |||| || ||| ||| | | || ||||||||  |||||| || ||||| ||||  |
Db    2815 TGTGAAGAGTACATATTTTCACCAGAGGCTTCAGAGTGGAATCAACATAAACATGTT--- 2872

Qy     469 CACTGGTTTTCTGACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTAC 528
             |    | |||| ||| |  |||||| ||  | ||||| || | |||||| ||||
Db    2872 --TTTTCCTCCTGATCTTGTTCCTGACAAGGATAATAGGGGCAGATTCTGGGTCTCTTAA 2929

Qy     529 ACTTCAGCTCCCAATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAG 588
             |  | ||||||| |||||||||||| |||  ||| | ||||||||||| |||||||||
Db    2930 CTTGTATCTCCCAAATAGATGTGAGCATCTTTGCTTGTATTCCTAGGTGATCTGAATGAG 2989

Qy     589 GAGCCAAGGGACCTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACAT 648
           |||||||    | || | ||||||| |||  ||||||||||||  ||  ||||||||  |
Db    2990 GAGCCAATAAATCTTCTCAGGGTACCTCTGAGAGCAACCCTGG--ACCTTCTTCACATGT 3047

Qy     649 CCTGACCAAGTTCAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAG 708
             ||||                                    | ||||||||||||||
Db    3048 ACTGA-----------------------------------CAAGAATGTGGATGGAT 3069

Qy     709 CCAGTCACCCAACCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAG 768
```

```
             |  |||||||| |||| | ||     ||| |   || ||| | |||| |  |||||  |
Db    3070 CAGGTCACCCAGCCAGACTTT-----TGACATTTATTTTGCTTTGCTTCTGTGTGATGAT 3124

Qy     769 GCAGAAAATCTGCTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATG 828
           |    | ||        | |   |||  |    ||  ||| || | ||||||  |||| |||
Db    3125 G----ACATAAAAAAAATCTGCTATTGCTACTGTTGGTCACTCGGTGAGGGGCAGCTTATG 3180

Qy     829 CTCATGTGGCTAGAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCT 888
           || |      ||| ||||||||||  ||| || |||||||||    |  |
Db    3181 CTAACCCAACTAAAGCTTTGCTTATACAATACTAGGCAGGGATGGGTGC---------- 3230

Qy     889 TAAAAATACTTGCCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTT 948
             | |||| ||| || ||  |||||||||  | ||||  | || ||  |||||||||
Db    3230 ------TGCTTGTCCTGTTCCT--GGGACTCTGAGAAAGCCTTCTTGCTTGCTTTGACTT 3281

Qy     949 GGGAGCCTTGCTCTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAG 1008
           |||   |||| ||||||  | |  |||   |||||||||||||| || ||| |
Db    3282 GGGGTTCTTGTTCTTCTTCTACATAAATGTGGGCCTGCCTCTTAGTATTCAG-------- 3334

Qy    1009 CTTTTCCCGGATAGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGG 1068
            ||| || |||||||||  | | ||||||||  |||||||||  ||| ||||  ||||||
Db    3334 -TTTGTCCAGATAGGTGGAGCCTCATCATCAGAAGTGACAGAAGAGACAAGGTTCAGGGG 3392

Qy    1069 CTTTCAAGTCACTAGTGGTTCCGTTTAGTAGAT-GATTGTGCATTGTTTCAAAATGGTGC 1127
           |||||||||||||||||||||||||||||||||  | || ||||||||||||||||||||
Db    3393 CTTTCAAGTCACTAGTGGTTCCGTTTAGTAGATGGTTTTTGCATTGTTTCAAAATGGTGC 3452

Qy    1128 CCTAGTGACTACAAAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGC 1187
           |||||||||||||||||||||||||||||||||||||||||  ||||||||  ||||||||||
Db    3453 CCTAGTGACTACAAAGCCCCAGAGCCAGCATCATCAGTGAAGCAATGTCAGTAGGTAAGC 3512

Qy    1188 ACCAGACCTCCTTGGGAGTGAGGAGGATTCTTGAGGAGAAAAAGAGGTCTTCTTTCTCCTC 1247
           | ||  ||                  | | | ||| |  ||| ||||||||||| | |
Db    3513 AACATCTCT----------------TACTGTGGAGAAAGAAATAGGTCTTCTTTTTTCAT 3556

Qy    1248 TG-CTGGAGACTAGTTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGA 1306
           || || ||||||| ||  |||| |  | |  |  ||||| |||| |||||| |||| |
Db    3557 TGACTAGAGACTACTTATTCTGAATTCATACTGTCTTCACTGTC--AGTTATTTTTGAGT 3614

Qy    1307 CTGGTCTCAAACTCTTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTA 1366
           | ||| || |||||| |||||| | ||||||||||  ||| || | || || || | ||
Db    3615 CAGGT-TCCAACTCTCCCAGTTTGACCCTGGGGCACTTCTTTCTAGCTAGAACACACAT- 3673

Qy    1367 CGTGCTCGGCGATTAAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGA 1426
              | |      ||   || |  |||||||  ||  ||||| |||  ||||||||||||
Db    3673 ---GTACTCATTTTTCAGGGTTTAAATGCAGCAGTGCCCTGCAACTTGGGCCATCTTGGA 3729

Qy    1427 CCTTGATCCAGAGAATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGA 1486
           ||||    |||||  | |||||||||||||||||| ||| ||| ||||| || ||  ||
Db    3730 CCTTACAGCAGAG--TTTCTGCTTCAGGAGCTTCTCAGAAAGTGCAGCCTTGTCTGTAGT 3787

Qy    1487 GAGAGGCTTGCCCTTCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAG 1546
             ||         |||||||| ||||||| |||||||||| | ||| ||    | | |||
Db    3788 AAGTAAACCATCCTTCACTGGTGGCTGTTGAGCCTCTGAGGAAATCTTGCCAC-GATCAA 3846

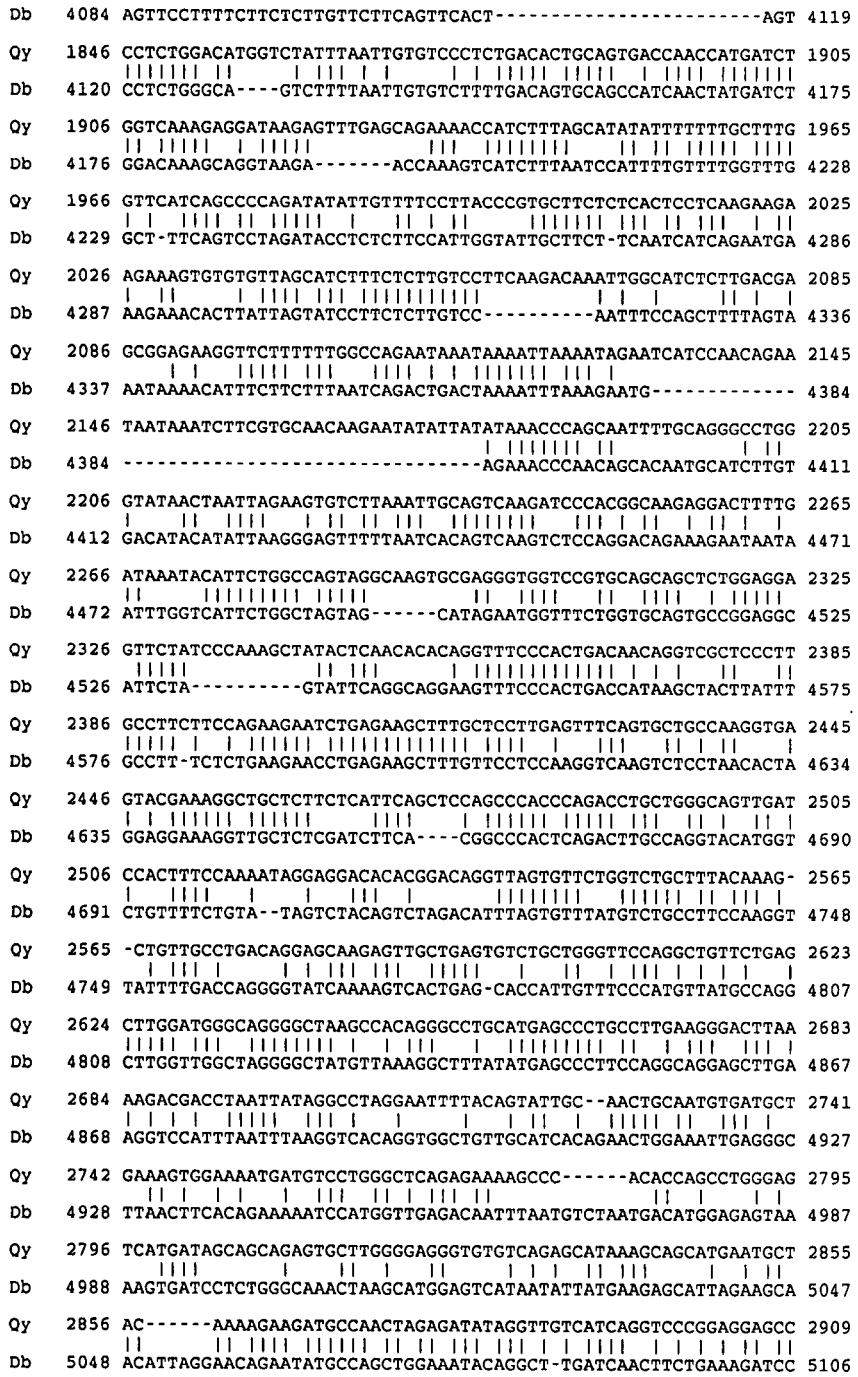
Qy    1547 GAATTCACTGTCTTACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAA 1606
           ||  |||   |||||||||||| ||   |||||| ||||||   ||| | ||||| ||||
Db    3847 GAGGTCAGCATCTTACAAGGAGATTATTTTCTTCCCTAGACGTCTCTTTCCATCAGAAAA 3906

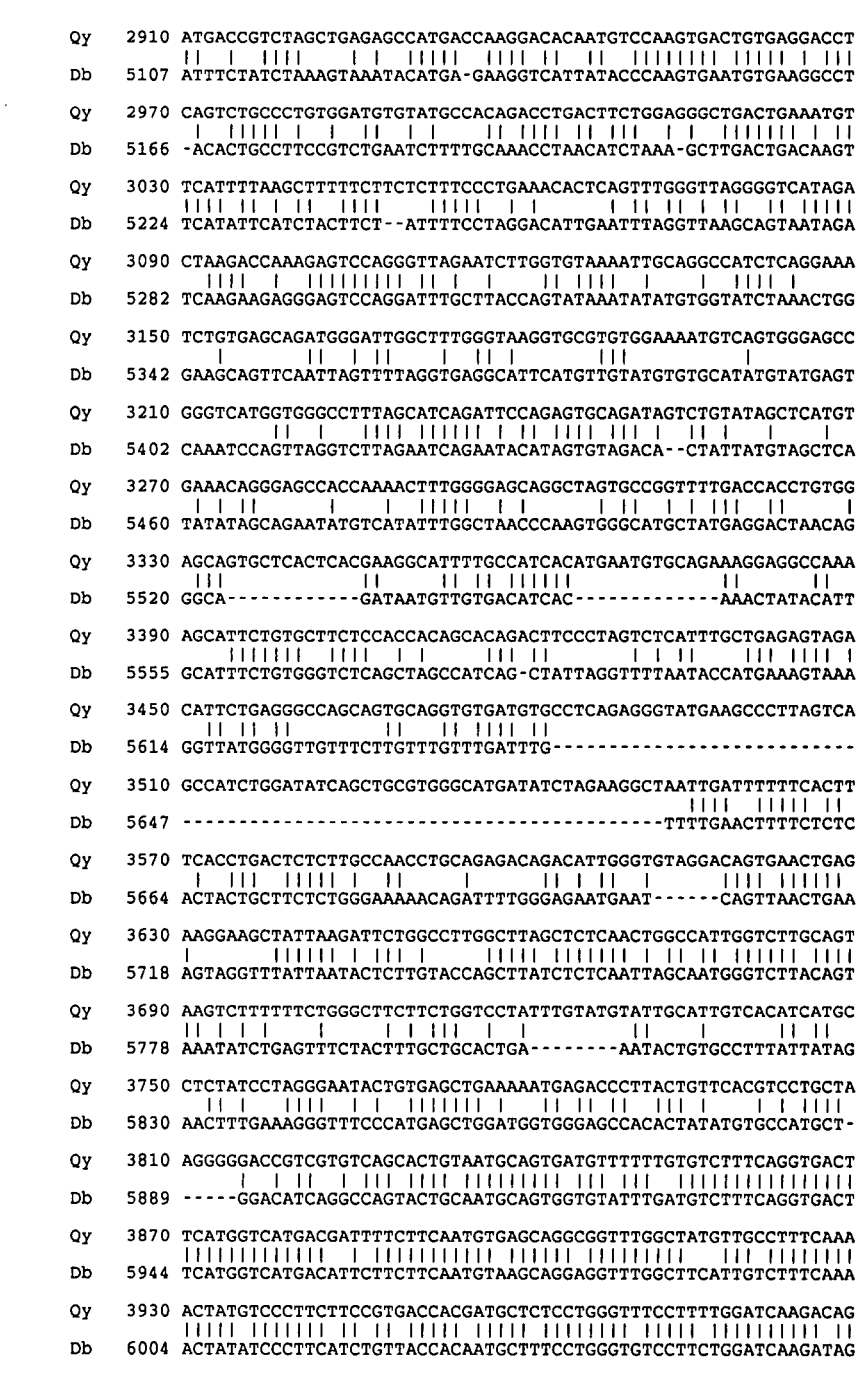
Qy    1607 CTCTCCCTGTTCTTCTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTT 1666
           ||| | ||  ||  ||| |||| |||| |||||||  |  || ||| |    ||||||||
Db    3907 TTCTTCTTGCTCATCTAAAATGGGAGTTTCTGGAACATTTACCCATCAGATCTAGTTCTT 3966

Qy    1667 TTTCCT-TGGAACTGTCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTA 1725
           |||||  | ||||  |||| |||||||| |  |          ||   |    | |  ||
Db    3967 TTTCCCCTATAACTACCCAGTTTACATTAATTTAAGGTACTCTTTCAAAAGTCAAATGTA 4026

Qy    1726 AACGATCAACATCATCATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTA 1785
           ||      |  | ||||   |       |  || ||| |||       | |   ||
Db    4027 AAGATCTAGGGTTAACATTAGAGCACACATTTGTATTCTATTGGGACTCTCCT---CCCT 4083

Qy    1786 GTTTATTTTTCTTCCCTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGT 1845
             ||  |||||||| ||| |||||||   |  |                      |||
```


Db 4084 AGTTCCTTTTCTTCTCTTGTTCTTCAGTTCACT----------AGT 4119
Qy 1846 CCTCTGGACATGGTCTATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCT 1905
Db 4120 CCTCTGGGCA----GTCTTTTAATTGTGTCTTTTGACAGTGCAGCCATCAACTATGATCT 4175
Qy 1906 GGTCAAAGAGGATAAGAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTG 1965
Db 4176 GGACAAAGCAGGTAAGA-------ACCAAAGTCATCTTTAATCCATTTTGTTTTGGTTTG 4228
Qy 1966 GTTCATCAGCCCCAGATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGA 2025
Db 4229 GCT-TTCAGTCCTAGATACCTCTCTTCCATTGGTATTGCTTCT-TCAATCATCAGAATGA 4286
Qy 2026 AGAAAGTGTGTGTTAGCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGA 2085
Db 4287 AAGAAACACTTATTAGTATCCTTCTCTTGTCC----------AATTTCCAGCTTTTAGTA 4336
Qy 2086 GCGGAGAAGGTTCTTTTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAA 2145
Db 4337 AATAAAACATTTCTTCTTTAATCAGACTGACTAAAATTTAAAGAATG------------ 4384
Qy 2146 TAATAAATCTTCGTGCAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGG 2205
Db 4384 ------------------------------AGAAACCCAACAGCACAATGCATCTTGT 4411
Qy 2206 GTATAACTAATTAGAAGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTG 2265
Db 4412 GACATACATATTAAGGGAGTTTTTAATCACAGTCAAGTCTCCAGGACAGAAAGAATAATA 4471
Qy 2266 ATAAATACATTCTGGCCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGA 2325
Db 4472 ATTTGGTCATTCTGGCTAGTAG------CATAGAATGGTTTCTGGTGCAGTGCCGGAGGC 4525
Qy 2326 GTTCTATCCCAAAGCTATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTT 2385
Db 4526 ATTCTA----------GTATTCAGGCAGGAAGTTTCCCACTGACCATAAGCTACTTATTT 4575
Qy 2386 GCCTTCTTCCAGAAGAATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGA 2445
Db 4576 GCCTT-TCTCTGAAGAACCTGAGAAGCTTTGTTCCTCCAAGGTCAAGTCTCCTAACACTA 4634
Qy 2446 GTACGAAAGGCTGCTCTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGAT 2505
Db 4635 GGAGGAAAGGTTGCTCTCGATCTTCA----CGGCCCACTCAGACTTGCCAGGTACATGGT 4690
Qy 2506 CCACTTTCCAAAATAGGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAG- 2565
Db 4691 CTGTTTTCTGTA--TAGTCTACAGTCTAGACATTTAGTGTTTATGTCTGCCTTCCAAGGT 4748
Qy 2565 -CTGTTGCCTGACAGGAGCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAG 2623
Db 4749 TATTTTGACCAGGGGTATCAAAAGTCACTGAG-CACCATTGTTTCCCATGTTATGCCAGG 4807
Qy 2624 CTTGGATGGGCAGGGGCTAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAA 2683
Db 4808 CTTGGTTGGCTAGGGGCTATGTTAAAGGCTTTATATGAGCCCTTCCAGGCAGGAGCTTGA 4867
Qy 2684 AAGACGACCTAATTATAGGCCTAGGAATTTTACAGTATTGC--AACTGCAATGTGATGCT 2741
Db 4868 AGGTCCATTTAATTTAAGGTCACAGGTGGCTGTTGCATCACAGAACTGGAAATTGAGGGC 4927
Qy 2742 GAAAGTGGAAAATGATGTCCTGGGCTCAGAGAAAAGCCC------ACACCAGCCTGGGAG 2795
Db 4928 TTAACTTCACAGAAAAATCCATGGTTGAGACAATTTAATGTCTAATGACATGGAGAGTAA 4987
Qy 2796 TCATGATAGCAGCAGAGTGCTTGGGGAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCT 2855
Db 4988 AAGTGATCCTCTGGGCAAACTAAGCATGGAGTCATAATATTATGAAGAGCATTAGAAGCA 5047
Qy 2856 AC------AAAAGAAGATGCCAACTAGAGATATAGGTTGTCATCAGGTCCCGGAGGAGCC 2909
Db 5048 ACATTAGGAACAGAATATGCCAGCTGGAAATACAGGCT-TGATCAACTTCTGAAAGATCC 5106


Qy 2910 ATGACCGTCTAGCTGAGAGCCATGACCAAGGACACAATGTCCAAGTGACTGTGAGGACCT 2969
Db 5107 ATTTCTATCTAAAGTAAATACATGA-GAAGGTCATTATACCCAAGTGAATGTGAAGGCCT 5165
Qy 2970 CAGTCTGCCCTGTGGATGTGTATGCCACAGACCTGACTTCTGGAGGGCTGACTGAAATGT 3029
Db 5166 -ACACTGCCTTCCGTCTGAATCTTTTGCAAACCTAACATCTAAA-GCTTGACTGACAAGT 5223
Qy 3030 TCATTTTAAGCTTTTTCTTCTCTTTCCCTGAAACACTCAGTTTGGGTTAGGGGTCATAGA 3089
Db 5224 TCATATTCATCTACTTCT--ATTTTCCTAGGACATTGAATTTAGGTTAAGCAGTAATAGA 5281
Qy 3090 CTAAGACCAAAGAGTCCAGGGTTAGAATCTTGGTGTAAAATTGCAGGCCATCTCAGGAAA 3149
Db 5282 TCAAGAAGAGGGAGTCCAGGATTTGCTTACCAGTATAAATATATGTGGTATCTAAACTGG 5341
Qy 3150 TCTGTGAGCAGATGGGATTGGCTTTGGGTAAGGTGCGTGTGGAAAATGTCAGTGGGAGCC 3209
Db 5342 GAAGCAGTTCAATTAGTTTTAGGTGAGGCATTCATGTTGTATGTGTGCATATGTATGAGT 5401
Qy 3210 GGGTCATGGTGGGCCTTTAGCATCAGATTCCAGAGTGCAGATAGTCTGTATAGCTCATGT 3269
Db 5402 CAAATCCAGTTAGGTCTTAGAATCAGAATACATAGTGTAGACA--CTATTATGTAGCTCA 5459
Qy 3270 GAAACAGGGAGCCACCAAAACTTTGGGGAGCAGGCTAGTGCCGGTTTTGACCACCTGTGG 3329
Db 5460 TATATAGCAGAATATGTCATATTTGGCTAACCCAAGTGGGCATGCTATGAGGACTAACAG 5519
Qy 3330 AGCAGTGCTCACTCACGAAGGCATTTTGCCATCACATGAATGTGCAGAAAGGAGGCCAAA 3389
Db 5520 GGCA-----------GATAATGTTGTGACATCAC-----------AAACTATACATT 5554
Qy 3390 AGCATTCTGTGCTTCTCCACCACAGCACAGACTTCCCTAGTCTCATTTGCTGAGAGTAGA 3449
Db 5555 GCATTTCTGTGGGTCTCAGCTAGCCATCAG-CTATTAGGTTTTAATACCATGAAAGTAAA 5613
Qy 3450 CATTCTGAGGGCCAGCAGTGCAGGTGTGATGTGCCTCAGAGGGTATGAAGCCCTTAGTCA 3509
Db 5614 GGTTATGGGGTTGTTTCTTGTTTGTTTGATTTG------------------------- 5647
Qy 3510 GCCATCTGGATATCAGCTGCGTGGGCATGATATCTAGAAGGCTAATTGATTTTTTCACTT 3569
Db 5647 --TTTTGAACTTTTCTCTC 5663
Qy 3570 TCACCTGACTCTCTTGCCAACCTGCAGAGACAGACATTGGGTGTAGGACAGTGAACTGAG 3629
Db 5664 ACTACTGCTTCTCTGGGAAAAACAGATTTTGGGAGAATGAAT------CAGTTAACTGAA 5717
Qy 3630 AAGGAAGCTATTAAGATTCTGGCCTTGGCTTAGCTCTCAACTGGCCATTGGTCTTGCAGT 3689
Db 5718 AGTAGGTTTATTAATACTCTTGTACCAGCTTATCTCTCAATTAGCAATGGGTCTTACAGT 5777
Qy 3690 AAGTCTTTTTTCTGGGCTTCTTCTGGTCCTATTTGTATGTATTGCATTGTCACATCATGC 3749
Db 5778 AAATATCTGAGTTTCTACTTTGCTGCACTGA--------AATACTGTGCCTTTATTATAG 5829
Qy 3750 CTCTATCCTAGGGAATACTGTGAGCTGAAAAATGAGACCCTTACTGTTCACGTCCTGCTA 3809
Db 5830 AACTTTGAAAGGGTTTCCCATGAGCTGGATGGTGGGAGCCACACTATATGTGCCATGCT- 5889
Qy 3810 AGGGGGACCGTCGTGTCAGCACTGTAATGCAGTGATGTTTTTTGTGTCTTTCAGGTGACT 3869
Db 5889 -----GGACATCAGGCCAGTACTGCAATGCAGTGGTGTATTTGATGTCTTTCAGGTGACT 5943
Qy 3870 TCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAA 3929
Db 5944 TCATGGTCATGACATTCTTCTTCAATGTAAGCAGGAGGTTTGGCTTCATTGTCTTTCAAA 6003
Qy 3930 ACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAG 3989
Db 6004 ACTATATCCCTTCATCTGTTACCACAATGCTTTCCTGGGTGTCCTTCTGGATCAAGATAG 6063

```
Qy   3990 AGTCTGCTCCAGCCCGGACCTC------------------------------------ 4012
          |  ||||| | ||| || ||||
Db   6064 AAGCTGCTGCTGCCAGGGCCTCTGTAGGTAAGAAAGTATGGTGATCTTAAATGTGATCAT 6123

Qy   4012 ------------------------------------------------------------ 4012

Db   6124 ATGTCATAGATTAACATTGCCTTCTCCTGTTGTCCTGCAGCACTGTCAGGAGCTTAGCCC 6183

Qy   4012 ------------------TCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCAC 4053
                             | ||||| ||| ||||| || |||||| |||| |||| ||
Db   6184 ACCTTCACTCCTTGCTCTTATAGGGGTCAGTTCTGTGCTCACCATGGCCACACTGGGTAC 6243

Qy   4054 CTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGC 4113
          |||||||||||||||||||| |||||||||||| ||||||| ||||| |||||||| ||
Db   6244 CTTTTCTCGTAAGAATTTCCCTCGTGTCTCCTATCTCACAGCTTTGGACTTCTATATTGC 6303

Qy   4114 CATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGAT 4173
           || || |||||||| |||||||| |||| | |||||  |||||||||||||||||||
Db   6304 AATTTGTTTCGTCTTGTGCTTCTGTACTCTACTAGAGTTCACTGTGCTCAACTTCCTGAC 6363

Qy   4174 CTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCA 4215
          ||||||  | |   ||   || |||||||| ||  ||  |||
Db   6364 CTACAATAATATTGAACGACAGGCTTCTCCAAAGTTCTACCA 6405
```

RESULT 8
US-09-030-832-6
; Sequence 6, Application US/09030832
; GENERAL INFORMATION:
; APPLICANT: Hanna, Michael C.
; APPLICANT: Kirkness, Ewen F.
; TITLE OF INVENTION: GABAA Receptor Epsilon Subunit
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,832
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/888,012
; FILING DATE: 03-JUL-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0950001/EKS/SGW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7479 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-030-832-6

Query Match 10.6%; Score 654.4; DB 35; Length 7479;
Best Local Similarity 57.7%; Pred. No. 1.9e-193;
Matches 2515; Conservative 0; Mismatches 1341; Indels 506; Gaps 55;

```
Qy      2 TCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTATG 61
          ||| |||  |||||| ||||||||||||||||||||||||||||||||||  || |||||
Db   2402 TCTCATATATGCTAAACACTTACAACTGTTTGCAGAGGAAACTGAGACTTCATAGCTATG 2461

Qy     62 TCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAAG 121
          |||||||||||||||||||||||||||||||||||||||||||| ||||||  |  ||||||
Db   2462 TCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCCCCTTGAAGGACGGGGTAAG 2521

Qy    122 TAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGC-------TGGCTTTTTCATGCAGACC 174
          |||||| |  | ||   |  || | ||||  | |       ||  ||||  ||
Db   2522 TAGATATATGTTTGTAACCTTCAGTATGTTAATCTACCTTTTGAGTTTTAGATCTTTTGT 2581

Qy    175 CTTCAGTTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTC-GT 233
          || | ||||    ||| | | |||||    || ||  || |||||||  ||  ||| ||
Db   2582 ATTTAATTTCTTTCTTATATCACTGACTAACTTAGACAACATTGGGGAGGGGTACTCTGT 2641

Qy    234 GTGAGTTCTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTC-----C 288
          |||| ||  ||| | || ||||||   ||   ||||||| ||||||| ||   |
Db   2642 GTGATTTTACCAAATCCTGAACCAGGTCAAGTTGGTTGAGTGGGAAGGAAGACCACCCTA 2701

Qy    289 ATTGTAGTGGGAGGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTC 348
            | ||   || |||||  |||||||   |||| | |||||  || || | |   ||||
Db   2702 GCAGGAGGTAGAAGTGGAAACTAGAGTGACAATGGCGGCTAG--TAGGGATTGAGGAGTC 2759

Qy    349 TGGAGGAAGTTACAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAG 408
          || ||   |||||  ||| | || ||||| | | | |      ||||||||||||| |||
Db   2760 TGCAGATGGTTAC-TCAGGTGCAATGGCTACAGTAAT----ATTATCTTAAAGGAGCAAC 2814

Qy    409 TCTGAAAAGCACAGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGC 468
          | |||| || ||| ||| | | || |||||||| |||| || ||||| |||| |
Db   2815 TGTGAAGAGTACATATTTTCACCAGAGGCTTCAGAGTGGAATCAACATAAACATGTT--- 2872

Qy    469 CACTGGTTTTCTGACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTAC 528
            |   | |||| ||| |  ||||||| ||  | ||||| || | |||||| |||||
Db   2872 --TTTTCCTCCTGATCTTGTTCCTGACAAGGATAATAGGGGCAGATTCTGGGTCTCTTAA 2929

Qy    529 ACTTCAGCTCCCAATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAG 588
          |  | ||||||| |||||||||||| |||  ||| | |||||||||| |||||||||
Db   2930 CTTGTATCTCCCAAATAGATGTGAGCATCTTTGCTTGTATTCCTAGGTGATCTGAATGAG 2989

Qy    589 GAGCCAAGGGACCTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACAT 648
          |||||||   | || | ||||||| |||  |||||||||||||  ||  |||||||| |
Db   2990 GAGCCAATAAATCTTCTCAGGGTACCTCTGAGAGCAACCCTGG--ACCTTCTTCACATGT 3047

Qy    649 CCTGACCAAGTTCAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAG 708
           ||||                                        |||||||||||||||
Db   3048 ACTGA-----------------------------------CAAGAATGTGGATGGAT 3069

Qy    709 CCAGTCACCCAACCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAG 768
          |  |||||||| |||| | ||      ||| |   || ||| | |||| |  |||||  |
Db   3070 CAGGTCACCCAGCCAGACTTT-----TGACATTTATTTTGCTTTGCTTCTGTGTGATGAT 3124

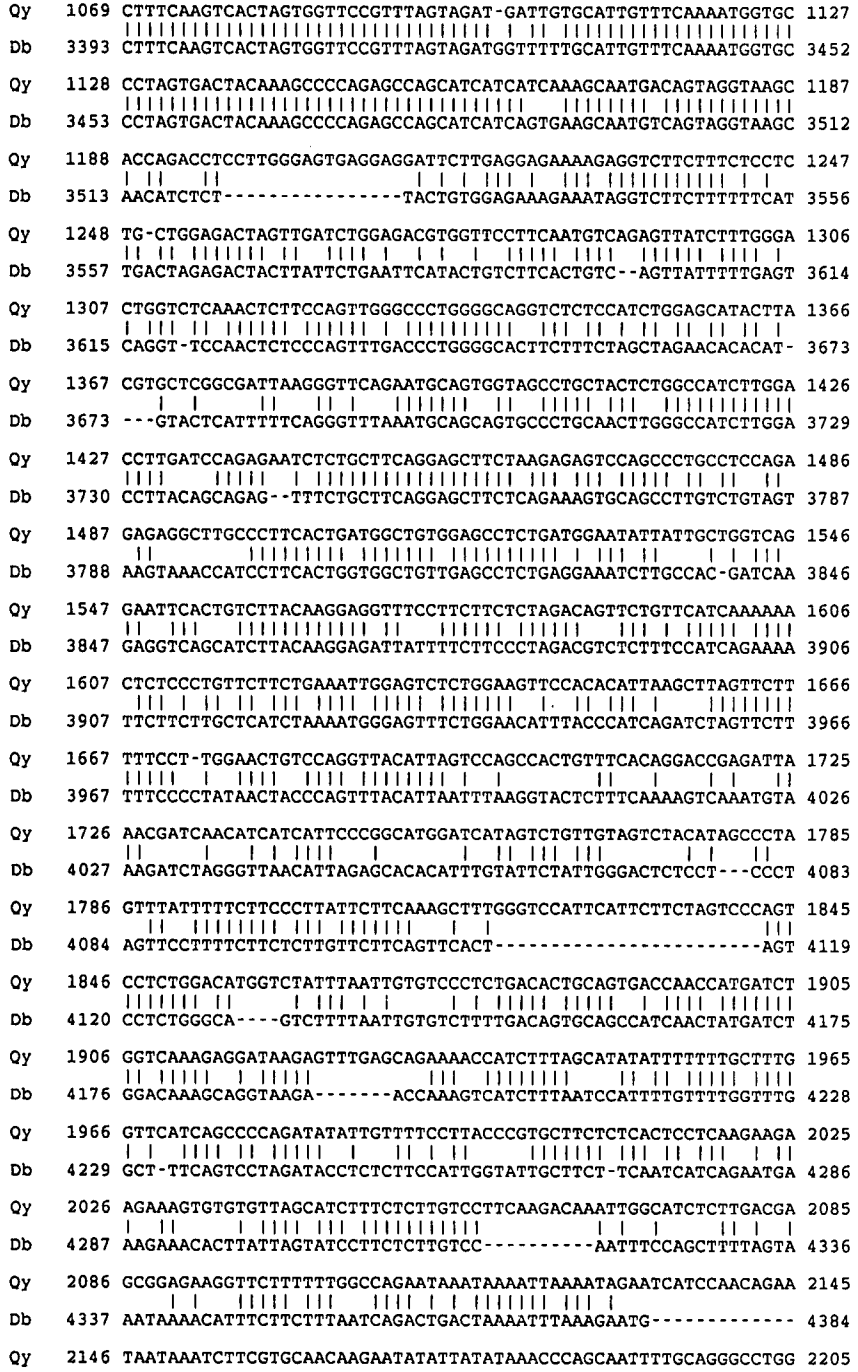
Qy    769 GCAGAAAATCTGCTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATG 828
          |    | ||       | |   |||  |   ||  ||| || | ||||||  |||| |||
Db   3125 G----ACATAAAAAAAATCTGCTATTGCTACTGTTGGTCACTCGGTGAGGGGCAGCTTATG 3180

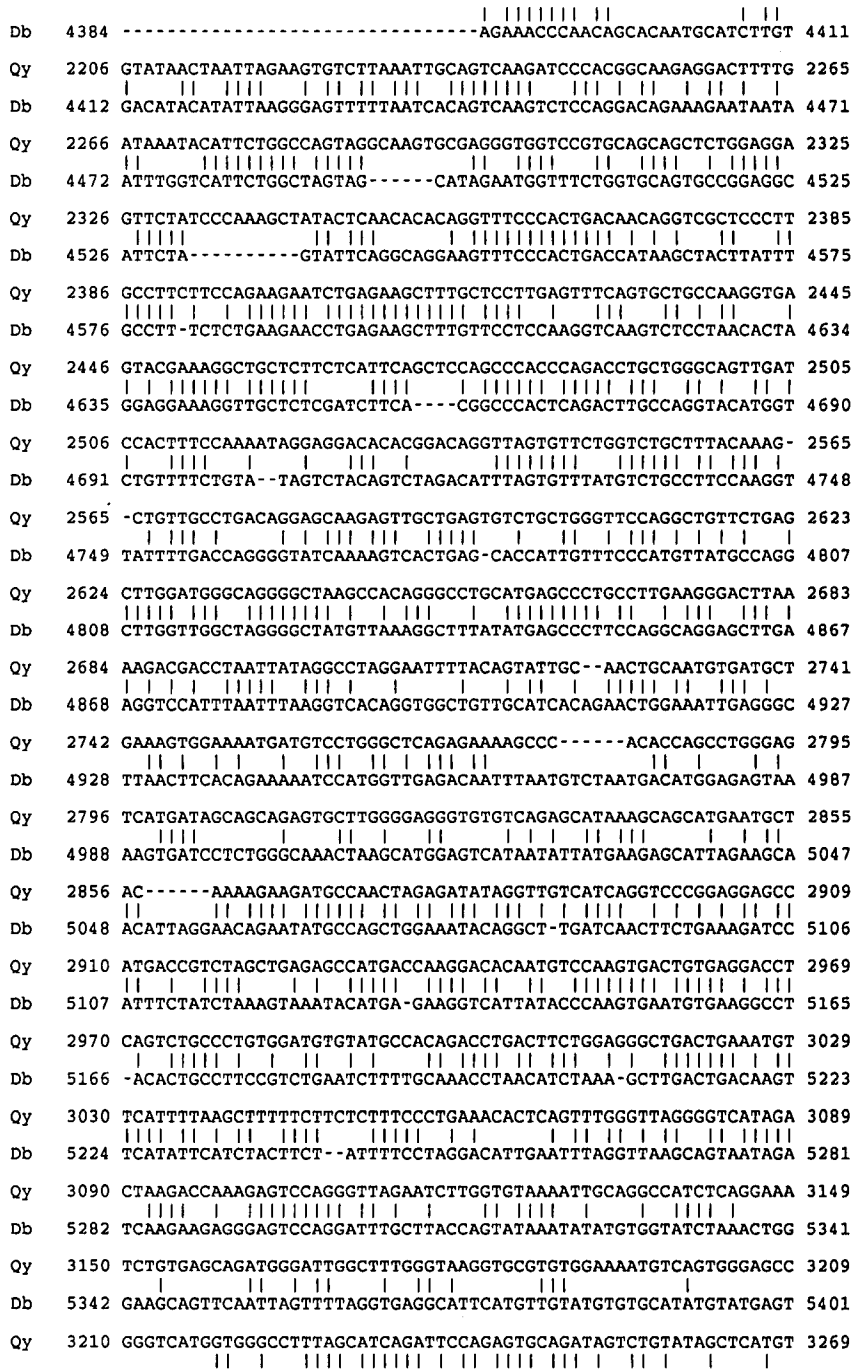
Qy    829 CTCATGTGGCTAGAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCT 888
          || |     ||| |||||||||| ||| || |||||||||   |  |
Db   3181 CTAACCCAACTAAAGCTTTGCTTATACAATACTAGGCAGGGATGGGTGC---------- 3230

Qy    889 TAAAAATACTTGCCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTT 948
            | |||| ||| || ||  |||||||| | ||||  | || ||  |||||||||
Db   3230 ------TGCTTGTCCTGTTCCT--GGGACTCTGAGAAAGCCTTCTTGCTTGCTTTGACTT 3281

Qy    949 GGGAGCCTTGCTCTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAG 1008
          |||   |||| |||||| | |  |||   |||||||||||||| || ||| |
Db   3282 GGGGTTCTTGTTCTTCTTCTACATAAATGTGGGCCTGCCTCTTAGTATTCAG-------- 3334

Qy   1009 CTTTTCCCGGATAGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGG 1068
          |||  || |||||||| | | |||||||| |||||||||  ||| ||||  ||||||
Db   3334 -TTTGTCCAGATAGGTGGAGCCTCATCATCAGAAGTGACAGAAGAGACAAGGTTCAGGGG 3392
```





```
Db    5402 CAAATCCAGTTAGGTCTTAGAATCAGAATACATAGTGTAGACA--CTATTATGTAGCTCA 5459

Qy    3270 GAAACAGGGAGCCACCAAAACTTTGGGGAGCAGGCTAGTGCCGGTTTTGACCACCTGTGG 3329

Db    5460 TATATAGCAGAATATGTCATATTTGGCTAACCCAAGTGGGCATGCTATGAGGACTAACAG 5519

Qy    3330 AGCAGTGCTCACTCACGAAGGCATTTTGCCATCACATGAATGTGCAGAAAGGAGGCCAAA 3389

Db    5520 GGCA------------GATAATGTTGTGACATCAC-------------AAACTATACATT 5554

Qy    3390 AGCATTCTGTGCTTCTCCACCACAGCACAGACTTCCCTAGTCTCATTTGCTGAGAGTAGA 3449

Db    5555 GCATTTCTGTGGGTCTCAGCTAGCCATCAG-CTATTAGGTTTTAATACCATGAAAGTAAA 5613

Qy    3450 CATTCTGAGGGCCAGCAGTGCAGGTGTGATGTGCCTCAGAGGGTATGAAGCCCTTAGTCA 3509

Db    5614 GGTTATGGGGTTGTTTCTTGTTTGTTTGATTTG---------------------------- 5647

Qy    3510 GCCATCTGGATATCAGCTGCGTGGGCATGATATCTAGAAGGCTAATTGATTTTTTCACTT 3569

Db    5647 ----------------------------------------------TTTTGAACTTTTCTCTC 5663

Qy    3570 TCACCTGACTCTCTTGCCAACCTGCAGAGACAGACATTGGGTGTAGGACAGTGAACTGAG 3629

Db    5664 ACTACTGCTTCTCTGGGAAAAACAGATTTTGGGAGAATGAAT------CAGTTAACTGAA 5717

Qy    3630 AAGGAAGCTATTAAGATTCTGGCCTTGGCTTAGCTCTCAACTGGCCATTGGTCTTGCAGT 3689

Db    5718 AGTAGGTTTATTAATACTCTTGTACCAGCTTATCTCTCAATTAGCAATGGGTCTTACAGT 5777

Qy    3690 AAGTCTTTTTTCTGGGCTTCTTCTGGTCCTATTTGTATGTATTGCATTGTCACATCATGC 3749

Db    5778 AAATATCTGAGTTTCTACTTTGCTGCACTGA--------AATACTGTGCCTTTATTATAG 5829

Qy    3750 CTCTATCCTAGGGAATACTGTGAGCTGAAAAATGAGACCCTTACTGTTCACGTCCTGCTA 3809

Db    5830 AACTTTGAAAGGGTTTCCCATGAGCTGGATGGTGGGAGCCACACTATATGTGCCATGCT- 5889

Qy    3810 AGGGGGACCGTCGTGTCAGCACTGTAATGCAGTGATGTTTTTTGTGTCTTTCAGGTGACT 3869

Db    5889 -----GGACATCAGGCCAGTACTGCAATGCAGTGGTGTATTTGATGTCTTTCAGGTGACT 5943

Qy    3870 TCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAA 3929

Db    5944 TCATGGTCATGACATTCTTCTTCAATGTAAGCAGGAGGTTTGGCTTCATTGTCTTTCAAA 6003

Qy    3930 ACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAG 3989

Db    6004 ACTATATCCCTTCATCTGTTACCACAATGCTTTCCTGGGTGTCCTTCTGGATCAAGATAG 6063

Qy    3990 AGTCTGCTCCAGCCCGGACCTC---------------------------------------- 4012

Db    6064 AAGCTGCTGCTGCCAGGGCCTCTGTAGGTAAGAAAGTATGGTGATCTTAAATGTGATCAT 6123

Qy    4012 ---------------------------------------------------------- 4012

Db    6124 ATGTCATAGATTAACATTGCCTTCTCCTGTTGTCCTGCAGCACTGTCAGGAGCTTAGCCC 6183

Qy    4012 ------------------TCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCAC 4053

Db    6184 ACCTTCACTCCTTGCTCTTATAGGGGTCAGTTCTGTGCTCACCATGGCCACACTGGGTAC 6243

Qy    4054 CTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGC 4113

Db    6244 CTTTTCTCGTAAGAATTTCCCTCGTGTCTCCTATCTCACAGCTTTGGACTTCTATATTGC 6303

Qy    4114 CATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGAT 4173

Db    6304 AATTTGTTTCGTCTTGTGCTTCTGTACTCTACTAGAGTTCACTGTGCTCAACTTCCTGAC 6363

Qy    4174 CTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCA 4215

Db    6364 CTACAATAATATTGAACGACAGGCTTCTCCAAAGTTCTACCA 6405
```

```
RESULT   9
US-60-160-190-439/c
; Sequence 439, Application US/60160190
; GENERAL INFORMATION:
;  APPLICANT: BONAZZI, VIVIEN
;  TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: CL000115
;  CURRENT APPLICATION NUMBER: US/60/160,190
;  CURRENT FILING DATE: 1998-10-19
;  NUMBER OF SEQ ID NOS: 2384
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 439
;   LENGTH: 523
;   TYPE: DNA
;   ORGANISM: HUMAN
US-60-160-190-439


  Query Match             7.3%;  Score 445.8;  DB 86;  Length 523;
  Best Local Similarity   96.4%;  Pred. No. 1.2e-128;
  Matches  456;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy    4191 CCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 4250

Db     473 CCCACTTCTTTCCTTGTCCATTTTAGCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 414

Qy    4251 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 4310

Db     413 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 354

Qy    4311 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 4370

Db     353 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 294

Qy    4371 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 4430

Db     293 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 234

Qy    4431 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 4490

Db     233 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 174

Qy    4491 GCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 4550

Db     173 GCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 114

Qy    4551 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTG 4610

Db     113 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTG 54

Qy    4611 GTACCCTGTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCA 4663

Db      53 GTACCCTGTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTCCAA 1
```

```
RESULT  10
US-60-168-603-89
; Sequence 89, Application US/60168603
; GENERAL INFORMATION:
;  APPLICANT: Hodgson, David M.                    Jones, Anissa L.
;  APPLICANT: Lincoln, Stephen E.                  Yu, Jimmy Y.
;  APPLICANT: Russo, Frank D.                      Greenawalt, Lila B.
;  APPLICANT: Spiro, Peter A.                      Panzer, Scott R.
;  APPLICANT: Banville, Steve C.                   Roseberry, Ann M.
;  APPLICANT: Bratcher, Shawn R.                   Wright, Rachel J.
;  APPLICANT: Dufour, Gerard E.                    Chen, Wensheng
;  APPLICANT: Cohen, Howard J.                     Liu, Tommy
;  APPLICANT: Rosen, Bruce                         Yap, Pierre E.
;  APPLICANT: Shah, Purvi                          Stockdreher, Theresa K.
```

```
;  APPLICANT: Chalup, Michael S.           Amshey, Stefan
;  APPLICANT: Hillman, Jennifer L.              Fong, Willy Tuen
;  TITLE OF INVENTION: MEMBRANE TRANSPORT MOLECULES
;  FILE REFERENCE: PT-0095 P
;  CURRENT APPLICATION NUMBER: US/60/168,603
;  CURRENT FILING DATE: 1999-12-01
;  NUMBER OF SEQ ID NOS: 153
;  SOFTWARE: PERL Program
; SEQ ID NO 89
;   LENGTH: 599
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 425535.2
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 35
;   OTHER INFORMATION: a, t, c, g, or other
US-60-168-603-89


  Query Match             6.5%;  Score 401;  DB 86;  Length 599;
  Best Local Similarity   77.1%;  Pred. No. 1.7e-114;
  Matches  598;  Conservative    0;  Mismatches    1;  Indels  177;  Gaps    2;

Qy   3397 TGTGCTTCTCCACCACAGCACAGACTTCCCTAGTCTCATTTGCTGAGAGTAGACATTCTG 3456
          ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db      1 tgtgcttctccaccacagcacagacttccctagtntcatttgctgagagtagacattctg 60

Qy   3457 AGGGCCAGCAGTGCAGGTGTGATGTGCCTCAGAGGGTATGAAGCCCTTAGTCAGCCATCT 3516
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 agggccagcagtgcaggtgtgatgtgcctcagagggtatgaagcccttagtcagccatct 120

Qy   3517 GGATATCAGCTGCGTGGGCATGATATCTAGAAGGCTAATTGATTTTTTCACTTTCACCTG 3576
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ggatatcagctgcgtgggcatgatatctagaaggctaattgatttttttcactttcacctg 180

Qy   3577 ACTCTCTTGCCAACCTGCAGAGACAGACATTGGGTGTAGGACAGTGAACTGAGAAGGAAG 3636
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 actctcttgccaacctgcagagacagacattgggtgtaggacagtgaactgagaaggaag 240

Qy   3637 CTATTAAGATTCTGGCCTTGGCTTAGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTT 3696
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ctattaagattctggccttggcttagctctcaactggccattggtcttgca--------- 292

Qy   3697 TTTTCTGGGCTTCTTCTGGTCCTATTTGTATGTATTGCATTGTCACATCATGCCTCTATC 3756

Db    292 ------------------------------------------------------------ 292

Qy   3757 CTAGGGAATACTGTGAGCTGAAAAATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGA 3816

Db    292 ------------------------------------------------------------ 292

Qy   3817 CCGTCGTGTCAGCACTGTAATGCAGTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGGT 3876
                                                 ||||||||||||||
Db    292 ----------------------------------------------gtgacttcatggt 304

Qy   3877 CATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGT 3936
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 catgacgattttcttcaatgtgagcaggcggtttggctatgttgcctttcaaaactatgt 364

Qy   3937 CCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGC 3996
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 cccttcttccgtgaccacgatgctctcctgggtttccttttggatcaagacagagtctgc 424

Qy   3997 TCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTT 4056
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425 tccagcccggacctctctagggatcacctctgttctgaccatgaccacgttgggcacctt 484

Qy   4057 TTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCAT 4116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485 ttctcgtaagaatttcccgcgtgtctcctatatcacagccttggatttctatatcgccat 544

Qy   4117 CTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGA 4172
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    545 ctgcttcgtcttctgcttctgcgctctgttggag-ttgctgtgctcaacttcctga 599


RESULT  11
US-09-277-227-869
; Sequence 869, Application US/09277227
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-766
;  CURRENT APPLICATION NUMBER: US/09/277,227
;  CURRENT FILING DATE: 1999-03-25
;  NUMBER OF SEQ ID NOS: 23680
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 869
;   LENGTH: 467
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(467)
;   OTHER INFORMATION: n = A,T,C or G
US-09-277-227-869


  Query Match             6.5%;  Score 398.8;  DB 44;  Length 467;
  Best Local Similarity   99.5%;  Pred. No. 7e-114;
  Matches  400;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   4525 CTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGT 4584
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     66 ctactcgagagttgttttcccagtgactttcttcttcttcaatgtgctctactggctttt 125

Qy   4585 TTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCAGG 4644
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 ttgccttaacttgtaggtaccagctggtaccctgtggggcaacctctccagttccccagg 185

Qy   4645 AGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGCGACTA 4704
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 aggtccaagcccctgccaagggagttgggggaaagcagcagcagcagcaggagcgacta 245

Qy   4705 GAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCC 4764
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 gagtttttcctgccccattccccaaacagaagcttgcagagggtttgtctttgctgcccc 305

Qy   4765 TCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAATAA 4824
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    306 tctcccctacctggcccattcactgagttttctcagcagaccatttcaaattattaataa 365

Qy   4825 ATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACAGC 4884
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 atgggccacctccctcttcttcaaggagcatccgtgatgctcagtgttcaaaaccacagc 425

Qy   4885 CACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGC 4926
          |||||||||||||||||||||||||||||||||||||||||
Db    426 cacttagtgatcagctccctaaaaccatgcctaagtacaggc 467


RESULT  12
US-09-287-618-34164
; Sequence 34164, Application US/09287618
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-768
;  CURRENT APPLICATION NUMBER: US/09/287,618
;  CURRENT FILING DATE: 1999-04-02
;  NUMBER OF SEQ ID NOS: 35865
```

```
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 34164
;   LENGTH: 406
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-287-618-34164


  Query Match             6.5%;  Score 397.6;  DB 45;  Length 406;
  Best Local Similarity   99.0%;  Pred. No. 1.5e-113;
  Matches  400;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   4525 CTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGT 4584
           |||||||||||||||||||||| |||||||||||||||||||||||||||||||||| |
Db      3 ctactcgagagttgttttcccagagactttcttcttcttcaatgtgctctactggctttt 62

Qy   4585 TTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCAGG 4644
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     63 ttgccttaacttggaggtaccagctggtaccctgtggggcaacctctccagttccccagg 122

Qy   4645 AGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGCGACTA 4704
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 aggtccaagcccttgccaagggagttgggggaaagcagcagcagcagcaggagcgactа 182

Qy   4705 GAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCC 4764
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 gagtttttcctgccccattccccaaacagaagcttgcagagggtttgtctttgctgcccc 242

Qy   4765 TCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAATAA 4824
           |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    243 tctcccctacctggcccattcactgagttttctcagcagaccatttcaaattattaataa 302

Qy   4825 ATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACAGC 4884
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 atgggccacctccctcttcttcaaggagcatccgtgatgctcagtgttcaaaaccacagc 362

Qy   4885 CACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGG 4928
           |||||||||||||||||||||||||||||||||||||||||||
Db    363 cacttagtgatcagctccctaaaaccatgcctaagtacaggcgg 406


RESULT  13
US-09-332-782-13902
; Sequence 13902, Application US/09332782
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-754CON1
;  CURRENT APPLICATION NUMBER: US/09/332,782
;  CURRENT FILING DATE: 1999-06-14
;  EARLIER APPLICATION NUMBER: US 09/181,430
;  EARLIER FILING DATE: 1998-10-28
;  NUMBER OF SEQ ID NOS: 21027
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13902
;   LENGTH: 406
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(406)
;   OTHER INFORMATION: n = A,T,C or G
US-09-332-782-13902


  Query Match             6.4%;  Score 392.4;  DB 48;  Length 406;
  Best Local Similarity   99.3%;  Pred. No. 6.5e-112;
  Matches  404;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy   4665 GGGAGTTGGGGGAAAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTC 4724
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 gggagttgggggaaagcagcagcagcaggagcgactagagtttttcctgccccattc 60

Qy   4725 CCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATT 4784
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 cccaaacagaagcttgcagagggtttgtctttgctgcccctctccctacctggcccatt 120

Qy   4785 CACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCT 4844
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    121 cactgagtcttctcagcagaccatttcaaattattaataaatgggccacctccctnttct 180

Qy   4845 TCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCT 4904
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 tcaaggagcatccgtgatgctcagtgttcaaaaccacagccacttagtgatcagctccct 240

Qy   4905 AAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAA 4964
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 aaaaccatgcctaagtacaggcggattagctatcttccaacaatgctgaccaccagacaa 300

Qy   4965 TTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTTCTGGC 5024
           |||||||||||||||||||||||||||||||||||| |||||||||| ||||||||||
Db    301 ttactgcatttttccagaagcccactattgcctttgcagtgctttcgg-ccagttctggc 359

Qy   5025 CTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATACCTGGCACC 5071
           |||||||||||||||||||||||||||||||||||||||||||||
Db    360 ctcagcctcaaagtgcaccgactagttgcttgcctatacctggcacc 406


RESULT  14
US-09-362-510-41441
; Sequence 41441, Application US/09362510
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-759CON1
;  CURRENT APPLICATION NUMBER: US/09/362,510
;  CURRENT FILING DATE: 1999-07-27
;  EARLIER APPLICATION NUMBER: US 09/221,820
;  EARLIER FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 62165
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 41441
;   LENGTH: 382
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-362-510-41441


  Query Match             6.2%;  Score 381;  DB 51;  Length 382;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-108;
  Matches  381;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   4994 GCCTTTGTAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGC 5053
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 gcctttgtagtgctttcggcccagttctggcctcagcctcaaagtgcaccgactagttgc 60

Qy   5054 TTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGATC 5113
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ttgcctatacctggcacctcattaagatgctgggcagcagtataacaggaggaagagatc 120

Qy   5114 CCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTG 5173
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 cctctcctttggtcagattattatgttctcagttctctctccctgctacccctttctctg 180

Qy   5174 CAGATAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTA 5233
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 cagatagatagacactggcattatccctttaggaagaggggggggcagcaagagagccta 240

Qy   5234 TTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCA 5293
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 tttgggacagcattcctctctctctgctgctgtgacatctccctctccttgctggctcca 300

Qy   5294 TCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGT 5353
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    301 tctttcgtctgcactaccaattcaatgcccttcatccaatgggtatctatttttgtgtgt 360

Qy   5354 GATTATAGTAACTACTCCCTG 5374
          |||||||||||||||||||||
Db    361 gattatagtaactactccctg 381


RESULT  15
US-09-431-517-25013
; Sequence 25013, Application US/09431517
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-751CON1
;  CURRENT APPLICATION NUMBER: US/09/431,517
;  CURRENT FILING DATE: 1999-11-01
;  EARLIER APPLICATION NUMBER: US 09/170,294
;  EARLIER FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 31760
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25013
;   LENGTH: 380
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(380)
;   OTHER INFORMATION: n = A,T,C or G
US-09-431-517-25013


  Query Match             6.1%;  Score 377.4;  DB 53;  Length 380;
  Best Local Similarity   99.5%;  Pred. No. 3.3e-107;
  Matches  378;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   4665 GGGAGTTGGGGGAAAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTC 4724
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 gggagttgggggaaagcagcagcagcaggagcgactagagtttttcctgccccattc 60

Qy   4725 CCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATT 4784
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 cccaaacagaagcttgcagagggtttgtctttgctgcccctctccccctacctggcccatt 120

Qy   4785 CACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCT 4844
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 cactgagtcttctcagcagaccatttcaaattattaataaatgggccacctccctcttct 180

Qy   4845 TCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCT 4904
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 tcaaggagcatccgtgatgctcagtgttcaaaaccacagccacttagtgatcagctccct 240

Qy   4905 AAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAA 4964
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 aaaaccatgcctaagtacaggcggattagctatcttccaacaatgctgaccaccagacaa 300

Qy   4965 TTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTTCTGGC 5024
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    301 ttactgcatttttccagaagcccactattgcctttgcagtgctttcggcccagttctggc 360

Qy   5025 CTCAGCCTCAAAGTGCACCG 5044
          |||||||||||||| ||||||
Db    361 ctcagcctcaaagngcaccg 380


Search completed: March 10, 2000, 08:58:29
Job time: 8987 sec
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2000, 23:36:57 ; Search time 4946.18 Seconds
(without alignments)
-3772.935 Million cell updates/sec

Title: US-09-030-832-1
Perfect score: 6146
Sequence: 1 GTCTTATAATTGCTAAGCAC.....TCACCATCATCTGAAATGGG 6146

Scoring table: IDENTITY_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl:*

Word size : 0

Number of hits that pass the threshold : 1642386

1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pr1:*
10: gb_pr2:*
11: gb_pr3:*
12: gb_ro:*
13: gb_sts:*
14: gb_sy:*
15: gb_un:*
16: gb_vi:*
17: em_fun:*
18: em_hum1:*
19: em_hum2:*
20: em_in:*
21: em_om:*
22: em_or:*
23: em_ov:*
24: em_pat:*
25: em_ph:*
26: em_pl:*
27: em_ro:*
28: em_sts:*
29: em_sy:*
30: em_un:*
31: em_vi:*
32: gb_htg1:*
33: gb_htg2:*
34: gb_in1:*
35: gb_in2:*
36: em_ba1:*
37: em_ba2:*
38: em_hum3:*
39: em_hum4:*
40: gb_pr4:*
41: gb_htg3:*
42: gb_htg4:*
43: gb_htg5:*
44: gb_htg6:*
45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6146	100.0	6146	11	HSU92285	U92285 Human GABA-
c 2	5703	92.8	158898	11	U82696	U82696 Homo sapien
3	5542.2	90.2	9631	11	HSGABRE3	U92283 Human GABA-
4	5096	82.9	10897	10	HSY09764	Y09764 Homo sapien
5	2284	37.2	3154	10	HSU66661	U66661 Human GABA-
6	2268.8	36.9	3150	10	HSY09765	Y09765 Homo sapien
7	2128	34.6	3153	9	HSGABACHL	Y07637 H.sapiens m
8	654.4	10.6	7479	12	RNU92284	U92284 Rattus norv
9	173.6	2.8	1572	4	GGGABAA	X73533 G.domesticu
10	144.4	2.3	1745	9	HSGABAAS	X15376 Human mRNA
11	142.8	2.3	1428	3	BOVGABAARG	M55563 Bovine gamm
12	140.4	2.3	2231	12	MUSGABAAG2	M62374 Mus musculu
13	140.4	2.3	2036	12	MUSGABAAR	M86572 Mouse gamma
14	140	2.3	346	12	AF090376	AF090376 Mus muscu
15	140	2.3	1838	12	RATGABAAI	L08497 Rattus ratt
16	134.4	2.2	1843	12	RATGABAAE	L08493 Rattus ratt
17	134.4	2.2	1843	12	S55933	S55933 GABAA recep
18	134	2.2	1565	5	A46959	A46959 Sequence 7
19	134	2.2	1536	10	S82769	S82769 GABAA recep
20	134	2.2	1654	12	RATGABAA	M81142 Rat GABA-A
21	134	2.2	1930	12	RNGABAG3	X63324 R.norvegicu
22	130.6	2.1	2206	4	GDGABAAR	X54944 Chicken mRN
23	129.2	2.1	1598	12	MMGSGABA	X59300 Mouse mRNA
24	128	2.1	1408	5	A28106	A28106 Human GABAa
25	128	2.1	1408	5	A39278	A39278 Sequence 3
26	128	2.1	1732	5	I88880	I88880 Sequence 17
27	126.4	2.1	1732	10	S81944	S81944 gamma-amino
28	125.6	2.0	1707	5	A50024	A50024 Sequence 7
29	124	2.0	1742	9	HSGABAAA1	X14766 Human mRNA
30	123.6	2.0	1345	4	CAGABANTS	X94342 C.auratus m
31	123.2	2.0	1555	12	MMGABAA1S	X61430 M.musculus
32	123.2	2.0	1728	12	MUSGABA1A	M86566 Mouse GABA-
33	123.2	2.0	2664	12	MUSGABAAS	M63436 Mouse GABA-
34	122.4	2.0	1679	10	HSU30461	U30461 Human GABAA
35	121.6	2.0	2353	3	BTGABARA	X05717 Bovine mRNA
36	120.8	2.0	1629	34	LSGABAA	X58638 L.stagnalis
37	119.8	1.9	1439	4	GGGABAA6S	X94343 G.gallus mR
38	119.6	1.9	2310	5	A28104	A28104 Human GABAa
39	119.6	1.9	2310	5	A39276	A39276 Sequence 1
40	119.6	1.9	2310	5	I88879	I88879 Sequence 15
41	119.6	1.9	2318	9	HUMGABRA5Y	L08485 Human GABA-
42	119.2	1.9	1336	4	GLGABABRA	Z25467 Gallus dome
43	118.6	1.9	1700	12	MUSGABA3A	M86568 Mouse GABA-
44	118.4	1.9	1651	12	RATGABAAA	L08490 Rattus ratt
45	117	1.9	1792	12	RNGABAA3	X51991 R.norvegicu

ALIGNMENTS

RESULT 1
HSU92285
LOCUS HSU92285 6146 bp mRNA PRI 04-FEB-1998
DEFINITION Human GABA-A receptor epsilon subunit (GABRE) RNA, alternative transcript.
ACCESSION U92285
VERSION U92285.1 GI:2735330
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
REFERENCE   1  (bases 1 to 6146)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6146)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .6146
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq28"
     misc_RNA        1. .6146
                     /gene="GABRE"
                     /note="RNA transcript is initiated from within the GABRE
                     gene, and therefore contains intron sequence with respect
                     to the subunit transcript"
     misc_feature    1. .3863
                     /gene="GABRE"
                     /note="intron 6 of GABRE; GABRE gene sequence deposited in
                     GenBank Accession Number U92283"
     gene            1. .6146
                     /gene="GABRE"
     stem_loop       12. .96
                     /gene="GABRE"
     stem_loop       1065. .1147
                     /gene="GABRE"
     misc_feature    3864. .6146
                     /gene="GABRE"
                     /note="exons 7, 8 and 9 of GABRE; GABRE gene sequence
                     deposited in GenBank Accession Number U92283"
BASE COUNT     1440 a   1519 c   1458 g   1729 t
ORIGIN

  Query Match             100.0%;  Score 6146;  DB 11;  Length 6146;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 6146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTAT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GTCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTAT 60

Qy      61 GTCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GTCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAA 120

Qy     121 GTAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGCTGGCTTTTTCATGCAGACCCTTCAG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GTAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGCTGGCTTTTTCATGCAGACCCTTCAG 180

Qy     181 TTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTCGTGTGAGTT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTCGTGTGAGTT 240

Qy     241 CTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTCCATTGTAGTGGGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTCCATTGTAGTGGGA 300

Qy     301 GGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTCTGGAGGAAGTTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTCTGGAGGAAGTTA 360

Qy     361 CAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAGTCTGAAAAGCAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAGTCTGAAAAGCAC 420

Qy     421 AGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGCCACTGGTTTTCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGCCACTGGTTTTCT 480

Qy     481 GACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTACACTTCAGCTCCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTACACTTCAGCTCCC 540

Qy     541 AATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAGGAGCCAAGGGAC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAGGAGCCAAGGGAC 600

Qy     601 CTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACATCCTGACCAAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACATCCTGACCAAGTT 660

Qy     661 CAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAGCCAGTCACCCAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAGCCAGTCACCCAA 720

Qy     721 CCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAGGCAGAAAATCTG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAGGCAGAAAATCTG 780

Qy     781 CTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATGCTCATGTGGCTA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATGCTCATGTGGCTA 840

Qy     841 GAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCTTAAAAATACTTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCTTAAAAATACTTG 900

Qy     901 CCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTTGGGAGCCTTGCT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 CCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTTGGGAGCCTTGCT 960

Qy     961 CTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAGCTTTTCCCGGAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAGCTTTTCCCGGAT 1020

Qy    1021 AGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGGCTTTCAAGTCAC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 AGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGGCTTTCAAGTCAC 1080

Qy    1081 TAGTGGTTCCGTTTAGTAGATGATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTACA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 TAGTGGTTCCGTTTAGTAGATGATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTACA 1140

Qy    1141 AAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAGACCTCCTT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAGACCTCCTT 1200

Qy    1201 GGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTGGAGACTAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTGGAGACTAG 1260

Qy    1261 TTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTCTCAAACTC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTCTCAAACTC 1320

Qy    1321 TTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCTCGGCGATT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 TTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCTCGGCGATT 1380

Qy    1381 AAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGATCCAGAGA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 AAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGATCCAGAGA 1440

Qy    1441 ATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGGCTTGCCCT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGGCTTGCCCT 1500

Qy    1501 TCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAGGAATTCACTGTCTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   1501 TCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAGGAATTCACTGTCTT 1560
Qy   1561 ACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAACTCTCCCTGTTCTT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAACTCTCCCTGTTCTT 1620

Qy   1621 CTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTTTTTCCTTGGAACTG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTTTTTCCTTGGAACTG 1680

Qy   1681 TCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTAAACGATCAACATCAT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTAAACGATCAACATCAT 1740

Qy   1741 CATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTAGTTTATTTTTCTTCC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTAGTTTATTTTTCTTCC 1800

Qy   1801 CTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGTCCTCTGGACATGGTC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGTCCTCTGGACATGGTC 1860

Qy   1861 TATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCTGGTCAAAGAGGATAA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCTGGTCAAAGAGGATAA 1920

Qy   1921 GAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTGGTTCATCAGCCCCAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 GAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTGGTTCATCAGCCCCAG 1980

Qy   1981 ATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGAAGAAAGTGTGTGTTA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGAAGAAAGTGTGTGTTA 2040

Qy   2041 GCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGAGCGGAGAAGGTTCTT 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGAGCGGAGAAGGTTCTT 2100

Qy   2101 TTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAATAATAAATCTTCGTG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAATAATAAATCTTCGTG 2160

Qy   2161 CAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGGGTATAACTAATTAGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 CAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGGGTATAACTAATTAGA 2220

Qy   2221 AGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTGATAAATACATTCTGG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTGATAAATACATTCTGG 2280

Qy   2281 CCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGAGTTCTATCCCAAAGC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGAGTTCTATCCCAAAGC 2340

Qy   2341 TATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTTGCCTTCTTCCAGAAG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTTGCCTTCTTCCAGAAG 2400

Qy   2401 AATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGAGTACGAAAGGCTGCT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 AATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGAGTACGAAAGGCTGCT 2460

Qy   2461 CTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGATCCACTTTCCAAAATA 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGATCCACTTTCCAAAATA 2520

Qy   2521 GGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAGCTGTTGCCTGACAGGA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 GGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAGCTGTTGCCTGACAGGA 2580

Qy   2581 GCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAGCTTGGATGGGCAGGGGC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 GCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAGCTTGGATGGGCAGGGGC 2640

Qy   2641 TAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAAAAGACGACCTAATTATA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 TAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAAAAGACGACCTAATTATA 2700

Qy   2701 GGCCTAGGAATTTTACAGTATTGCAACTGCAATGTGATGCTGAAAGTGGAAAATGATGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GGCCTAGGAATTTTACAGTATTGCAACTGCAATGTGATGCTGAAAGTGGAAAATGATGTC 2760

Qy   2761 CTGGGCTCAGAGAAAAGCCCACACCAGCCTGGGAGTCATGATAGCAGCAGAGTGCTTGGG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 CTGGGCTCAGAGAAAAGCCCACACCAGCCTGGGAGTCATGATAGCAGCAGAGTGCTTGGG 2820

Qy   2821 GAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCTACAAAAGAAGATGCCAACTAGAGAT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCTACAAAAGAAGATGCCAACTAGAGAT 2880

Qy   2881 ATAGGTTGTCATCAGGTCCCGGAGGAGCCATGACCGTCTAGCTGAGAGCCATGACCAAGG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 ATAGGTTGTCATCAGGTCCCGGAGGAGCCATGACCGTCTAGCTGAGAGCCATGACCAAGG 2940

Qy   2941 ACACAATGTCCAAGTGACTGTGAGGACCTCAGTCTGCCCTGTGGATGTGTATGCCACAGA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 ACACAATGTCCAAGTGACTGTGAGGACCTCAGTCTGCCCTGTGGATGTGTATGCCACAGA 3000

Qy   3001 CCTGACTTCTGGAGGGCTGACTGAAATGTTCATTTTAAGCTTTTTCTTCTCTTTCCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCTGACTTCTGGAGGGCTGACTGAAATGTTCATTTTAAGCTTTTTCTTCTCTTTCCCTGA 3060

Qy   3061 AACACTCAGTTTGGGTTAGGGGTCATAGACTAAGACCAAAGAGTCCAGGGTTAGAATCTT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AACACTCAGTTTGGGTTAGGGGTCATAGACTAAGACCAAAGAGTCCAGGGTTAGAATCTT 3120

Qy   3121 GGTGTAAAATTGCAGGCCATCTCAGGAAATCTGTGAGCAGATGGGATTGGCTTTGGGTAA 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGTGTAAAATTGCAGGCCATCTCAGGAAATCTGTGAGCAGATGGGATTGGCTTTGGGTAA 3180

Qy   3181 GGTGCGTGTGGAAAATGTCAGTGGGAGCCGGGTCATGGTGGGCCTTTAGCATCAGATTCC 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 GGTGCGTGTGGAAAATGTCAGTGGGAGCCGGGTCATGGTGGGCCTTTAGCATCAGATTCC 3240

Qy   3241 AGAGTGCAGATAGTCTGTATAGCTCATGTGAAACAGGGAGCCACCAAAACTTTGGGGAGC 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 AGAGTGCAGATAGTCTGTATAGCTCATGTGAAACAGGGAGCCACCAAAACTTTGGGGAGC 3300

Qy   3301 AGGCTAGTGCCGGTTTTGACCACCTGTGGAGCAGTGCTCACTCACGAAGGCATTTTGCCA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 AGGCTAGTGCCGGTTTTGACCACCTGTGGAGCAGTGCTCACTCACGAAGGCATTTTGCCA 3360

Qy   3361 TCACATGAATGTGCAGAAAGGAGGCCAAAAGCATTCTGTGCTTCTCCACCACAGCACAGA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TCACATGAATGTGCAGAAAGGAGGCCAAAAGCATTCTGTGCTTCTCCACCACAGCACAGA 3420

Qy   3421 CTTCCCTAGTCTCATTTGCTGAGAGTAGACATTCTGAGGGCCAGCAGTGCAGGTGTGATG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 CTTCCCTAGTCTCATTTGCTGAGAGTAGACATTCTGAGGGCCAGCAGTGCAGGTGTGATG 3480

Qy   3481 TGCCTCAGAGGGTATGAAGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGAT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 TGCCTCAGAGGGTATGAAGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGAT 3540

Qy   3541 ATCTAGAAGGCTAATTGATTTTTTCACTTTCACCTGACTCTCTTGCCAACCTGCAGAGAC 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ATCTAGAAGGCTAATTGATTTTTTCACTTTCACCTGACTCTCTTGCCAACCTGCAGAGAC 3600

Qy   3601 AGACATTGGGTGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCTT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 AGACATTGGGTGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCTT 3660

Qy   3661 AGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCTTCTGGTCCTA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 AGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCTTCTGGTCCTA 3720
```

```
Qy   3721 TTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGTGAGCTGAAAA 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGTGAGCTGAAAA 3780

Qy   3781 ATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCACTGTAATGCA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 ATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCACTGTAATGCA 3840

Qy   3841 GTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 GTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAG 3900

Qy   3901 CAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 CAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCT 3960

Qy   3961 CTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGAT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGAT 4020

Qy   4021 CACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTTCTCGTAAGAATTTCCCGCGTGT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 CACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTTCTCGTAAGAATTTCCCGCGTGT 4080

Qy   4081 CTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGC 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 CTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGC 4140

Qy   4141 TCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTC 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 TCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTC 4200

Qy   4201 TCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTC 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 TCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTC 4260

Qy   4261 CCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGG 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 CCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGG 4320

Qy   4321 AAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCC 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 AAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCC 4380

Qy   4381 TGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAA 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 TGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAA 4440

Qy   4441 GAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTG 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 GAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTG 4500

Qy   4501 CATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTT 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 CATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTT 4560

Qy   4561 CTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTG 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 CTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTG 4620

Qy   4621 GGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAG 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 GGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAG 4680

Qy   4681 CAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTG 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 CAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTG 4740

Qy   4741 CAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAG 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 CAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAG 4800

Qy   4801 CAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTG 4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 CAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTG 4860

Qy   4861 ATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 ATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGT 4920

Qy   4921 ACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTGCATTTTTCCA 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 ACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTGCATTTTTCCA 4980

Qy   4981 GAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 GAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGC 5040

Qy   5041 ACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACA 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 ACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACA 5100

Qy   5101 GGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCT 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 GGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCT 5160

Qy   5161 ACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCA 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 ACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCA 5220

Qy   5221 GCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTC 5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 GCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTC 5280

Qy   5281 CTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGTATC 5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5281 CTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGTATC 5340

Qy   5341 TATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTC 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTC 5400

Qy   5401 TTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGG 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5401 TTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGG 5460

Qy   5461 CACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGG 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 CACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGG 5520

Qy   5521 CATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCT 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCT 5580

Qy   5581 TGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCACAAT 5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 TGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCACAAT 5640

Qy   5641 CAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGAC 5700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 CAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGAC 5700

Qy   5701 AAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTA 5760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701 AAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTA 5760

Qy   5761 TCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACT 5820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 TCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACT 5820

Qy   5821 GGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCA 5880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 GGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCA 5880

Qy   5881 GTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGG 5940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    5881 GTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGG 5940

Qy    5941 CGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAAT 6000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5941 CGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAAT 6000

Qy    6001 CTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATG 6060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6001 CTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATG 6060

Qy    6061 CTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTAC 6120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6061 CTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTAC 6120

Qy    6121 TTTTTGTCACCATCATCTGAAATGGG 6146
           |||||||||||||||||||||||||
Db    6121 TTTTTGTCACCATCATCTGAAATGGG 6146


RESULT   2
U82696/c
LOCUS       U82696     158898 bp    DNA             PRI       01-JAN-1998
DEFINITION  Homo sapiens chromosome X map Xq28, complete sequence.
ACCESSION   U82696
VERSION     U82696.1  GI:2735037
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Hinzmann,B., Bauer,D., Drescher,B., Knop,A., Nordsiek,D.,
            Kioschis,P., Poustka,A., Rosenthal,A. and Gloeckner,G.
  TITLE     Location of GABA receptor gamma-4 subunit (GABRG4) on Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 158898)
  AUTHORS   Gloeckner,G., Rosenthal,A., Drescher,B., Schattevoy,R., Hinzmann,B.
            and Poustka,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-DEC-1996) Genome Analysis, Institut for Molecular
            Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
FEATURES             Location/Qualifiers
     source          1. .158898
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq28"
     misc_feature    1. .39138
                     /note="Region: cosmid IF064"
     repeat_region   1. .106
                     /rpt_family="L1PA11"
                     /evidence=not_experimental
     repeat_region   213. .282
                     /rpt_family="L1MB3"
                     /evidence=not_experimental
     exon            complement(1180. .1284)
                     /note="GRAIL, score = 43.000%, comment = marginal"
                     /evidence=not_experimental
     exon            complement(1683. .1767)
                     /note="MZEF, score = 60%"
                     /evidence=not_experimental
     exon            complement(2062. .2120)
                     /note="FEXHB, score = 11.76%"
                     /evidence=not_experimental
     repeat_region   complement(2637. .2710)
                     /rpt_family="L1ME2"
                     /evidence=not_experimental
     repeat_region   complement(2859. .3028)
                     /rpt_family="L1ME3A"
                     /evidence=not_experimental
     exon            complement(2911. .2978)
                     /note="MZEF, score = 79.7%"
                     /evidence=not_experimental
     exon            4250. .4431
                     /note="GRAIL, score = 52.000%, comment = good shadow"
                     /evidence=not_experimental
     repeat_region   complement(4639. .4866)
                     /rpt_family="L1MA2"
                     /evidence=not_experimental
     repeat_region   complement(4893. .5203)
                     /rpt_family="L1MA2"
                     /evidence=not_experimental
     exon            complement(4974. .5117)
                     /note="GRAIL, score = 61.000%, comment = good"
                     /evidence=not_experimental
     repeat_region   complement(5206. .5561)
                     /rpt_family="L1MA2"
                     /evidence=not_experimental
     repeat_region   complement(5562. .5602)
                     /rpt_family="L1MA9"
                     /evidence=not_experimental
     repeat_region   complement(5619. .5655)
                     /rpt_family="L1MA5"
                     /evidence=not_experimental
     repeat_region   complement(6084. .6254)
                     /rpt_family="MLT1D"
                     /evidence=not_experimental
     repeat_region   complement(6262. .6322)
                     /rpt_family="MLT1D"
                     /evidence=not_experimental
     repeat_region   complement(6384. .6549)
                     /rpt_family="MLT1D"
                     /evidence=not_experimental
     repeat_region   6664. .6771
                     /note="homology = 89.80%, score = 82, counts = 27"
                     /rpt_type=tandem
                     /rpt_unit=cctt
                     /evidence=not_experimental
     exon            6807. .6884
                     /note="FEXHB, score = 10.83%"
                     /evidence=not_experimental
     repeat_region   7337. .7454
                     /rpt_family="L1"
                     /evidence=not_experimental
     exon            7483. .7533
                     /note="FEXHB, score = 12.95%"
                     /evidence=not_experimental
     repeat_region   7950. .8010
                     /rpt_family="MSTA"
                     /evidence=not_experimental
     repeat_region   8147. .8238
                     /rpt_family="MSTA"
                     /evidence=not_experimental
     repeat_region   8245. .8286
                     /rpt_family="MSTA"
                     /evidence=not_experimental
     repeat_region   8287. .8361
                     /rpt_family="MSTC"
                     /evidence=not_experimental
     repeat_region   8878. .8921
                     /note="homology = 97.70%, score = 20, counts = 2"
                     /rpt_type=tandem
                     /rpt_unit=gattttaccttgtcaagtgcta
                     /evidence=not_experimental
     exon            complement(9471. .9526)
                     /note="MZEF, score = 85.6%"
                     /evidence=not_experimental
     exon            complement(9474. .9529)
                     /note="FEXHB, score = 12.02%"
                     /evidence=not_experimental
     repeat_region   9618. .9660
                     /rpt_family="MER3"
                     /evidence=not_experimental
     exon            10066. .10099
                     /note="GRAIL, score = 61.000%, comment = good"
                     /evidence=not_experimental
```

```
exon            11110. .11190
                /note="GRAIL, score = 76.000%, comment = excellent"
                /evidence=not_experimental
exon            11257. .11275
                /note="FEXHB, score = 19.61%"
                /evidence=not_experimental
repeat_region   11360. .11419
                /note="homology = 91.70%, score = 20, counts = 2"
                /rpt_type=tandem
                /rpt_unit=agggcaaatagctagaactattcatcaggc
                /evidence=not_experimental
exon            11613. .11637
                /note="Xpound exon prediction, score = 68% (0%)"
                /evidence=not_experimental
exon            complement(12630. .12662)
                /note="FEXHB, score = 13.07%"
                /evidence=not_experimental
repeat_region   13530. .13600
                /rpt_family="MLT2B2"
                /evidence=not_experimental
repeat_region   13607. .13760
                /rpt_family="MLT2B2"
                /evidence=not_experimental
exon            13820. .13947
                /note="GRAIL, score = 88.000%, comment = excellent"
                /evidence=not_experimental
repeat_region   13924. .13977
                /rpt_family="MLT2D"
                /evidence=not_experimental
repeat_region   13978. .14043
                /note="homology = 75.80%, score = 23, counts = 6"
                /rpt_type=tandem
                /rpt_unit=ctctctccttt
                /evidence=not_experimental
repeat_region   14054. .14087
                /note="homology = 94.10%, score = 28, counts = 17"
                /rpt_type=tandem
                /rpt_unit=tg
                /evidence=not_experimental
exon            complement(15048. .15137)
                /note="FEXHB, score = 12.14%"
                /evidence=not_experimental
exon            complement(15049. .15138)
                /note="MZEF, score = 83.8%"
                /evidence=not_experimental
misc_feature    15192. .57359
                /note="Region: Cosmid IG0799"
exon            complement(15720. .15884)
                /note="GRAIL, score = 53.000%, comment = good"
                /evidence=not_experimental
repeat_region   16505. .16631
                /rpt_family="L1MA9"
                /evidence=not_experimental
repeat_region   16659. .16746
                /rpt_family="MER4A"
                /evidence=not_experimental
repeat_region   16798. .16851
                /rpt_family="MER4A"
                /evidence=not_experimental
repeat_region   complement(16851. .16910)
                /rpt_family="THE1B"
                /evidence=not_experimental
repeat_region   complement(16920. .16972)
                /rpt_family="THE1B"
                /evidence=not_experimental
exon            complement(16931. .16963)
                /note="FEXHB, score = 12.61%"
                /evidence=not_experimental
repeat_region   complement(17023. .17178)
                /rpt_family="THE1B"
                /evidence=not_experimental
repeat_region   complement(17252. .17279)
                /rpt_family="THE1BR"
                /evidence=not_experimental
repeat_region   complement(17282. .17495)
```

Query Match 92.8%; Score 5703; DB 11; Length 158898;
Best Local Similarity 93.6%; Pred. No. 0;
Matches 6146; Conservative 0; Mismatches 0; Indels 423; Gaps 2;

```
Qy       1 GTCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTAT 60
Db   97177 GTCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTAT 97118

Qy      61 GTCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAA 120
Db   97117 GTCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAA 97058

Qy     121 GTAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGCTGGCTTTTTCATGCAGACCCTTCAG 180
Db   97057 GTAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGCTGGCTTTTTCATGCAGACCCTTCAG 96998

Qy     181 TTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTCGTGTGAGTT 240
Db   96997 TTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTCGTGTGAGTT 96938

Qy     241 CTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTCCATTGTAGTGGGA 300
Db   96937 CTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTCCATTGTAGTGGGA 96878

Qy     301 GGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTCTGGAGGAAGTTA 360
Db   96877 GGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTCTGGAGGAAGTTA 96818

Qy     361 CAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAGTCTGAAAAGCAC 420
Db   96817 CAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAGTCTGAAAAGCAC 96758

Qy     421 AGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGCCACTGGTTTTCT 480
Db   96757 AGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGCCACTGGTTTTCT 96698

Qy     481 GACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTACACTTCAGCTCCC 540
Db   96697 GACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTACACTTCAGCTCCC 96638

Qy     541 AATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAGGAGCCAAGGGAC 600
Db   96637 AATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAGGAGCCAAGGGAC 96578

Qy     601 CTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACATCCTGACCAAGTT 660
Db   96577 CTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACATCCTGACCAAGTT 96518

Qy     661 CAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAGCCAGTCACCCAA 720
Db   96517 CAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAGCCAGTCACCCAA 96458

Qy     721 CCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAGGCAGAAAATCTG 780
Db   96457 CCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAGGCAGAAAATCTG 96398

Qy     781 CTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATGCTCATGTGGCTA 840
Db   96397 CTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATGCTCATGTGGCTA 96338

Qy     841 GAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCTTAAAAATACTTG 900
Db   96337 GAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCTTAAAAATACTTG 96278

Qy     901 CCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTTGGGAGCCTTGCT 960
Db   96277 CCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTTGGGAGCCTTGCT 96218

Qy     961 CTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAGCTTTTCCCGGAT 1020
```

```
Db  96217 CTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAGCTTTTCCCGGAT 96158

Qy   1021 AGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGGCTTTCAAGTCAC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  96157 AGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGGCTTTCAAGTCAC 96098

Qy   1081 TAGTGGTTCCGTTTAGTAGATGATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTACA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  96097 TAGTGGTTCCGTTTAGTAGATGATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTACA 96038

Qy   1141 AAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAGACCTCCTT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  96037 AAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAGACCTCCTT 95978

Qy   1201 GGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTGGAGACTAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95977 GGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTGGAGACTAG 95918

Qy   1261 TTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTCTCAAACTC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95917 TTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTCTCAAACTC 95858

Qy   1321 TTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCTCGGCGATT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95857 TTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCTCGGCGATT 95798

Qy   1381 AAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGATCCAGAGA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95797 AAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGATCCAGAGA 95738

Qy   1441 ATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGGCTTGCCCT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95737 ATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGGCTTGCCCT 95678

Qy   1501 TCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAGGAATTCACTGTCTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95677 TCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAGGAATTCACTGTCTT 95618

Qy   1561 ACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAACTCTCCCTGTTCTT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95617 ACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAACTCTCCCTGTTCTT 95558

Qy   1621 CTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTTTTTCCTTGGAACTG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95557 CTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTTTTTCCTTGGAACTG 95498

Qy   1681 TCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTAAACGATCAACATCAT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95497 TCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTAAACGATCAACATCAT 95438

Qy   1741 CATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTAGTTTATTTTTCTTCC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95437 CATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTAGTTTATTTTTCTTCC 95378

Qy   1801 CTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGTCCTCTGGACATGGTC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95377 CTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGTCCTCTGGACATGGTC 95318

Qy   1861 TATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCTGGTCAAAGAGGATAA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95317 TATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCTGGTCAAAGAGGATAA 95258

Qy   1921 GAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTGGTTCATCAGCCCCAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95257 GAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTGGTTCATCAGCCCCAG 95198

Qy   1981 ATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGAAGAAAGTGTGTGTTA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95197 ATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGAAGAAAGTGTGTGTTA 95138

Qy   2041 GCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGAGCGGAGAAGGTTCTT 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95137 GCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGAGCGGAGAAGGTTCTT 95078

Qy   2101 TTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAATAATAAATCTTCGTG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95077 TTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAATAATAAATCTTCGTG 95018

Qy   2161 CAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGGGTATAACTAATTAGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  95017 CAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGGGTATAACTAATTAGA 94958

Qy   2221 AGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTGATAAATACATTCTGG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94957 AGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTGATAAATACATTCTGG 94898

Qy   2281 CCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGAGTTCTATCCCAAAGC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94897 CCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGAGTTCTATCCCAAAGC 94838

Qy   2341 TATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTTGCCTTCTTCCAGAAG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94837 TATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTTGCCTTCTTCCAGAAG 94778

Qy   2401 AATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGAGTACGAAAGGCTGCT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94777 AATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGAGTACGAAAGGCTGCT 94718

Qy   2461 CTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGATCCACTTTCCAAAATA 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94717 CTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGATCCACTTTCCAAAATA 94658

Qy   2521 GGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAGCTGTTGCCTGACAGGA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94657 GGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAGCTGTTGCCTGACAGGA 94598

Qy   2581 GCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAGCTTGGATGGGCAGGGGC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94597 GCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAGCTTGGATGGGCAGGGGC 94538

Qy   2641 TAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAAAAGACGACCTAATTATA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94537 TAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAAAAGACGACCTAATTATA 94478

Qy   2701 GGCCTAGGAATTTTACAGTATTGCAACTGCAATGTGATGCTGAAAGTGGAAAATGATGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94477 GGCCTAGGAATTTTACAGTATTGCAACTGCAATGTGATGCTGAAAGTGGAAAATGATGTC 94418

Qy   2761 CTGGGCTCAGAGAAAAGCCCACACCAGCCTGGGAGTCATGATAGCAGCAGAGTGCTTGGG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94417 CTGGGCTCAGAGAAAAGCCCACACCAGCCTGGGAGTCATGATAGCAGCAGAGTGCTTGGG 94358

Qy   2821 GAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCTACAAAAGAAGATGCCAACTAGAGAT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94357 GAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCTACAAAAGAAGATGCCAACTAGAGAT 94298

Qy   2881 ATAGGTTGTCATCAGGTCCCGGAGGAGCCATGACCGTCTAGCTGAGAGCCATGACCAAGG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94297 ATAGGTTGTCATCAGGTCCCGGAGGAGCCATGACCGTCTAGCTGAGAGCCATGACCAAGG 94238

Qy   2941 ACACAATGTCCAAGTGACTGTGAGGACCTCAGTCTGCCCTGTGGATGTGTATGCCACAGA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94237 ACACAATGTCCAAGTGACTGTGAGGACCTCAGTCTGCCCTGTGGATGTGTATGCCACAGA 94178

Qy   3001 CCTGACTTCTGGAGGGCTGACTGAAATGTTCATTTTAAGCTTTTTCTTCTCTTTCCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94177 CCTGACTTCTGGAGGGCTGACTGAAATGTTCATTTTAAGCTTTTTCTTCTCTTTCCCTGA 94118

Qy   3061 AACACTCAGTTTGGGTTAGGGGTCATAGACTAAGACCAAAGAGTCCAGGGTTAGAATCTT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94117 AACACTCAGTTTGGGTTAGGGGTCATAGACTAAGACCAAAGAGTCCAGGGTTAGAATCTT 94058

Qy   3121 GGTGTAAAATTGCAGGCCATCTCAGGAAATCTGTGAGCAGATGGGATTGGCTTTGGGTAA 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  94057 GGTGTAAAATTGCAGGCCATCTCAGGAAATCTGTGAGCAGATGGGATTGGCTTTGGGTAA 93998
```

```
Qy   3181 GGTGCGTGTGGAAAATGTCAGTGGGAGCCGGGTCATGGTGGGCCTTTAGCATCAGATTCC 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  93997 GGTGCGTGTGGAAAATGTCAGTGGGAGCCGGGTCATGGTGGGCCTTTAGCATCAGATTCC 93938

Qy   3241 AGAGTGCAGATAGTCTGTATAGCTCATGTGAAACAGGGAGCCACCAAAACTTTGGGGAGC 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  93937 AGAGTGCAGATAGTCTGTATAGCTCATGTGAAACAGGGAGCCACCAAAACTTTGGGGAGC 93878

Qy   3301 AGGCTAGTGCCGGTTTTGACCACCTGTGGAGCAGTGCTCACTCACGAAGGCATTTTGCCA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  93877 AGGCTAGTGCCGGTTTTGACCACCTGTGGAGCAGTGCTCACTCACGAAGGCATTTTGCCA 93818

Qy   3361 TCACATGAATGTGCAGAAAGGAGGCCAAAAGCATTCTGTGCTTCTCCACCACAGCACAGA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  93817 TCACATGAATGTGCAGAAAGGAGGCCAAAAGCATTCTGTGCTTCTCCACCACAGCACAGA 93758

Qy   3421 CTTCCCTAGTCTCATTTGCTGAGAGTAGACATTCTGAGGGCCAGCAGTGCAGGTGTGATG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  93757 CTTCCCTAGTCTCATTTGCTGAGAGTAGACATTCTGAGGGCCAGCAGTGCAGGTGTGATG 93698

Qy   3481 TGCCTCAGAGGGTATGAAGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGAT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  93697 TGCCTCAGAGGGTATGAAGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGAT 93638

Qy   3541 ATCTAGAAGGCTAATTGATTTTTTCACTTTCACCTGACTCTCTTGCCAACCTGCAGAGAC 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  93637 ATCTAGAAGGCTAATTGATTTTTTCACTTTCACCTGACTCTCTTGCCAACCTGCAGAGAC 93578

Qy   3601 AGACATTGGGTGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCTT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  93577 AGACATTGGGTGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCTT 93518

Qy   3661 AGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCTTCTGGTCCTA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  93517 AGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCTTCTGGTCCTA 93458

Qy   3721 TTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGTGAGCTGAAAA 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  93457 TTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGTGAGCTGAAAA 93398

Qy   3781 ATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCACTGTAATGCA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  93397 ATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCACTGTAATGCA 93338

Qy   3841 GTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  93337 GTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAG 93278

Qy   3901 CAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  93277 CAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCT 93218

Qy   3961 CTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCT------ 4015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||      
Db  93217 CTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGTAA 93158

Qy   4015 ------------------------------------------------------------ 4015

Db  93157 GAGGAGAAACAGGTATACGCATAGGCACATGGCTGGGAGTTGGCTGGGCCAGGGCAGAGT 93098

Qy   4015 ------------------------------------------------------------ 4015

Db  93097 TGCCTTGTCATGGAGTCTTTTAACCAATGTCGCACATAGGTCAGGAGCTGAGCCCATCAC 93038

Qy   4015 --------------AGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCT 4060
                         ||||||||||||||||||||||||||||||||||||||||||||||
Db  93037 TCTTGTGCTCTTGCAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCT 92978

Qy   4061 CGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGC 4120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92977 CGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGC 92918

Qy   4121 TTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAAC 4180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92917 TTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAAC 92858

Qy   4181 CAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCAT---------------------- 4217
          ||||||||||||||||||||||||||||||||||||                      
Db  92857 CAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATGTATGAGCTGGGTATGGGAGTGGT 92798

Qy   4217 ------------------------------------------------------------ 4217

Db  92797 GGCAAGGCTTTGGAGTGTAGAGACATGCTAGCAAGGGTACTGGGGTTATGGCACATGGGT 92738

Qy   4217 ------------------------------------------------------------ 4217

Db  92737 GGTCAGCTTGCTGAGTGATGGAATGTTACCCAGGGTGGTGGCGGGGTTGAATCAACTTCC 92678

Qy   4217 ------------------------------------------------------------ 4217

Db  92677 TGATGTAATGGTGAGAAGTTGGAGGAGAGAAGCCAAGATATGGTGTGCCAAAGACAGTTT 92618

Qy   4217 ------------------------------------------------------------ 4217

Db  92617 CCAGAAAATCCGGAGGCAGCACTTAGACTTGGGTTATCTTCCCTTGACTTTTCCCCACTT 92558

Qy   4217 ----------------------CCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACG 4257
                                 ||||||||||||||||||||||||||||||||||||||||
Db  92557 CTTTCCTTGTCCATTTTAGCCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACG 92498

Qy   4258 TTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGA 4317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92497 TTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGA 92438

Qy   4318 GGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAG 4377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92437 GGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAG 92378

Qy   4378 CCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTT 4437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92377 CCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTT 92318

Qy   4438 TAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCT 4497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92317 TAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCT 92258

Qy   4498 CTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTT 4557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92257 CTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTT 92198

Qy   4558 CTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCT 4617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92197 CTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCT 92138

Qy   4618 GTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGA 4677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92137 GTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGA 92078

Qy   4678 AAGCAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGC 4737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92077 AAGCAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGC 92018

Qy   4738 TTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCT 4797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92017 TTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCT 91958

Qy   4798 CAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCC 4857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  91957 CAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCC 91898

Qy   4858 GTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTA 4917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  91897 GTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTA 91838

Qy   4918 AGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTGCATTTTT 4977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db  91837 AGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTGCATTTTT 91778

Qy   4978 CCAGAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAG 5037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  91777 CCAGAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAG 91718

Qy   5038 TGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATA 5097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  91717 TGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATA 91658

Qy   5098 ACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCT 5157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  91657 ACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCT 91598

Qy   5158 GCTACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGG 5217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  91597 GCTACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGG 91538

Qy   5218 GCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCT 5277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  91537 GCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCT 91478

Qy   5278 CTCCTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGT 5337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  91477 CTCCTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGT 91418

Qy   5338 ATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTT 5397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  91417 ATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTT 91358

Qy   5398 CTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCC 5457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  91357 CTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCC 91298

Qy   5458 AGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAAC 5517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  91297 AGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAAC 91238

Qy   5518 AGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTT 5577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  91237 AGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTT 91178

Qy   5578 GCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCAC 5637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  91177 GCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCAC 91118

Qy   5638 AATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTT 5697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  91117 AATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTT 91058

Qy   5698 GACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTC 5757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  91057 GACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTC 90998

Qy   5758 TTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTC 5817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  90997 TTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTC 90938

Qy   5818 ACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGC 5877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  90937 ACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGC 90878

Qy   5878 TCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAA 5937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  90877 TCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAA 90818

Qy   5938 TGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCA 5997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  90817 TGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCA 90758

Qy   5998 AATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTAT 6057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  90757 AATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTAT 90698

Qy   6058 ATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATC 6117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  90697 ATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATC 90638

Qy   6118 TACTTTTTGTCACCATCATCTGAAATGGG 6146
          |||||||||||||||||||||||||||||
Db  90637 TACTTTTTGTCACCATCATCTGAAATGGG 90609


RESULT   3
HSGABRE3
LOCUS       HSGABRE3     9631 bp    DNA             PRI       03-JAN-1998
DEFINITION  Human GABA-A receptor epsilon subunit (GABRE) gene, exons 4-9, and
            complete cds.
ACCESSION   U92283
VERSION     U92283.1  GI:2735347
KEYWORDS    .
SEGMENT     3 of 3
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9631)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 9631)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .9631
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq28"
     mRNA            join(U92281.1:<162. .256,U92282.1:64. .281,
                     U92282.1:730. .797,301. .521,1577. .1659,2966. .3103,
                     7082. .7234,7375. .7574,7858. .>9631)
                     /gene="GABRE"
                     /product="GABA-A receptor epsilon subunit"
     gene            order(U92281.1:<162. .556,U92282.1:1. .1097,1. .>9631)
                     /gene="GABRE"
     CDS             join(U92281.1:201. .256,U92282.1:64. .281,U92282.1:730. .797,
                     301. .521,1577. .1659,2966. .3103,7082. .7234,7375. .7574,
                     7858. .8241)
                     /gene="GABRE"
                     /codon_start=1
                     /product="GABA-A receptor epsilon subunit"
                     /protein_id="AAB94645.1"
                     /db_xref="GI:2735349"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIS
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRR
                     FGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV
                     SYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRA
                     RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWC
                     KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
     intron          <1. .300
                     /gene="GABRE"
     exon            301. .521
                     /gene="GABRE"
     intron          522. .1576
                     /gene="GABRE"
     repeat_region   1095. .1134
                     /rpt_type=tandem
                     /rpt_unit=ttttg
```

```
     exon            1577. .1659
                     /gene="GABRE"
     intron          1660. .2965
                     /gene="GABRE"
     exon            2966. .3103
                     /gene="GABRE"
     intron          3104. .7081
                     /gene="GABRE"
     stem_loop       3230. .3314
                     /gene="GABRE"
     stem_loop       4283. .4365
                     /gene="GABRE"
     exon            7082. .7234
                     /gene="GABRE"
     intron          7235. .7374
                     /gene="GABRE"
     exon            7375. .7574
                     /gene="GABRE"
     intron          7575. .7857
                     /gene="GABRE"
     exon            7858. .>9631
                     /gene="GABRE"
     3'UTR           8242. .>9631
                     /gene="GABRE"
BASE COUNT     2267 a    2381 c    2249 g    2734 t
ORIGIN
```

Query Match 90.2%; Score 5542.2; DB 11; Length 9631;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 5987; Conservative 0; Mismatches 3; Indels 423; Gaps 2;

```
Qy       1 GTCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTAT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3219 GTCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTAT 3278

Qy      61 GTCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3279 GTCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAA 3338

Qy     121 GTAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGCTGGCTTTTTCATGCAGACCCTTCAG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3339 GTAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGCTGGCTTTTTCATGCAGACCCTTCAG 3398

Qy     181 TTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTCGTGTGAGTT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3399 TTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTCGTGTGAGTT 3458

Qy     241 CTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTCCATTGTAGTGGGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3459 CTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTCCATTGTAGTGGGA 3518

Qy     301 GGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTCTGGAGGAAGTTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3519 GGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTCTGGAGGAAGTTA 3578

Qy     361 CAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAGTCTGAAAAGCAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3579 CAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAGTCTGAAAAGCAC 3638

Qy     421 AGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGCCACTGGTTTTCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3639 AGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGCCACTGGTTTTCT 3698

Qy     481 GACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTACACTTCAGCTCCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3699 GACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTACACTTCAGCTCCC 3758

Qy     541 AATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAGGAGCCAAGGGAC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3759 AATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAGGAGCCAAGGGAC 3818

Qy     601 CTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACATCCTGACCAAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3819 CTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACATCCTGACCAAGTT 3878

Qy     661 CAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAGCCAGTCACCCAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3879 CAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAGCCAGTCACCCAA 3938

Qy     721 CCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAGGCAGAAAATCTG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3939 CCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAGGCAGAAAATCTG 3998

Qy     781 CTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATGCTCATGTGGCTA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3999 CTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATGCTCATGTGGCTA 4058

Qy     841 GAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCTTAAAAATACTTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4059 GAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCTTAAAAATACTTG 4118

Qy     901 CCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTTGGGAGCCTTGCT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4119 CCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTTGGGAGCCTTGCT 4178

Qy     961 CTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAGCTTTTCCCGGAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4179 CTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAGCTTTTCCCGGAT 4238

Qy    1021 AGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGGCTTTCAAGTCAC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4239 AGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGGCTTTCAAGTCAC 4298

Qy    1081 TAGTGGTTCCGTTTAGTAGATGATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTACA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4299 TAGTGGTTCCGTTTAGTAGATGATTGTGCATTGTTTCAAAATGGTGCCCTAGTGACTACA 4358

Qy    1141 AAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAGACCTCCTT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4359 AAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAGACCTCCTT 4418

Qy    1201 GGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTGGAGACTAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4419 GGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTGGAGACTAG 4478

Qy    1261 TTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTCTCAAACTC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4479 TTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTCTCAAACTC 4538

Qy    1321 TTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCTCGGCGATT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4539 TTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCTCGGCGATT 4598

Qy    1381 AAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGATCCAGAGA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4599 AAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGATCCAGAGA 4658

Qy    1441 ATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGGCTTGCCCT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4659 ATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGGCTTGCCCT 4718

Qy    1501 TCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAGGAATTCACTGTCTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4719 TCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAGGAATTCACTGTCTT 4778

Qy    1561 ACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAACTCTCCCTGTTCTT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4779 ACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAACTCTCCCTGTTCTT 4838

Qy    1621 CTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTTTTTCCTTGGAACTG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4839 CTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTTTTTCCTTGGAACTG 4898

Qy    1681 TCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTAAACGATCAACATCAT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   4899 TCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTAAACGATCAACATCAT 4958

Qy   1741 CATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTAGTTTATTTTTCTTCC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4959 CATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTAGTTTATTTTTCTTCC 5018

Qy   1801 CTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGTCCTCTGGACATGGTC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5019 CTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGTCCTCTGGACATGGTC 5078

Qy   1861 TATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCTGGTCAAAGAGGATAA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5079 TATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCTGGTCAAAGAGGATAA 5138

Qy   1921 GAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTGGTTCATCAGCCCCAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5139 GAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTGGTTCATCAGCCCCAG 5198

Qy   1981 ATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGAAGAAAGTGTGTGTTA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5199 ATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGAAGAAAGTGTGTGTTA 5258

Qy   2041 GCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGAGCGGAGAAGGTTCTT 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5259 GCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGAGCGGAGAAGGTTCTT 5318

Qy   2101 TTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAATAATAAATCTTCGTG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5319 TTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAATAATAAATCTTCGTG 5378

Qy   2161 CAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGGGTATAACTAATTAGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5379 CAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGGGTATAACTAATTAGA 5438

Qy   2221 AGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTGATAAATACATTCTGG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5439 AGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTGATAAATACATTCTGG 5498

Qy   2281 CCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGAGTTCTATCCCAAAGC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5499 CCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGAGTTCTATCCCAAAGC 5558

Qy   2341 TATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTTGCCTTCTTCCAGAAG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5559 TATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTTGCCTTCTTCCAGAAG 5618

Qy   2401 AATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGAGTACGAAAGGCTGCT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5619 AATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGAGTACGAAAGGCTGCT 5678

Qy   2461 CTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGATCCACTTTCCAAAATA 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5679 CTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGATCCACTTTCCAAAATA 5738

Qy   2521 GGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAGCTGTTGCCTGACAGGA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5739 GGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAGCTGTTGCCTGACAGGA 5798

Qy   2581 GCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAGCTTGGATGGGCAGGGGC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5799 GCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAGCTTGGATGGGCAGGGGC 5858

Qy   2641 TAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAAAAGACGACCTAATTATA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5859 TAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAAAAGACGACCTAATTATA 5918

Qy   2701 GGCCTAGGAATTTTACAGTATTGCAACTGCAATGTGATGCTGAAAGTGGAAAATGATGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5919 GGCCTAGGAATTTTACAGTATTGCAACTGCAATGTGATGCTGAAAGTGGAAAATGATGTC 5978

Qy   2761 CTGGGCTCAGAGAAAAGCCCACACCAGCCTGGGAGTCATGATAGCAGCAGAGTGCTTGGG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5979 CTGGGCTCAGAGAAAAGCCCACACCAGCCTGGGAGTCATGATAGCAGCAGAGTGCTTGGG 6038

Qy   2821 GAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCTACAAAAGAAGATGCCAACTAGAGAT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6039 GAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCTACAAAAGAAGATGCCAACTAGAGAT 6098

Qy   2881 ATAGGTTGTCATCAGGTCCCGGAGGAGCCATGACCGTCTAGCTGAGAGCCATGACCAAGG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6099 ATAGGTTGTCATCAGGTCCCGGAGGAGCCATGACCGTCTAGCTGAGAGCCATGACCAAGG 6158

Qy   2941 ACACAATGTCCAAGTGACTGTGAGGACCTCAGTCTGCCCTGTGGATGTGTATGCCACAGA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6159 ACACAATGTCCAAGTGACTGTGAGGACCTCAGTCTGCCCTGTGGATGTGTATGCCACAGA 6218

Qy   3001 CCTGACTTCTGGAGGGCTGACTGAAATGTTCATTTTAAGCTTTTTCTTCTCTTTCCCTGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6219 CCTGACTTCTGGAGGGCTGACTGAAATGTTCATTTTAAGCTTTTTCTTCTCTTTCCCTGA 6278

Qy   3061 AACACTCAGTTTGGGTTAGGGGTCATAGACTAAGACCAAAGAGTCCAGGGTTAGAATCTT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6279 AACACTCAGTTTGGGTTAGGGGTCATAGACTAAGACCAAAGAGTCCAGGGTTAGAATCTT 6338

Qy   3121 GGTGTAAAATTGCAGGCCATCTCAGGAAATCTGTGAGCAGATGGGATTGGCTTTGGGTAA 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6339 GGTGTAAAATTGCAGGCCATCTCAGGAAATCTGTGAGCAGATGGGATTGGCTTTGGGTAA 6398

Qy   3181 GGTGCGTGTGGAAAATGTCAGTGGGAGCCGGGTCATGGTGGGCCTTTAGCATCAGATTCC 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6399 GGTGCGTGTGGAAAATGTCAGTGGGAGCCGGGTCATGGTGGGCCTTTAGCATCAGATTCC 6458

Qy   3241 AGAGTGCAGATAGTCTGTATAGCTCATGTGAAACAGGGAGCCACCAAAACTTTGGGGAGC 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6459 AGAGTGCAGATAGTCTGTATAGCTCATGTGAAACAGGGAGCCACCAAAACTTTGGGGAGC 6518

Qy   3301 AGGCTAGTGCCGGTTTTGACCACCTGTGGAGCAGTGCTCACTCACGAAGGCATTTTGCCA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6519 AGGCTAGTGCCGGTTTTGACCACCTGTGGAGCAGTGCTCACTCACGAAGGCATTTTGCCA 6578

Qy   3361 TCACATGAATGTGCAGAAAGGAGGCCAAAAGCATTCTGTGCTTCTCCACCACAGCACAGA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6579 TCACATGAATGTGCAGAAAGGAGGCCAAAAGCATTCTGTGCTTCTCCACCACAGCACAGA 6638

Qy   3421 CTTCCCTAGTCTCATTTGCTGAGAGTAGACATTCTGAGGGCCAGCAGTGCAGGTGTGATG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6639 CTTCCCTAGTCTCATTTGCTGAGAGTAGACATTCTGAGGGCCAGCAGTGCAGGTGTGATG 6698

Qy   3481 TGCCTCAGAGGGTATGAAGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGAT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6699 TGCCTCAGAGGGTATGAAGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGAT 6758

Qy   3541 ATCTAGAAGGCTAATTGATTTTTTCACTTTCACCTGACTCTCTTGCCAACCTGCAGAGAC 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6759 ATCTAGAAGGCTAATTGATTTTTTCACTTTCACCTGACTCTCTTGCCAACCTGCAGAGAC 6818

Qy   3601 AGACATTGGGTGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCTT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6819 AGACATTGGGTGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCTT 6878

Qy   3661 AGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCTTCTGGTCCTA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6879 AGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCTTCTGGTCCTA 6938

Qy   3721 TTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGTGAGCTGAAAA 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6939 TTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGTGAGCTGAAAA 6998

Qy   3781 ATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCACTGTAATGCA 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6999 ATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCACTGTAATGCA 7058

Qy   3841 GTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7059 GTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAG 7118
```

```
Qy   3901 CAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7119 CAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCT 7178

Qy   3961 CTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCT------ 4015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7179 CTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGTAA 7238

Qy   4015 ------------------------------------------------------------ 4015

Db   7239 GAGGAGAAACAGGTATACGCATAGGCACATGGCTGGGAGTTGGCTGGGCCAGGGCAGAGT 7298

Qy   4015 ------------------------------------------------------------ 4015

Db   7299 TGCCTTGTCATGGAGTCTTTTAACCAATGTCGCACATAGGTCAGGAGCTGAGCCCATCAC 7358

Qy   4015 -------------AGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCT 4060
                       ||||||||||||||||||||||||||||||||||||||||||||||
Db   7359 TCTTGTGCTCTTGCAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCT 7418

Qy   4061 CGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGC 4120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7419 CGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGC 7478

Qy   4121 TTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAAC 4180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7479 TTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAAC 7538

Qy   4181 CAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCAT---------------------- 4217
          |||||||||||||||||||||||||||||||||
Db   7539 CAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATGTATGAGCTGGGTATGGGAGTGGT 7598

Qy   4217 ------------------------------------------------------------ 4217

Db   7599 GGCAAGGCTTTGGAGTGTAGAGACATGCTAGCAAGGGTACTGGGGTTATGGCACATGGGT 7658

Qy   4217 ------------------------------------------------------------ 4217

Db   7659 GGTCAGCTTGCTGAGTGATGGAATGTTACCCAGGGTGGTGGCGGGGTTGAATCAACTTCC 7718

Qy   4217 ------------------------------------------------------------ 4217

Db   7719 TGATGTAATGGTGAGAAGTTGGAGGAGAGAAGCCAAGATATGGTGTGCCAAAGACAGTTT 7778

Qy   4217 ------------------------------------------------------------ 4217

Db   7779 CCAGAAAATCCGGAGGCAGCACTTAGACTTGGGTTATCTTCCCTTGACTTTTCCCCACTT 7838

Qy   4217 -------------------CCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACG 4257
                              |||||||||||||||||||||||||||||||||||||||||
Db   7839 CTTTCCTTGTCCATTTTAGCCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACG 7898

Qy   4258 TTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGA 4317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7899 TTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGA 7958

Qy   4318 GGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAG 4377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7959 GGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAG 8018

Qy   4378 CCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTT 4437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8019 CCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTT 8078

Qy   4438 TAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCT 4497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8079 TAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCT 8138

Qy   4498 CTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTT 4557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8139 CTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTT 8198

Qy   4558 CTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCT 4617
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8199 CTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCT 8258

Qy   4618 GTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGA 4677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8259 GTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGA 8318

Qy   4678 AAGCAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGC 4737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8319 AAGCAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGC 8378

Qy   4738 TTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCT 4797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8379 TTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCT 8438

Qy   4798 CAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCC 4857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8439 CAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCC 8498

Qy   4858 GTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTA 4917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8499 GTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTA 8558

Qy   4918 AGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTGCATTTTT 4977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8559 AGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTGCATTTTT 8618

Qy   4978 CCAGAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAG 5037
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   8619 CCAGAAGCCCACTATTGCCTTTGCAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAG 8678

Qy   5038 TGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATA 5097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8679 TGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATA 8738

Qy   5098 ACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCT 5157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8739 ACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCT 8798

Qy   5158 GCTACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGG 5217
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   8799 GCTACCCCTTTCTCTGCAGTTAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGG 8858

Qy   5218 GCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCT 5277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8859 GCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCT 8918

Qy   5278 CTCCTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGT 5337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8919 CTCCTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGT 8978

Qy   5338 ATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTT 5397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8979 ATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTT 9038

Qy   5398 CTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCC 5457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9039 CTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCC 9098

Qy   5458 AGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAAC 5517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9099 AGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAAC 9158

Qy   5518 AGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTT 5577
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9159 AGGCATTGCTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTT 9218

Qy   5578 GCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCAC 5637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9219 GCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCAC 9278

Qy   5638 AATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTT 5697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    9279 AATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTT 9338

Qy    5698 GACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTC 5757
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    9339 GACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTC 9398

Qy    5758 TTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTC 5817
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    9399 TTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTC 9458

Qy    5818 ACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGC 5877
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    9459 ACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGC 9518

Qy    5878 TCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAA 5937
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    9519 TCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAA 9578

Qy    5938 TGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCC 5990
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    9579 TGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCC 9631


RESULT   4
HSY09764
LOCUS       HSY09764    10897 bp    DNA             PRI       31-OCT-1997
DEFINITION  Homo sapiens GABRE gene, exon 2-8.
ACCESSION   Y09764
VERSION     Y09764.1  GI:2285959
KEYWORDS    GABA receptor; GABRE gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10897)
  AUTHORS   Wilke,K., Gaul,R., Klauck,S.M. and Poustka,A.
  TITLE     A gene in human chromosome band Xq28 (GABRE) defines a putative new
            subunit class of the GABAA neurotransmitter receptor
  JOURNAL   Genomics 45 (1), 1-10 (1997)
  MEDLINE   97480709
REFERENCE   2  (bases 1 to 10897)
  AUTHORS   Wilke,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1996) K. Wilke, Deutsches Krebsforschungszentrum,
            Abteilung Molekulare Genomanalyse (840), Im Neuenheimer Feld 280,
            D-69120 Heidelberg, FRG
FEATURES             Location/Qualifiers
     source          1. .10897
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="q28"
                     /clone="cosmid Qc11C8"
     gene            1334. .10897
                     /gene="GABRE"
     exon            1334. .1551
                     /gene="GABRE"
                     /number=2
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            2000. .2288
                     /gene="GABRE"
                     /number=3
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            3346. .3428
                     /gene="GABRE"
                     /number=4
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            4736. .4873
                     /gene="GABRE"
                     /number=5
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            8163. .8315
                     /gene="GABRE"
                     /number=6
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            8456. .8655
                     /gene="GABRE"
                     /number=7
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            8939. .10897
                     /gene="GABRE"
                     /number=8
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
BASE COUNT     2630 a   2703 c   2465 g   3099 t
ORIGIN


  Query Match             82.9%;  Score 5096;  DB 10;  Length 10897;
  Best Local Similarity   92.7%;  Pred. No. 0;
  Matches 5559;  Conservative    0;  Mismatches   15;  Indels  424;  Gaps    3;

Qy     572 TAGGTGACCTGAATGAGGAGCCAAGGGACCTCCCCAGGGTAGCTCCCAGAGCAACCCTGG 631
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4871 TTGGTGACCTGAATGAGGAGCCAAGGGACCTCCCCAGGGTAGCTCCCAGAGCAACCCTGG 4930

Qy     632 AAACACTCTTCACACATCCTGACCAAGTTCAGGGCAGTGAAGGCACTGCCCTCATCGTTT 691
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4931 AAACACTCTTCACACATCCTGACCAAGTTCAGGGCAGTGAAGGCACTGCCCTCATCGTTT 4990

Qy     692 CCAGAATGTGGATGGAGCCAGTCACCCAACCAGCCATTTGTCGTGAGAGGCATCTTGTTC 751
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4991 CCAGAATGTGGATGGAGCCAGTCACCCAACCAGCCATTTGTCGTGAGAGGCATCTTGTTC 5050

Qy     752 TGCTACCATGTGACTAGGCAGAAAATCTGCTTTTGTTTCATTTATTGAGTCAGTCTCTGG 811
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5051 TGCTACCATGTGACTAGGCAGAAAATCTGCTTTTGTTTCATTTATTGAGTCAGTCTCTGG 5110

Qy     812 ATGAGGGAAAGCTCATGCTCATGTGGCTAGAGCTTTGCTTGCACAGTATTAGGCAGGGGC 871
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5111 ATGAGGGAAAGCTCATGCTCATGTGGCTAGAGCTTTGCTTGCACAGTATTAGGCAGGGGC 5170

Qy     872 AGAGGGCTGGGCTACCTTAAAAATACTTGCCCTTTTTCTTGGGGACTCTGGGGAAGCGGT 931
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    5171 AGAGGGCTGGGCTACCTAAAAAATACTTGCCCTTTTTCTTGGGGACTCTGGGGAAGCGGT 5230

Qy     932 TTTACTACCTTTGACTTGGGAGCCTTGCTCTTCTGCCAGCTAACCATGGGCCTGCCTCTT 991
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5231 TTTACTACCTTTGACTTGGGAGCCTTGCTCTTCTGCCAGCTAACCATGGGCCTGCCTCTT 5290

Qy     992 GGTTTTCTGCACCTCAGCTTTTCCCGGATAGGTGGGGACCCATCATCAAAAGTGACAGAG 1051
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5291 GGTTTTCTGCACCTCAGCTTTTCCCGGATAGGTGGGGACCCATCATCAAAAGTGACAGAG 5350

Qy    1052 AAGATAAGGCCCAGGGGCTTTCAAGTCACTAGTGGTTCCGTTTAGTAGATGATTGTGCAT 1111
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5351 AAGATAAGGCCCAGGGGCTTTCAAGTCACTAGTGGTTCCGTTTAGTAGATGATTGTGCAT 5410

Qy    1112 TGTTTCAAAATGGTGCCCTAGTGACTACAAAGCCCCAGAGCCAGCATCATCATCAAAGCA 1171
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5411 TGTTTCAAAATGGTGCCCTAGTGACTACAAAGCCCCAGAGCCAGCATCATCATCAAAGCA 5470

Qy    1172 ATGACAGTAGGTAAGCACCAGACCTCCTTGGGAGTGAGGAGGATTCTTGAGGAGAAAAGA 1231
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5471 ATGACAGTAGGTAAGCACCAGACCTCCTTGGGAGTGAGGAGGATTCTTGAGGAGAAAAGA 5530

Qy    1232 GGTCTTCTTTCTCCTCTGCTGGAGACTAGTTGATCTGGAGACGTGGTTCCTTCAATGTCA 1291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5531 GGTCTTCTTTCTCCTCTGCTGGAGACTAGTTGATCTGGAGACGTGGTTCCTTCAATGTCA 5590
```

```
Qy   1292 GAGTTATCTTTGGGACTGGTCTCAAACTCTTCCAGTTGGGCCCTGGGGCAGGTCTCTCCA 1351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5591 GAGTTATCTTTGGGACTGGTCTCAAACTCTTCCAGTTGGGCCCTGGGGCAGGTCTCTCCA 5650

Qy   1352 TCTGGAGCATACTTACGTGCTCGGCGATTAAGGGTTCAGAATGCAGTGGTAGCCTGCTAC 1411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5651 TCTGGAGCATACTTACGTGCTCGGCGATTAAGGGTTCAGAATGCAGTGGTAGCCTGCTAC 5710

Qy   1412 TCTGGCCATCTTGGACCTTGATCCAGAGAATCTCTGCTTCAGGAGCTTCTAAGAGAGTCC 1471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5711 TCTGGCCATCTTGGACCTTGATCCAGAGAATCTCTGCTTCAGGAGCTTCTAAGAGAGTCC 5770

Qy   1472 AGCCCTGCCTCCAGAGAGAGGCTTGCCCTTCACTGATGGCTGTGGAGCCTCTGATGGAAT 1531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5771 AGCCCTGCCTCCAGAGAGAGGCTTGCCCTTCACTGATGGCTGTGGAGCCTCTGATGGAAT 5830

Qy   1532 ATTATTGCTGGTCAGGAATTCACTGTCTTACAAGGAGGTTTCCTTCTTCTCTAGACAGTT 1591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5831 ATTATTGCTGGTCAGGAATTCACTGTCTTACAAGGAGGTTTCCTTCTTCTCTAGACAGTT 5890

Qy   1592 CTGTTCATCAAAAAACTCTCCCTGTTCTTCTGAAATTGGAGTCTCTGGAAGTTCCACACA 1651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5891 CTGTTCATCAAAAAACTCTCCCTGTTCTTCTGAAATTGGAGTCTCTGGAAGTTCCACACA 5950

Qy   1652 TTAAGCTTAGTTCTTTTTCCTTGGAACTGTCCAGGTTACATTAGTCCAGCCACTGTTTCA 1711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5951 TTAAGCTTAGTTCTTTTTCCTTGGAACTGTCCAGGTTACATTAGTCCAGCCACTGTTTCA 6010

Qy   1712 CAGGACCGAGATTAAACGATCAACATCATCATTCCCGGCATGGATCATAGTCTGTTGTAG 1771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6011 CAGGACCGAGATTAAACGATCAACATCATCATTCCCGGCATGGATCATAGTCTGTTGTAG 6070

Qy   1772 TCTACATAGCCCTAGTTTATTTTTCTTCCCTTATTCTTCAAAGCTTTGGGTCCATTCATT 1831
          ||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db   6071 TCTACATAGCCCTAGTTTATTTTTCTTCCCTTATTCTTCAAAGGTGGGGGTCCATTCATT 6130

Qy   1832 CTTCTAGTCCCAGTCCTCTGGACATGGTCTATTTAATTGTGTCCCTCTGACACTGCAGTG 1891
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   6131 CTTCTAGTCCCAGTCCTCTGGACATGGTCTATTTAATTGTGTCCCTCTGACACTGCAATG 6190

Qy   1892 ACCAACCATGATCTGGTCAAAGAGGATAAGAGTTTGAGCAGAAAACCATCTTTAGCATAT 1951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6191 ACCAACCATGATCTGGTCAAAGAGGATAAGAGTTTGAGCAGAAAACCATCTTTAGCATAT 6250

Qy   1952 ATTTTTTTGCTTTGGTTCATCAGCCCCAGATATATTGTTTTCCTTACCCGTGCTTCTCTC 2011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6251 ATTTTTTTGCTTTGGTTCATCAGCCCCAGATATATTGTTTTCCTTACCCGTGCTTCTCTC 6310

Qy   2012 ACTCCTCAAGAAGAAGAAAGTGTGTGTTAGCATCTTTCTCTTGTCCTTCAAGACAAATTG 2071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6311 ACTCCTCAAGAAGAAGAAAGTGTGTGTTAGCATCTTTCTCTTGTCCTTCAAGACAAATTG 6370

Qy   2072 GCATCTCTTGACGAGCGGAGAAGGTTCTTTTTTGGCCAGAATAAATAAAATTAAAATAGA 2131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6371 GCATCTCTTGACGAGCGGAGAAGGTTCTTTTTTGGCCAGAATAAATAAAATTAAAATAGA 6430

Qy   2132 ATCATCCAACAGAATAATAAATCTTCGTGCAACAAGAATATATTATATAAACCCAGCAAT 2191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6431 ATCATCCAACAGAATAATAAATCTTCGTGCAACAAGAATATATTATATAAACCCAGCAAT 6490

Qy   2192 TTTGCAGGGCCTGGGTATAACTAATTAGAAGTGTCTTAAATTGCAGTCAAGATCCCACGG 2251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6491 TTTGCAGGGCCTGGGTATAACTAATTAGAAGTGTCTTAAATTGCAGTCAAGATCCCACGG 6550

Qy   2252 CAAGAGGACTTTTGATAAATACATTCTGGCCAGTAGGCAAGTGCGAGGGTGGTCCGTGCA 2311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6551 CAAGAGGACTTTTGATAAATACATTCTGGCCAGTAGGCAAGTGCGAGGGTGGTCCGTGCA 6610

Qy   2312 GCAGCTCTGGAGGAGTTCTATCCCAAAGCTATACTCAACACACAGGTTTCCCACTGACAA 2371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6611 GCAGCTCTGGAGGAGTTCTATCCCAAAGCTATACTCAACACACAGGTTTCCCACTGACAA 6670

Qy   2372 CAGGTCGCTCCCTTGCCTTCTTCCAGAAGAATCTGAGAAGCTTTGCTCCTTGAGTTTCAG 2431
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6671 CAGGTCGCTCCCTTGCCTTCTTCCAGAAGAATCTGAGAAGCTTTGCTCCTTGAGTTTCAG 6730

Qy   2432 TGCTGCCAAGGTGAGTACGAAAGGCTGCTCTTCTCATTCAGCTCCAGCCCACCCAGACCT 2491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6731 TGCTGCCAAGGTGAGTACGAAAGGCTGCTCTTCTCATTCAGCTCCAGCCCACCCAGACCT 6790

Qy   2492 GCTGGGCAGTTGATCCACTTTCCAAAATAGGAGGACACACGGACAGGTTAGTGTTCTGGT 2551
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   6791 GCTGGGCAGTTGATCCACTTTCCCAAATAGGAGGACACACGGACAGGTTAGTGTTCTGGT 6850

Qy   2552 CTGCTTTACAAAGCTGTTGCCTGACAGGAGCAAGAGTTGCTGAGTGTCTGCTGGGTTCCA 2611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6851 CTGCTTTACAAAGCTGTTGCCTGACAGGAGCAAGAGTTGCTGAGTGTCTGCTGGGTTCCA 6910

Qy   2612 GGCTGTTCTGAGCTTGGATGGGCAGGGGCTAAGCCACAGGGCCTGCATGAGCCCTGCCTT 2671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6911 GGCTGTTCTGAGCTTGGATGGGCAGGGGCTAAGCCACAGGGCCTGCATGAGCCCTGCCTT 6970

Qy   2672 GAAGGGACTTAAAAGACGACCTAATTATAGGCCTAGGAATTTTACAGTATTGCAACTGCA 2731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6971 GAAGGGACTTAAAAGACGACCTAATTATAGGCCTAGGAATTTTACAGTATTGCAACTGCA 7030

Qy   2732 ATGTGATGCTGAAAGTGGAAAATGATGTCCTGGGCTCAGAGAAAAGCCCACACCAGCCTG 2791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7031 ATGTGATGCTGAAAGTGGAAAATGATGTCCTGGGCTCAGAGAAAAGCCCACACCAGCCTG 7090

Qy   2792 GGAGTCATGATAGCAGCAGAGTGCTTGGGGAGGGTGTGTCAGAGCATAAAGCAGCATGAA 2851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7091 GGAGTCATGATAGCAGCAGAGTGCTTGGGGAGGGTGTGTCAGAGCATAAAGCAGCATGAA 7150

Qy   2852 TGCTACAAAAGAAGATGCCAACTAGAGATATAGGTTGTCATCAGGTCCCGGAGGAGCCAT 2911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7151 TGCTACAAAAGAAGATGCCAACTAGAGATATAGGTTGTCATCAGGTCCCGGAGGAGCCAT 7210

Qy   2912 GACCGTCTAGCTGAGAGCCATGACCAAGGACACAATGTCCAAGTGACTGTGAGGACCTCA 2971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7211 GACCGTCTAGCTGAGAGCCATGACCAAGGACACAATGTCCAAGTGACTGTGAGGACCTCA 7270

Qy   2972 GTCTGCCCTGTGGATGTGTATGCCACAGACCTGACTTCTGGAGGGCTGACTGAAATGTTC 3031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7271 GTCTGCCCTGTGGATGTGTATGCCACAGACCTGACTTCTGGAGGGCTGACTGAAATGTTC 7330

Qy   3032 ATTTTAAGCTTTTTCTTCTCTTTCCCTGAAACACTCAGTTTGGGTTAGGGGTCATAGACT 3091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7331 ATTTTAAGCTTTTTCTTCTCTTTCCCTGAAACACTCAGTTTGGGTTAGGGGTCATAGACT 7390

Qy   3092 AAGACCAAAGAGTCCAGGGTTAGAATCTTGGTGTAAAATTGCAGGCCATCTCAGGAAATC 3151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7391 AAGACCAAAGAGTCCAGGGTTAGAATCTTGGTGTAAAATTGCAGGCCATCTCAGGAAATC 7450

Qy   3152 TGTGAGCAGATGGGATTGGCTTTGGGTAAGGTGCGTGTGGAAAATGTCAGTGGGAGCCGG 3211
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   7451 TGTGAGCAGATGGGAATGGCTTTGGGTAAGGTGCGTGTGGAAAATGTCAGTGGGAGCCGG 7510

Qy   3212 GTCATGGTGGGCCTTTAGCATCAGATTCCAGAGTGCAGATAGTCTGTATAGCTCATGTGA 3271
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   7511 GTCATGGTGGGCCTTTAGCATCAGATTCCAGAATGCAGATAGTCTGTATAGCTCATGTGA 7570

Qy   3272 AACAGGGAGCCACCAAAACTTTGGGGAGCAGGCTAGTGCCGGTTTTGACCACCTGTGGAG 3331
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   7571 AACAGGGAGCCACCAAAACTTTGGGGAGCAGGCTAGTGCCGGTCTTGACCACCTGTGGAG 7630

Qy   3332 CAGTGCTCACTCACGAAGGCATTTTGCCATCACATGAATGTGCAGAAAGGAGGCCAAAAG 3391
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   7631 CAGTGCTCACTCACGAAGGCATTTTGGCATCACATGAATGTGCAGAAAGGAGGCCAAAAG 7690

Qy   3392 CATTCTGTGCTTCTCCACCACAGCACAGACTTCCCTAGTCTCATTTGCTGAGAGTAGACA 3451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7691 CATTCTGTGCTTCTCCACCACAGCACAGACTTCCCTAGTCTCATTTGCTGAGAGTAGACA 7750

Qy   3452 TTCTGAGGGCCAGCAGTGCAGGTGTGATGTGCCTCAGAGGGTATGAAGCCCTTAGTCAGC 3511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```



```
Qy   5249 CTCTCTCTCTGCTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTCTGCACT 5308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9971 CTCTCTCTCTGCTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTCTGCACT 10030

Qy   5309 ACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGTAACTAC 5368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10031 ACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGTAACTAC 10090

Qy   5369 TCCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACT 5428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10091 TCCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACT 10150

Qy   5429 TTCCCAGTGACTTCCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCTGGGGCC 5488
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  10151 TTCCCAGTGACTTCCCCTAGCCCTGA-CCAGGCACTAGGCCTTGGTGACTTCCTGGGGCC 10209

Qy   5489 AAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACC 5548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10210 AAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACC 10269

Qy   5549 CAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCAC 5608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10270 CAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCAC 10329

Qy   5609 TGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTA 5668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10330 TGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTA 10389

Qy   5669 TGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGAT 5728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10390 TGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGAT 10449

Qy   5729 AGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAG 5788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10450 AGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAG 10509

Qy   5789 TCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACC 5848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10510 TCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACC 10569

Qy   5849 TTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTC 5908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10570 TTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTC 10629

Qy   5909 TGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGC 5968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10630 TGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGC 10689

Qy   5969 CTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAA 6028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10690 CTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAA 10749

Qy   6029 TGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGT 6088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10750 TGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGT 10809

Qy   6089 TGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGG 6146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10810 TGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGG 10867
```

```
RESULT   5
HSU66661
LOCUS       HSU66661     3154 bp    mRNA            PRI       11-MAR-1997
DEFINITION  Human GABA-A receptor epsilon subunit mRNA, complete cds.
ACCESSION   U66661
VERSION     U66661.1  GI:1857125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3154)
  AUTHORS   Davies,P.A., Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Insensitivity to anaesthetic agents conferred by a class of GABA(A)
            receptor subunit
  JOURNAL   Nature 385 (6619), 820-823 (1997)
  MEDLINE   97192095
REFERENCE   2  (bases 1 to 3154)
  AUTHORS   Davies,P.A., Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-1996) Department of Cellular and Molecular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .3154
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             41. .1561
                     /codon_start=1
                     /product="GABA-A receptor epsilon subunit"
                     /protein_id="AAB49284.1"
                     /db_xref="GI:1857126"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIA
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRR
                     FGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV
                     SYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRA
                     RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWC
                     KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
BASE COUNT      725 a    886 c    686 g    857 t
ORIGIN
```

```
  Query Match           37.2%;  Score 2284;  DB 10;  Length 3154;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2284;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3863 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 3922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    824 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 883

Qy   3923 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 3982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    884 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 943

Qy   3983 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 4042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    944 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 1003

Qy   4043 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGAT 4102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1004 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGAT 1063

Qy   4103 TTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTC 4162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1064 TTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTC 1123

Qy   4163 AACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGT 4222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1124 AACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGT 1183

Qy   4223 ATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACAT 4282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1184 ATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACAT 1243

Qy   4283 CAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCG 4342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1244 CAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCG 1303

Qy   4343 TCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCCGCAGCCTCTGC 4402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1304 TCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCCGCAGCCTCTGC 1363
```

```
Qy   4403 TCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCC 4462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1364 TCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCC 1423

Qy   4463 GATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGAT 4522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1424 GATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGAT 1483

Qy   4523 AACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTT 4582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1484 AACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTT 1543

Qy   4583 GTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCA 4642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1544 GTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCA 1603

Qy   4643 GGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGCGAC 4702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1604 GGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGCGAC 1663

Qy   4703 TAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCC 4762
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1664 TAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCC 1723

Qy   4763 CCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAAT 4822
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1724 CCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAAT 1783

Qy   4823 AAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACA 4882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1784 AAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACA 1843

Qy   4883 GCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCC 4942
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1844 GCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCC 1903

Qy   4943 AACAATGCTGACCACCAGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTA 5002
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1904 AACAATGCTGACCACCAGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTA 1963

Qy   5003 GTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATA 5062
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1964 GTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATA 2023

Qy   5063 CCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTT 5122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2024 CCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTT 2083

Qy   5123 TGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGAT 5182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2084 TGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGAT 2143

Qy   5183 AGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACA 5242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2144 AGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACA 2203

Qy   5243 GCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTC 5302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2204 GCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTC 2263

Qy   5303 TGCACTACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGT 5362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2264 TGCACTACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGT 2323

Qy   5363 AACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCT 5422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2324 AACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCT 2383

Qy   5423 GTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCT 5482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2384 GTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCT 2443

Qy   5483 GGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTG 5542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2444 GGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTG 2503

Qy   5543 CCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCA 5602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2504 CCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCA 2563

Qy   5603 GTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAA 5662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2564 GTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAA 2623

Qy   5663 TTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTT 5722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2624 TTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTT 2683

Qy   5723 CATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAAC 5782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2684 CATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAAC 2743

Qy   5783 CCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACT 5842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2744 CCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACT 2803

Qy   5843 GTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGT 5902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2804 GTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGT 2863

Qy   5903 CACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTT 5962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2864 CACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTT 2923

Qy   5963 CTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCA 6022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2924 CTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCA 2983

Qy   6023 GTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTA 6082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2984 GTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTA 3043

Qy   6083 ATTTGTTGGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAA 6142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3044 ATTTGTTGGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAA 3103

Qy   6143 TGGG 6146
          ||||
Db   3104 TGGG 3107
```

```
RESULT   6
HSY09765
LOCUS       HSY09765     3150 bp    mRNA            PRI       31-OCT-1997
DEFINITION  Homo sapiens mRNA for putative GABA receptor epsilon subunit.
ACCESSION   Y09765
VERSION     Y09765.1  GI:2285960
KEYWORDS    GABA receptor; GABRE gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3150)
  AUTHORS   Wilke,K., Gaul,R., Klauck,S.M. and Poustka,A.
  TITLE     A gene in human chromosome band Xq28 (GABRE) defines a putative new
            subunit class of the GABAA neurotransmitter receptor
  JOURNAL   Genomics 45 (1), 1-10 (1997)
  MEDLINE   97480709
REFERENCE   2  (bases 1 to 3150)
  AUTHORS   Wilke,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1996) K. Wilke, Deutsches Krebsforschungszentrum,
            Abteilung Molekulare Genomanalyse (840), Im Neuenheimer Feld 280,
            D-69120 Heidelberg, FRG
FEATURES             Location/Qualifiers
     source          1. .3150
```

```
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /map="q28"
     CDS             55. .1575
                     /note="putative"
                     /codon_start=1
                     /product="GABA receptor epsilon subunit"
                     /protein_id="CAA70904.1"
                     /db_xref="GI:2285961"
                     /db_xref="SPTREMBL:O15346"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIS
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRR
                     FGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV
                     SYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRA
                     RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWC
                     KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
BASE COUNT      712 a    889 c    690 g    859 t
ORIGIN
```

Query Match 36.9%; Score 2268.8; DB 10; Length 3150;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2281; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
Qy   3863 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 3922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    838 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 897

Qy   3923 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 3982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    898 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 957

Qy   3983 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 4042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    958 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 1017

Qy   4043 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGAT 4102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1018 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGAT 1077

Qy   4103 TTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTC 4162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1078 TTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTC 1137

Qy   4163 AACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGT 4222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1138 AACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGT 1197

Qy   4223 ATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACAT 4282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1198 ATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACAT 1257

Qy   4283 CAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCG 4342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1258 CAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCG 1317

Qy   4343 TCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGC 4402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1318 TCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGC 1377

Qy   4403 TCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCC 4462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1378 TCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCC 1437

Qy   4463 GATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGAT 4522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1438 GATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGAT 1497

Qy   4523 AACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTT 4582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1498 AACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTT 1557

Qy   4583 GTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCA 4642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1558 GTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCA 1617

Qy   4643 GGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGCGAC 4702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1618 GGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGGAGCGAC 1677

Qy   4703 TAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCC 4762
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1678 TAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCC 1737

Qy   4763 CCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAAT 4822
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   1738 CCTCTCCCCTACCTGGCCCATTCACTGAGTTTTCTCAGCAGACCATTTCAAATTATTAAT 1797

Qy   4823 AAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACA 4882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1798 AAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACA 1857

Qy   4883 GCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCC 4942
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1858 GCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCC 1917

Qy   4943 AACAATGCTGACCACCAGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTA 5002
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   1918 AACAATGCTGACCACCAGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGCA 1977

Qy   5003 GTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATA 5062
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1978 GTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATA 2037

Qy   5063 CCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTT 5122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2038 CCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTT 2097

Qy   5123 TGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGAT 5182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2098 TGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGAT 2157

Qy   5183 AGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACA 5242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2158 AGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACA 2217

Qy   5243 GCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTC 5302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2218 GCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTC 2277

Qy   5303 TGCACTACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGT 5362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2278 TGCACTACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGT 2337

Qy   5363 AACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCT 5422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2338 AACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCT 2397

Qy   5423 GTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCT 5482
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   2398 GTAACTTTCCCAGTGACTTCCCCTAGCCCTGA-CCAGGCACTAGGCCTTGGTGACTTCCT 2456

Qy   5483 GGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTG 5542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2457 GGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTG 2516

Qy   5543 CCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCA 5602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2517 CCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCA 2576
```

```
Qy   5603 GTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAA 5662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2577 GTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAA 2636

Qy   5663 TTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTT 5722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2637 TTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTT 2696

Qy   5723 CATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAAC 5782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2697 CATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAAC 2756

Qy   5783 CCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACT 5842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2757 CCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACT 2816

Qy   5843 GTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGT 5902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2817 GTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGT 2876

Qy   5903 CACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTT 5962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2877 CACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTT 2936

Qy   5963 CTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCA 6022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2937 CTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCA 2996

Qy   6023 GTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTA 6082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2997 GTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTA 3056

Qy   6083 ATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAA 6142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3057 ATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAA 3116

Qy   6143 TGGG 6146
          ||||
Db   3117 TGGG 3120
```

```
RESULT   7
HSGABACHL
LOCUS       HSGABACHL    3153 bp    mRNA            PRI       03-MAR-1997
DEFINITION  H.sapiens mRNA for putative GABA-gated chloride channel.
ACCESSION   Y07637
VERSION     Y07637.1  GI:1747370
KEYWORDS    GABA-gated chloride channel.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3153)
  AUTHORS   Garret,M., Bascles,L., Boue-Grabot,E., Sartor,P., Charron,G.,
            Bloch,B. and Margolskee,R.F.
  TITLE     An mRNA encoding a putative GABA-gated chloride channel is
            expressed in the human cardiac conduction system
  JOURNAL   J. Neurochem. 68 (4), 1382-1389 (1997)
  MEDLINE   97238072
REFERENCE   2  (bases 1 to 3153)
  AUTHORS   Garret,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-AUG-1996) M. Garret, CNRS UMR5543, Laboratoire de
            Neurophysiologie, Universite de Bordeaux2, 146 rue Leo Saignat,
            33076 Bordeaux Cedex, FRANCE
FEATURES             Location/Qualifiers
     source          1. .3153
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             51. .1568
                     /function="expressed in cardiac conduction system"
                     /codon_start=1
                     /product="putative GABA-gated chloride channel"
                     /protein_id="CAA68914.1"
                     /db_xref="GI:1747371"
                     /db_xref="SPTREMBL:Q99520"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIA
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPGDFMVMTIFFNVSRRF
                     GYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVS
                     YITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRAR
                     SRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCK
                     RFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
     polyA_signal    3118. .3123
BASE COUNT      726 a    885 c    687 g    855 t
ORIGIN
```

```
  Query Match             34.6%;  Score 2128;  DB 9;  Length 3153;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 2255;  Conservative    0;  Mismatches   20;  Indels   15;  Gaps   10;

Qy   3861 CAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTG 3920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    829 CAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTG 888

Qy   3921 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 3980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    889 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 948

Qy   3981 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 4040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    949 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 1008

Qy   4041 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGG 4100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1009 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGG 1068

Qy   4101 ATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGC 4160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1069 ATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGC 1128

Qy   4161 TCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTC 4220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1129 TCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTC 1188

Qy   4221 GTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAAC 4280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1189 GTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAAC 1248

Qy   4281 ATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCC 4340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1249 ATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCC 1308

Qy   4341 CGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCT 4400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309 CGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCT 1368

Qy   4401 GCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCC 4460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1369 GCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCC 1428

Qy   4461 CCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGG 4520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1429 CCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGG 1488

Qy   4521 ATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGC 4580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1489 ATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGC 1548

Qy   4581 TTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTT-CC 4639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   1549 TTGTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCC 1608
```

```
Qy   4640 CCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGC 4699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1609 CCAGGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGGAGC 1668

Qy   4700 GACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCT 4759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1669 GACTAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCT 1728

Qy   4760 GCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATT 4819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1729 GCCCCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATT 1788

Qy   4820 AATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACC 4879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1789 AATAAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACC 1848

Qy   4880 ACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCT 4939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1849 ACAGCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCT 1908

Qy   4940 TCCAACAATGCTGACCACCAGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTT 4999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1909 TCCAACAATGCTGACCACCAGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTT 1968

Qy   5000 GTAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCT 5059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1969 GTAGTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCT 2028

Qy   5060 ATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTC 5119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2029 ATACCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTC 2088

Qy   5120 CTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATA 5179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2089 CTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATA 2148

Qy   5180 GATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGGCAGCAAGAGAGCCTATTTGGG 5239
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   2149 GATAGACACTGGCATTATCCCTTTAGGAAGGGGGGGGGGCAGCAAGAGAGCCTATTTGGG 2208

Qy   5240 ACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTCCTTGCTGG-CTCCATCTTT 5298
          |||||||||||||||||| |||||||||||||||||||||||||||| |||||||||
Db   2209 ACAGCATTCCTCTCTCTCCTGCTGTGACATCTCCCTCTCCTTGCTGGCCTCCATCTTT 2268

Qy   5299 CGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTA 5358
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2269 CGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTA 2328

Qy   5359 TAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCT 5418
          |||||||||||||||||||||||||| |||||||||||||||  ||||||||||||||
Db   2329 TAGTAACTACTCCCTGCTTTATATGCC-CCCTCTTCCTTCTCTTTACCCCCTGTGACTCT 2387

Qy   5419 TTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACT 5478
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2388 TTCTGT-ACTTTCCCAGTGACTTGCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACT 2446

Qy   5479 TCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATT 5538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2447 TCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATT 2506

Qy   5539 GGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAA 5598
          |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db   2507 -GTGCCCACCCAGGGCACACTGATGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAA 2565

Qy   5599 ACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCT 5658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2566 ACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCT 2625

Qy   5659 TAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGA 5718
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2626 TAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGA 2685

Qy   5719 GCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATG- 5778
          |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db   2686 GCTTCATGATAGCCTTGTGACATCTT--AGGCAGGATTCTTATCCCCATTTTGCAGATGA 2743

Qy   5778 AAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAG-CTATCCAAGAG 5836
          |||||||||||| ||||||||||||||||||||||||||||||||| ||||||||||
Db   2744 AAAACCCTGAGTCTCAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCCTATCCAAGAG 2803

Qy   5837 CCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTC 5896
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db   2804 CCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATCTTT 2863

Qy   5897 TTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCT 5956
          |  |||||||||||||||||||||||||||    |  ||||||||||||||||
Db   2864 TGTCA----CTCTGCTGGCACACCAGTGGCAAGGCC--AGAATGCGACCTCTCTTTAGCT 2917

Qy   5957 CAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGT 6016
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2918 CAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGT 2977

Qy   6017 AACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTG 6076
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2978 AACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTG 3037

Qy   6077 TCTGTAATTTGTTGGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCAT 6136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3038 TCTGTAATTTGTTGGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCAT 3097

Qy   6137 CTGAAATGGG 6146
          ||||||||||
Db   3098 CTGAAATGGG 3107
```

```
RESULT   8
RNU92284
LOCUS       RNU92284     7479 bp    DNA             ROD       01-JAN-1998
DEFINITION  Rattus norvegicus GABA-A receptor epsilon subunit gene, partial
            cds.
ACCESSION   U92284
VERSION     U92284.1  GI:2735328
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 7479)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 7479)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .7479
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
     mRNA            join(<1. .200,895. .977,2138. .2275,5938. .6090,6207. .6406,
                     6654. .>7479)
                     /product="GABA-A receptor epsilon subunit"
     exon            <1. .200
                     /number=4
     CDS             join(<1. .200,895. .977,2138. .2275,5938. .6090,6207. .6406,
                     6654. .7034)
                     /codon_start=1
                     /product="GABA-A receptor epsilon subunit"
                     /protein_id="AAB93879.1"
                     /db_xref="GI:2735329"
                     /translation="FYQTWYDERLCYNDTFETLILHGNVVSQLWIPDTFFRNSKRTQE
                     YDITIPNQMALIHKDGKVLYTVRMTIDARCSLHMLNFPMDSHSCPLSFSSFSYDEHEM
                     IYKWENFKLKIDAKNTWKLLEFDFTGVNNKTEIISTPVGDFMVMTFFFNVSRRFGFIV
```

```
                     FQNYIPSSVTTMLSWVSFWIKIEAAAARASVGVSSVLTMATLGTFSRKNFPRVSYLTA
                     LDFYIAICFVLCFCTLLEFTVLNFLTYNNIERQASPKFYQFPTNSRANARTRARARTR
                     ARARARARQQQEVFVCEIVTYEENAEEGYQWSPRSRRPQCPWRRCGRSYVCFRVLRKY
                     FCMVPGCEGNSWQRGRICIHVYRLDNYSRVLFPITFFFFNVVYWVICLNL"
     intron          201. .894
                     /number=4
     exon            895. .977
                     /number=5
     intron          978. .2137
                     /number=5
     exon            2138. .2275
                     /number=6
     intron          2276. .5937
                     /number=6
     stem_loop       2412. .2496
     stem_loop       3389. .3472
     exon            5938. .6090
                     /number=7
     intron          6091. .6206
                     /number=7
     exon            6207. .6406
                     /number=8
     intron          6407. .6653
                     /number=8
     exon            6654. .>7479
                     /number=9
     3'UTR           7032. .>7479
BASE COUNT     1931 a   1620 c   1557 g   2371 t
ORIGIN
```

Query Match 10.6%; Score 654.4; DB 12; Length 7479;
Best Local Similarity 57.7%; Pred. No. 4.6e-169;
Matches 2515; Conservative 0; Mismatches 1341; Indels 506; Gaps 55;

```
Qy       2 TCTTATAATTGCTAAGCACTTACAACTGTTTGCAGAGGAAACTGAGACTTTGTAACTATG 61
Db    2402 TCTCATATATGCTAAACACTTACAACTGTTTGCAGAGGAAACTGAGACTTCATAGCTATG 2461

Qy      62 TCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCTCCTTGAGAGGTTAGGTAAG 121
Db    2462 TCTCAGTCTCATCTGCAAAGAAGTAAGTGCTTTGCCAAGCCCCTTGAAGGACGGGGTAAG 2521

Qy     122 TAGATAAAGTTCTGCTGCTGTCGGAATGTGCAGC-------TGGCTTTTTCATGCAGACC 174
Db    2522 TAGATATATGTTTGTAACCTTCAGTATGTTAATCTACCTTTTGAGTTTTAGATCTTTTGT 2581

Qy     175 CTTCAGTTTCGAGGTTACAACTCTGACCTCTTTGGATGACTTTGGGGAATGGAGCTC-GT 233
Db    2582 ATTTAATTTCTTTCTTATATCACTGACTAACTTAGACAACATTGGGGAGGGGTACTCTGT 2641

Qy     234 GTGAGTTCTCCATACCCAGAACCAATCCAGTCTGGTTGAATGGGAAGCAAAGTC-----C 288
Db    2642 GTGATTTTACCAAATCCTGAACCAGGTCAAGTTGGTTGAGTGGGAAGGAAGACCACCCTA 2701

Qy     289 ATTGTAGTGGGAGGTGGAGGCTAGAGTTCTAATGTCAGCTAGTTTAAGGCTGGGAAAGTC 348
Db    2702 GCAGGAGGTAGAAGTGGAAACTAGAGTGACAATGGCGGCTAG--TAGGGATTGAGGAGTC 2759

Qy     349 TGGAGGAAGTTACAGCAGCTACACTGGCTGCTGCATTGACATTTATCTTAAAGGAACAAG 408
Db    2760 TGCAGATGGTTAC-TCAGGTGCAATGGCTACAGTAAT----ATTATCTTAAAGGAGCAAC 2814

Qy     409 TCTGAAAAGCACAGATTCTTATCAAAGGCTTCATGGTGGATTCCACATAGACATAGTGGC 468
Db    2815 TGTGAAGAGTACATATTTTCACCAGAGGCTTCAGAGTGGAATCAACATAAACATGTT--- 2872

Qy     469 CACTGGTTTTCTGACCTTTTCTCTGACAAAGACTAAAGGGGAAGGTCCTGGGTATCTTAC 528
Db    2872 --TTTTCCTCCTGATCTTGTTCCTGACAAGGATAATAGGGGCAGATTCTGGGTCTCTTAA 2929

Qy     529 ACTTCAGCTCCCAATTAGATGTGAGCACCTTCACTTATGTTCCTAGGTGACCTGAATGAG 588
```

```
Db    2930 CTTGTATCTCCCAAATAGATGTGAGCATCTTTGCTTGTATTCCTAGGTGATCTGAATGAG 2989

Qy     589 GAGCCAAGGGACCTCCCCAGGGTAGCTCCCAGAGCAACCCTGGAAACACTCTTCACACAT 648
Db    2990 GAGCCAATAAATCTTCTCAGGGTACCTCTGAGAGCAACCCTGG--ACCTTCTTCACATGT 3047

Qy     649 CCTGACCAAGTTCAGGGCAGTGAAGGCACTGCCCTCATCGTTTCCAGAATGTGGATGGAG 708
Db    3048 ACTGA-----------------------------------CAAGAATGTGGATGGAT 3069

Qy     709 CCAGTCACCCAACCAGCCATTTGTCGTGAGAGGCATCTTGTTCTGCTACCATGTGACTAG 768
Db    3070 CAGGTCACCCAGCCAGACTTT-----TGACATTTATTTTGCTTTGCTTCTGTGTGATGAT 3124

Qy     769 GCAGAAAATCTGCTTTTGTTTCATTTATTGAGTCAGTCTCTGGATGAGGGAAAGCTCATG 828
Db    3125 G----ACATAAAAAAAATCTGCTATTGCTACTGTTGGTCACTCGGTGAGGGGCAGCTTATG 3180

Qy     829 CTCATGTGGCTAGAGCTTTGCTTGCACAGTATTAGGCAGGGGCAGAGGGCTGGGCTACCT 888
Db    3181 CTAACCCAACTAAAGCTTTGCTTATACAATACTAGGCAGGGATGGGTGC----------- 3230

Qy     889 TAAAAATACTTGCCCTTTTTCTTGGGGACTCTGGGGAAGCGGTTTTACTACCTTTGACTT 948
Db    3230 ------TGCTTGTCCTGTTCCT--GGGACTCTGAGAAAGCCTTCTTGCTTGCTTTGACTT 3281

Qy     949 GGGAGCCTTGCTCTTCTGCCAGCTAACCATGGGCCTGCCTCTTGGTTTTCTGCACCTCAG 1008
Db    3282 GGGGTTCTTGTTCTTCTTCTACATAAATGTGGGCCTGCCTCTTAGTATTCAG-------- 3334

Qy    1009 CTTTTCCCGGATAGGTGGGGACCCATCATCAAAAGTGACAGAGAAGATAAGGCCCAGGGG 1068
Db    3334 -TTTGTCCAGATAGGTGGAGCCTCATCATCAGAAGTGACAGAAGAGACAAGGTTCAGGGG 3392

Qy    1069 CTTTCAAGTCACTAGTGGTTCCGTTTAGTAGAT-GATTGTGCATTGTTTCAAAATGGTGC 1127
Db    3393 CTTTCAAGTCACTAGTGGTTCCGTTTAGTAGATGGTTTTTGCATTGTTTCAAAATGGTGC 3452

Qy    1128 CCTAGTGACTACAAAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGC 1187
Db    3453 CCTAGTGACTACAAAGCCCCAGAGCCAGCATCATCAGTGAAGCAATGTCAGTAGGTAAGC 3512

Qy    1188 ACCAGACCTCCTTGGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTC 1247
Db    3513 AACATCTCT----------------TACTGTGGAGAAAGAAATAGGTCTTCTTTTTTCAT 3556

Qy    1248 TG-CTGGAGACTAGTTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGA 1306
Db    3557 TGACTAGAGACTACTTATTCTGAATTCATACTGTCTTCACTGTC--AGTTATTTTTGAGT 3614

Qy    1307 CTGGTCTCAAACTCTTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTA 1366
Db    3615 CAGGT-TCCAACTCTCCCAGTTTGACCCTGGGGCACTTCTTTCTAGCTAGAACACACAT- 3673

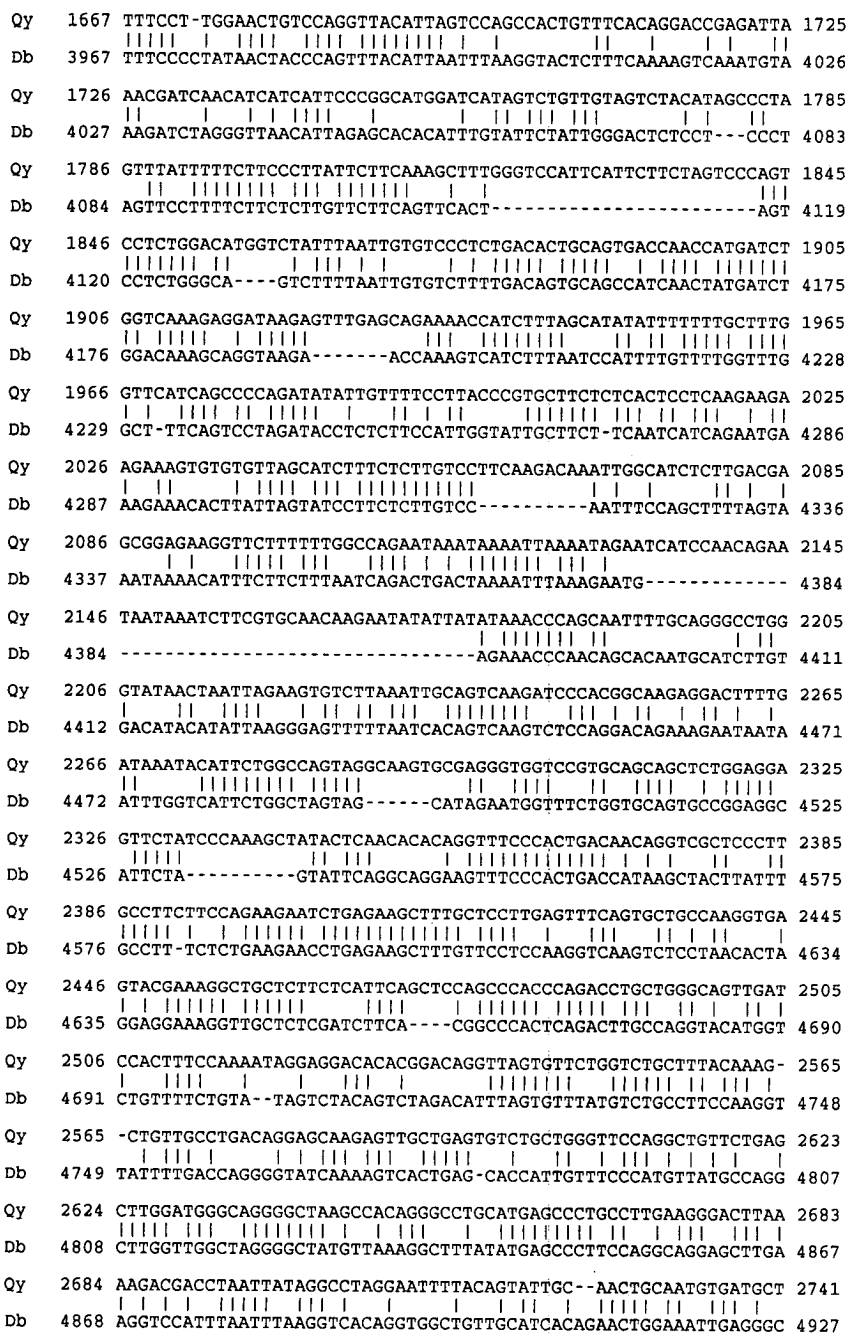
Qy    1367 CGTGCTCGGCGATTAAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGA 1426
Db    3673 ---GTACTCATTTTTCAGGGTTTAAATGCAGCAGTGCCCTGCAACTTGGGCCATCTTGGA 3729

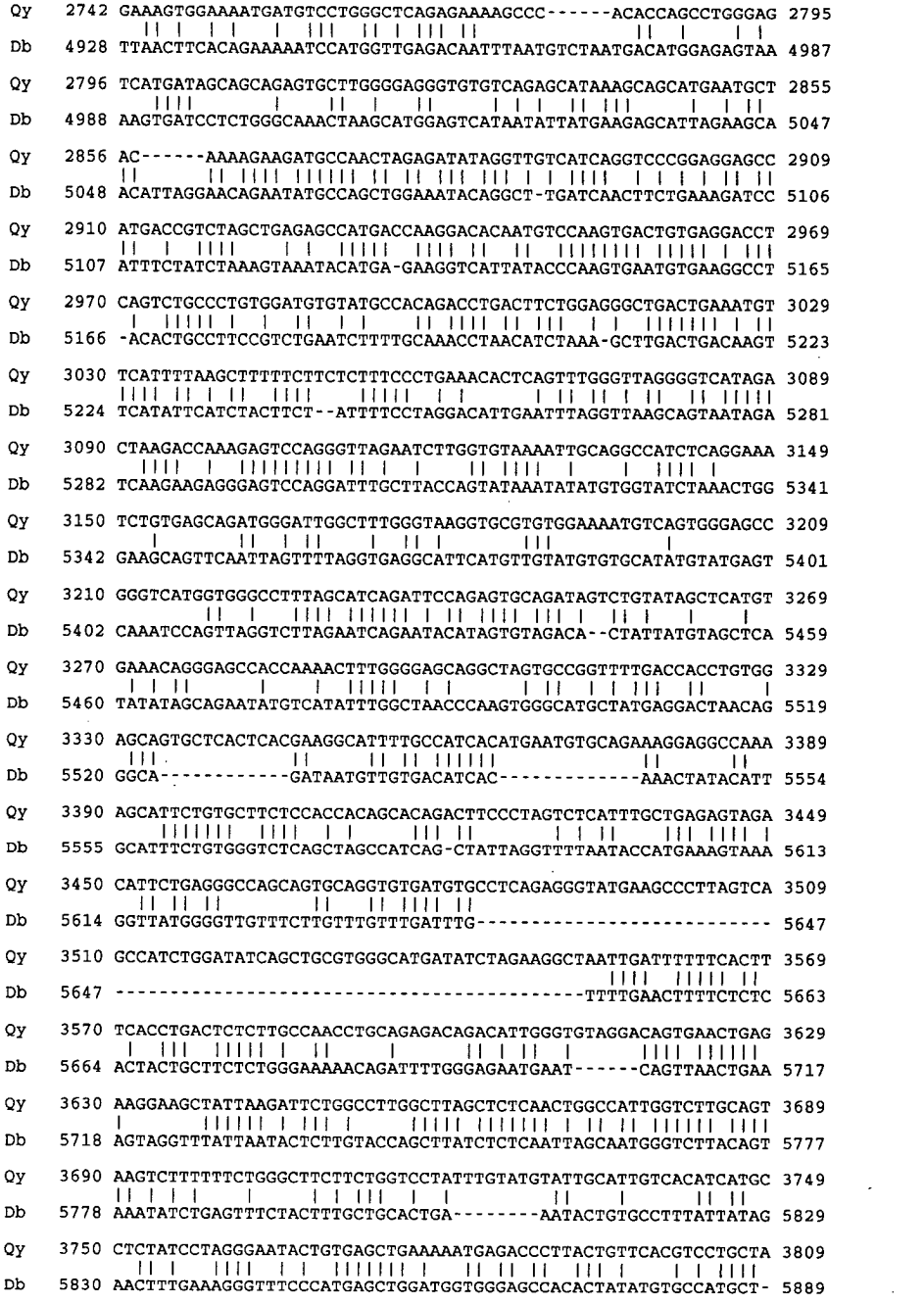
Qy    1427 CCTTGATCCAGAGAATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGA 1486
Db    3730 CCTTACAGCAGAG--TTTCTGCTTCAGGAGCTTCTCAGAAAGTGCAGCCTTGTCTGTAGT 3787

Qy    1487 GAGAGGCTTGCCCTTCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAG 1546
Db    3788 AAGTAAACCATCCTTCACTGGTGGCTGTTGAGCCTCTGAGGAAATCTTGCCAC-GATCAA 3846

Qy    1547 GAATTCACTGTCTTACAAGGAGGTTTCCTTCTTCTCTAGACAGTTCTGTTCATCAAAAAA 1606
Db    3847 GAGGTCAGCATCTTACAAGGAGATTATTTTCTTCCCTAGACGTCTCTTTCCATCAGAAAA 3906

Qy    1607 CTCTCCCTGTTCTTCTGAAATTGGAGTCTCTGGAAGTTCCACACATTAAGCTTAGTTCTT 1666
Db    3907 TTCTTCTTGCTCATCTAAAATGGGAGTTTCTGGAACATTTACCCATCAGATCTAGTTCTT 3966
```


Qy 1667 TTTCCT-TGGAACTGTCCAGGTTACATTAGTCCAGCCACTGTTTCACAGGACCGAGATTA 1725
Db 3967 TTTCCCCTATAACTACCCAGTTTACATTAATTTAAGGTACTCTTTCAAAAGTCAAATGTA 4026
Qy 1726 AACGATCAACATCATCATTCCCGGCATGGATCATAGTCTGTTGTAGTCTACATAGCCCTA 1785
Db 4027 AAGATCTAGGGTTAACATTAGAGCACACATTTGTATTCTATTGGGACTCTCCT---CCCT 4083
Qy 1786 GTTTATTTTTCTTCCCTTATTCTTCAAAGCTTTGGGTCCATTCATTCTTCTAGTCCCAGT 1845
Db 4084 AGTTCCTTTTCTTCTCTTGTTCTTCAGTTCACT----------AGT 4119
Qy 1846 CCTCTGGACATGGTCTATTTAATTGTGTCCCTCTGACACTGCAGTGACCAACCATGATCT 1905
Db 4120 CCTCTGGGCA----GTCTTTTAATTGTGTCTTTTGACAGTGCAGCCATCAACTATGATCT 4175
Qy 1906 GGTCAAAGAGGATAAGAGTTTGAGCAGAAAACCATCTTTAGCATATATTTTTTTGCTTTG 1965
Db 4176 GGACAAAGCAGGTAAGA-------ACCAAAGTCATCTTTAATCCATTTTGTTTTGGTTTG 4228
Qy 1966 GTTCATCAGCCCCAGATATATTGTTTTCCTTACCCGTGCTTCTCTCACTCCTCAAGAAGA 2025
Db 4229 GCT-TTCAGTCCTAGATACCTCTCTTCCATTGGTATTGCTTCT-TCAATCATCAGAATGA 4286
Qy 2026 AGAAAGTGTGTGTTAGCATCTTTCTCTTGTCCTTCAAGACAAATTGGCATCTCTTGACGA 2085
Db 4287 AAGAAACACTTATTAGTATCCTTCTCTTGTCC----------AATTTCCAGCTTTTAGTA 4336
Qy 2086 GCGGAGAAGGTTCTTTTTTGGCCAGAATAAATAAAATTAAAATAGAATCATCCAACAGAA 2145
Db 4337 AATAAAACATTTCTTCTTTAATCAGACTGACTAAAATTTAAAGAATG------------ 4384
Qy 2146 TAATAAATCTTCGTGCAACAAGAATATATTATATAAACCCAGCAATTTTGCAGGGCCTGG 2205
Db 4384 ----------AGAAACCCAACAGCACAATGCATCTTGT 4411
Qy 2206 GTATAACTAATTAGAAGTGTCTTAAATTGCAGTCAAGATCCCACGGCAAGAGGACTTTTG 2265
Db 4412 GACATACATATTAAGGGAGTTTTTAATCACAGTCAAGTCTCCAGGACAGAAAGAATAATA 4471
Qy 2266 ATAAATACATTCTGGCCAGTAGGCAAGTGCGAGGGTGGTCCGTGCAGCAGCTCTGGAGGA 2325
Db 4472 ATTTGGTCATTCTGGCTAGTAG------CATAGAATGGTTTCTGGTGCAGTGCCGGAGGC 4525
Qy 2326 GTTCTATCCCAAAGCTATACTCAACACACAGGTTTCCCACTGACAACAGGTCGCTCCCTT 2385
Db 4526 ATTCTA----------GTATTCAGGCAGGAAGTTTCCCACTGACCATAAGCTACTTATTT 4575
Qy 2386 GCCTTCTTCCAGAAGAATCTGAGAAGCTTTGCTCCTTGAGTTTCAGTGCTGCCAAGGTGA 2445
Db 4576 GCCTT-TCTCTGAAGAACCTGAGAAGCTTTGTTCCTCCAAGGTCAAGTCTCCTAACACTA 4634
Qy 2446 GTACGAAAGGCTGCTCTTCTCATTCAGCTCCAGCCCACCCAGACCTGCTGGGCAGTTGAT 2505
Db 4635 GGAGGAAAGGTTGCTCTCGATCTTCA----CGGCCCACTCAGACTTGCCAGGTACATGGT 4690
Qy 2506 CCACTTTCCAAAATAGGAGGACACACGGACAGGTTAGTGTTCTGGTCTGCTTTACAAAG- 2565
Db 4691 CTGTTTTCTGTA--TAGTCTACAGTCTAGACATTTAGTGTTTATGTCTGCCTTCCAAGGT 4748
Qy 2565 -CTGTTGCCTGACAGGAGCAAGAGTTGCTGAGTGTCTGCTGGGTTCCAGGCTGTTCTGAG 2623
Db 4749 TATTTTGACCAGGGGTATCAAAAGTCACTGAG-CACCATTGTTTCCCATGTTATGCCAGG 4807
Qy 2624 CTTGGATGGGCAGGGGCTAAGCCACAGGGCCTGCATGAGCCCTGCCTTGAAGGGACTTAA 2683
Db 4808 CTTGGTTGGCTAGGGGCTATGTTAAAGGCTTTATATGAGCCCTTCCAGGCAGGAGCTTGA 4867
Qy 2684 AAGACGACCTAATTATAGGCCTAGGAATTTTACAGTATTGC--AACTGCAATGTGATGCT 2741
Db 4868 AGGTCCATTTAATTTAAGGTCACAGGTGGCTGTTGCATCACAGAACTGGAAATTGAGGGC 4927


Qy 2742 GAAAGTGGAAAATGATGTCCTGGGCTCAGAGAAAAGCCC------ACACCAGCCTGGGAG 2795
Db 4928 TTAACTTCACAGAAAAATCCATGGTTGAGACAATTTAATGTCTAATGACATGGAGAGTAA 4987
Qy 2796 TCATGATAGCAGCAGAGTGCTTGGGGAGGGTGTGTCAGAGCATAAAGCAGCATGAATGCT 2855
Db 4988 AAGTGATCCTCTGGGCAAACTAAGCATGGAGTCATAATATTATGAAGAGCATTAGAAGCA 5047
Qy 2856 AC------AAAAGAAGATGCCAACTAGAGATATAGGTTGTCATCAGGTCCCGGAGGAGCC 2909
Db 5048 ACATTAGGAACAGAATATGCCAGCTGGAAATACAGGCT-TGATCAACTTCTGAAAGATCC 5106
Qy 2910 ATGACCGTCTAGCTGAGAGCCATGACCAAGGACACAATGTCCAAGTGACTGTGAGGACCT 2969
Db 5107 ATTTCTATCTAAAGTAAATACATGA-GAAGGTCATTATACCCAAGTGAATGTGAAGGCCT 5165
Qy 2970 CAGTCTGCCCTGTGGATGTGTATGCCACAGACCTGACTTCTGGAGGGCTGACTGAAATGT 3029
Db 5166 -ACACTGCCTTCCGTCTGAATCTTTTGCAAACCTAACATCTAAA-GCTTGACTGACAAGT 5223
Qy 3030 TCATTTTAAGCTTTTTCTTCTCTTTCCCTGAAACACTCAGTTTGGGTTAGGGGTCATAGA 3089
Db 5224 TCATATTCATCTACTTCT--ATTTTCCTAGGACATTGAATTTAGGTTAAGCAGTAATAGA 5281
Qy 3090 CTAAGACCAAAGAGTCCAGGGTTAGAATCTTGGTGTAAAATTGCAGGCCATCTCAGGAAA 3149
Db 5282 TCAAGAAGAGGGAGTCCAGGATTTGCTTACCAGTATAAATATATGTGGTATCTAAACTGG 5341
Qy 3150 TCTGTGAGCAGATGGGATTGGCTTTGGGTAAGGTGCGTGTGGAAAATGTCAGTGGGAGCC 3209
Db 5342 GAAGCAGTTCAATTAGTTTTAGGTGAGGCATTCATGTTGTATGTGTGCATATGTATGAGT 5401
Qy 3210 GGGTCATGGTGGGCCTTTAGCATCAGATTCCAGAGTGCAGATAGTCTGTATAGCTCATGT 3269
Db 5402 CAAATCCAGTTAGGTCTTAGAATCAGAATACATAGTGTAGACA--CTATTATGTAGCTCA 5459
Qy 3270 GAAACAGGGAGCCACCAAAACTTTGGGGAGCAGGCTAGTGCCGGTTTTGACCACCTGTGG 3329
Db 5460 TATATAGCAGAATATGTCATATTTGGCTAACCCAAGTGGGCATGCTATGAGGACTAACAG 5519
Qy 3330 AGCAGTGCTCACTCACGAAGGCATTTTGCCATCACATGAATGTGCAGAAAGGAGGCCAAA 3389
Db 5520 GGCA-----------GATAATGTTGTGACATCAC-------------AAACTATACATT 5554
Qy 3390 AGCATTCTGTGCTTCTCCACCACAGCACAGACTTCCCTAGTCTCATTTGCTGAGAGTAGA 3449
Db 5555 GCATTTCTGTGGGTCTCAGCTAGCCATCAG-CTATTAGGTTTTAATACCATGAAAGTAAA 5613
Qy 3450 CATTCTGAGGGCCAGCAGTGCAGGTGTGATGTGCCTCAGAGGGTATGAAGCCCTTAGTCA 3509
Db 5614 GGTTATGGGGTTGTTTCTTGTTTGTTTGATTTG---------- 5647
Qy 3510 GCCATCTGGATATCAGCTGCGTGGGCATGATATCTAGAAGGCTAATTGATTTTTTCACTT 3569
Db 5647 ----------TTTTGAACTTTTCTCTC 5663
Qy 3570 TCACCTGACTCTCTTGCCAACCTGCAGAGACAGACATTGGGTGTAGGACAGTGAACTGAG 3629
Db 5664 ACTACTGCTTCTCTGGGAAAAACAGATTTTGGGAGAATGAAT------CAGTTAACTGAA 5717
Qy 3630 AAGGAAGCTATTAAGATTCTGGCCTTGGCTTAGCTCTCAACTGGCCATTGGTCTTGCAGT 3689
Db 5718 AGTAGGTTTATTAATACTCTTGTACCAGCTTATCTCTCAATTAGCAATGGGTCTTACAGT 5777
Qy 3690 AAGTCTTTTTTCTGGGCTTCTTCTGGTCCTATTTGTATGTATTGCATTGTCACATCATGC 3749
Db 5778 AAATATCTGAGTTTCTACTTTGCTGCACTGA--------AATACTGTGCCTTTATTATAG 5829
Qy 3750 CTCTATCCTAGGGAATACTGTGAGCTGAAAAATGAGACCCTTACTGTTCACGTCCTGCTA 3809
Db 5830 AACTTTGAAAGGGTTTCCCATGAGCTGGATGGTGGGAGCCACACTATATGTGCCATGCT- 5889
Qy 3810 AGGGGGACCGTCGTGTCAGCACTGTAATGCAGTGATGTTTTTTGTGTCTTTCAGGTGACT 3869

```
Db   5889 -----GGACATCAGGCCAGTACTGCAATGCAGTGGTGTATTTGATGTCTTTCAGGTGACT 5943

Qy   3870 TCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAA 3929

Db   5944 TCATGGTCATGACATTCTTCTTCAATGTAAGCAGGAGGTTTGGCTTCATTGTCTTTCAAA 6003

Qy   3930 ACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAG 3989

Db   6004 ACTATATCCCTTCATCTGTTACCACAATGCTTTCCTGGGTGTCCTTCTGGATCAAGATAG 6063

Qy   3990 AGTCTGCTCCAGCCCGGACCTC---------------------------------------- 4012

Db   6064 AAGCTGCTGCTGCCAGGGCCTCTGTAGGTAAGAAAGTATGGTGATCTTAAATGTGATCAT 6123

Qy   4012 ------------------------------------------------------------ 4012

Db   6124 ATGTCATAGATTAACATTGCCTTCTCCTGTTGTCCTGCAGCACTGTCAGGAGCTTAGCCC 6183

Qy   4012 ------------------TCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCAC 4053

Db   6184 ACCTTCACTCCTTGCTCTTATAGGGGTCAGTTCTGTGCTCACCATGGCCACACTGGGTAC 6243

Qy   4054 CTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGC 4113

Db   6244 CTTTTCTCGTAAGAATTTCCCTCGTGTCTCCTATCTCACAGCTTTGGACTTCTATATTGC 6303

Qy   4114 CATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGAT 4173

Db   6304 AATTTGTTTCGTCTTGTGCTTCTGTACTCTACTAGAGTTCACTGTGCTCAACTTCCTGAC 6363

Qy   4174 CTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCA 4215

Db   6364 CTACAATAATATTGAACGACAGGCTTCTCCAAAGTTCTACCA 6405
```

```
RESULT   9
GGGABAA
LOCUS       GGGABAA      1572 bp    mRNA            VRT       26-SEP-1994
DEFINITION  G.domesticus mRNA for GABA-A receptor gamma-4 subunit.
ACCESSION   X73533
VERSION     X73533.1  GI:414021
KEYWORDS    GABA-A receptor; GABA-A receptor gamma-4 subunit; glycoprotein;
            ligand gated ion channel; membrane spanning; multigene family;
            neurotransmitter receptor.
SOURCE      chicken.
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
            Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1572)
  AUTHORS   Harvey,R.J., Kim,H.C. and Darlison,M.G.
  TITLE     Molecular cloning reveals the existence of a fourth gamma subunit
            of the vertebrate brain GABAA receptor
  JOURNAL   FEBS Lett. 331 (3), 211-216 (1993)
  MEDLINE   93387470
REFERENCE   2  (bases 1 to 1572)
  AUTHORS   Darlison,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUN-1993) M. Darlison, Inst. fuer Zellbiochemie und
            Klinische Neurobiologie, Universitaet-Krankenhaus Eppendorf, Univ.
            Hamburg, 2000 Hamburg 20, FRG
FEATURES             Location/Qualifiers
     source          1. .1572
                     /organism="Gallus gallus"
                     /strain="Commercial Rhode Island cross"
                     /db_xref="taxon:9031"
                     /dev_stage="embryonic"
                     /tissue_type="whole brain"
                     /clone_lib="lambda gt10 cDNA library"
                     /clone="pcGR lambda4.1"
     CDS             88. .1461
                     /note="gamma-4 subunit"
                     /codon_start=1
                     /product="GABA-A receptor"
                     /protein_id="CAA51939.1"
                     /db_xref="GI:414022"
                     /db_xref="SWISS-PROT:P34904"
                     /translation="MPAMVLLLCLALGPALRSARCESTEEYDYDYLSINKTWVLTPKA
                     QETDATQILNSLLKNYDNKLRPDIGIKPTFIDVDIYVNSIGPVSVIQMEYTIDIFFAQ
                     TWYDRRLRFNSTLKALTLNTNMVSRIWIPDTFFRNSKRADSHWITTPNQLLRIWNDGK
                     VLYTLRLTIEAECLLQLQNFPMDTHSCPLVFSSYGYPREEIVYRWRRYSIEVSDQRTW
                     RLYQFDFTGLRNTSEVLRTGAGEYMVMTVSFDLSRRMGYFAIQTYIPCILTVVLSWVS
                     FWIKRDSTPARTSLGITTVLTMTTLSTISRKHLPRVSYITAMDLFVSVCFIFVFAALM
                     EYATLNYLVGNKKPLEHSSRKARLPPAGAQVMPSFTAININININMIMHWPPEIEEDEDD
                     DPGSPCLEGKECERFFCCIEDCQTGMWREGRVRIHISRLDSYSRVFFPTAFLLFNIVY
                     WIAYLYL"
     sig_peptide     88. .150
     mat_peptide     151. .1458
                     /product="GABA A receptor"
     misc_feature    151. .858
                     /note="large extracellular domain; putative"
     misc_feature    190. .198
                     /note="N-linked glycosylation site; putative"
     misc_feature    421. .429
                     /note="N-linked glycosylation site; putative"
     misc_feature    604. .648
                     /note="dicysteine loop; putative"
     misc_feature    775. .783
                     /note="N-linked glycosylation site; putative"
     misc_feature    859. .924
                     /note="membrane spanning domain; putative"
     misc_feature    937. .1002
                     /note="membrane spanning domain; putative"
     misc_feature    1036. .1104
                     /note="membrane spanning domain; putative"
     misc_feature    1105. .1386
                     /note="large intracellular loop; putative"
     misc_feature    1135. .1146
                     /note="casein kinase I phosphorylation site; putative"
     misc_feature    1141. .1149
                     /note="protein C kinase phosphorylation site; putative"
     misc_feature    1144. .1152
                     /note="protein C kinase phosphorylation site; putative"
     misc_feature    1375. .1386
                     /note="multifunctional calmodulin-dependent protein kinase
                     II phosphorylation site; putative"
     misc_feature    1387. .1458
                     /note="membrane spanning domain; putative"
BASE COUNT      356 a    443 c    385 g    388 t
ORIGIN
```

```
  Query Match             2.8%;  Score 173.6;  DB 4;  Length 1572;
  Best Local Similarity   71.0%;  Pred. No. 1.1e-36;
  Matches  230;  Conservative    0;  Mismatches   94;  Indels    0;  Gaps    0;

Qy   3861 CAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTG 3920

Db    803 CAGGGGAGTACATGGTGATGACGGTTTCCTTTGACTTAAGTAGACGTATGGGTTATTTTG 862

Qy   3921 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 3980

Db    863 CCATTCAGACCTACATTCCCTGCATCCTGACTGTTGTTCTGTCCTGGGTTTCCTTCTGGA 922

Qy   3981 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 4040

Db    923 TCAAGAGAGACTCTACACCAGCCAGGACATCCCTCGGTATCACCACTGTGCTAACAATGA 982

Qy   4041 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGG 4100

Db    983 CCACGCTGAGTACCATCTCCCGCAAGCACCTTCCACGTGTTTCCTATATCACAGCCATGG 1042

Qy   4101 ATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGC 4160

Db   1043 ACCTCTTTGTGTCTGTGTGCTTCATCTTCGTCTTTGCAGCTCTCATGGAGTATGCTACAC 1102
```

```
Qy   4161 TCAACTTCCTGATCTACAACCAGA 4184
          |||||| |||| |    ||| |||
Db   1103 TCAACTACCTGGTGGGAAACAAGA 1126


RESULT  10
HSGABAAS
LOCUS       HSGABAAS     1745 bp    mRNA            PRI       15-MAR-1991
DEFINITION  Human mRNA for GABA-A receptor, gamma 2 subunit.
ACCESSION   X15376
VERSION     X15376.1  GI:31636
KEYWORDS    GABA-A receptor; gamma subunit receptor; gamma-aminobutyric acid
            receptor.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1745)
  AUTHORS   Pritchett,D.B., Sontheimer,H., Shivers,B.D., Ymer,S.,
            Kettenmann,H., Schofield,P.R. and Seeburg,P.H.
  TITLE     Importance of a novel GABAA receptor subunit for benzodiazepine
            pharmacology
  JOURNAL   Nature 338 (6216), 582-585 (1989)
  MEDLINE   89181956
FEATURES             Location/Qualifiers
     source          1. .1745
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /dev_stage="fetal"
                     /tissue_type="brain"
                     /tissue_lib="fetal brain cDNA"
     mRNA            1. .>1745
                     /note="for GABA-A receptor gamma 2 subunit"
     sig_peptide     226. .342
     CDS             227. .1630
                     /codon_start=1
                     /product="GABA-A receptor gamma 2 subunit"
                     /protein_id="CAA33437.1"
                     /db_xref="GI:31637"
                     /db_xref="SWISS-PROT:P18507"
                     /translation="MSSPNIWSTGSSVYSTPVFSQKMTVWILLLLSLYPGFTSQKSDD
                     DYEDYASNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIG
                     PVNAINMEYTIDIFFAQMWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADA
                     HWITTPNRMLRIWNDGRVLYSLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEI
                     VYQWKRSSVEVGDTRSWRLYQFSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFT
                     IQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTA
                     MDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPAPTIDIRPRSATIQMN
                     NATHLQERDEEYGYECLDGKDCASFFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFP
                     TAFCLFNLVYWVSYLYL"
     mat_peptide     341. .1627
                     /product="GABA-A receptor gamma 2 subunit"
BASE COUNT      492 a    389 c    378 g    486 t
ORIGIN


  Query Match             2.3%;  Score 144.4;  DB 9;  Length 1745;
  Best Local Similarity   64.2%;  Pred. No. 1.2e-28;
  Matches  217;  Conservative    0;  Mismatches  121;  Indels    0;  Gaps    0;

Qy   3859 TTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGT 3918
          ||| || || |   |||||||| |  | | |||  || |||||||  |  | || ||  |
Db    991 TTCCGGAGATTATGTGGTCATGTCTGTCTACTTTGATCTGAGCAGAAGAATGGGATACTT 1050

Qy   3919 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 3978
          | || | || | |||| |||| |   |  | |      | || |||||||| || || ||
Db   1051 TACCATCCAGACCTATATCCCCTGCACACTCATTGTCGTCCTATCCTGGGTGTCTTTCTG 1110

Qy   3979 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 4038
          ||||||  |  ||  ||| ||||||| | || ||| |||| |||||| |||| ||||| ||
Db   1111 GATCAATAAGGATGCTGTTCCAGCCAGAACATCTTTAGGTATCACCACTGTCCTGACAAT 1170

Qy   4039 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 4098
          ||||||  |  ||||| || | || ||     ||||    ||||||||| |||||||  |

Db   1171 GACCACCCTCAGCACCATTGCCCGGAAATCGCTCCCCAAGGTCTCCTATGTCACAGCGAT 1230

Qy   4099 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 4158
          |||| ||| | |  |  | || ||| ||||   |||||  |||||| |||||| ||
Db   1231 GGATCTCTTTGTATCTGTTTGTTTCATCTTTGTCTTCTCTGCTCTGGTGGAGTATGGCAC 1290

Qy   4159 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATG 4196
          |  | |  |  ||  ||||| || |  |  | | |
Db   1291 CTTGCATTATTTTGTCAGCAACCGGAAACCAAGCAAGG 1328


RESULT  11
BOVGABAARG
LOCUS       BOVGABAARG   1428 bp    mRNA            MAM       27-APR-1993
DEFINITION  Bovine gamma-aminobutyrate receptor type A gamma-2 subunit mRNA,
            complete cds.
ACCESSION   M55563
VERSION     M55563.1  GI:163069
KEYWORDS    GABA-alpha receptor; gamma-aminobutyrate receptor type A.
SOURCE      Bovine cortex, cDNA to mRNA.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 1428)
  AUTHORS   Whiting,P.J., McKernan,R.M. and Iversen,L.L.
  TITLE     Another mechanism for creating diversity in gamma-aminobutyrate
            type A receptors: RNA splicing directs expression of two forms of
            gamma-2 subunit, one of which contains a protein kinase C
            phosphorylation site
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 87, 9966-9970 (1990)
  MEDLINE   91088632
FEATURES             Location/Qualifiers
     source          1. .1428
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /tissue_type="cortex"
     sig_peptide     1. .117
                     /gene="GABA-alpha receptor gamma-2 subunit"
     CDS             1. .1428
                     /gene="GABA-alpha receptor gamma-2 subunit"
                     /codon_start=1
                     /product="gamma-aminobutyrate receptor type A gamma-2
                     subuni"
                     /protein_id="AAA30531.1"
                     /db_xref="GI:163070"
                     /translation="MSSPNIWSTGSSVYSTPVFSQKMTLWILLLLSLYPGLTRQKSDD
                     DYEDYASNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIG
                     PVNAINMEYTIDIFFGQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADA
                     HWITTPNRMLRIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEI
                     VYQWKRSSVEVSDTRSWRLYQFSFVGLRNTTEVVKTTSGDYVVMTVYFDLSRRMGYFT
                     IQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTA
                     MDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPLLRMFSFKAPTIDIRP
                     RSATIQMNNATHLQERDEEYGYECLDGKDCASFFCCFEDCRTGAWRHGRIHIRIAKMD
                     SYARIFFPTAFCLFNLVYWVSYLYL"
     gene            1. .1428
                     /gene="GABA-alpha receptor gamma-2 subunit"
     mat_peptide     118. .1425
                     /gene="GABA-alpha receptor gamma-2 subunit"
                     /product="gamma-aminobutyrate receptor type A gamma-2
                     subuni"
BASE COUNT      399 a    325 c    303 g    401 t
ORIGIN


  Query Match             2.3%;  Score 142.8;  DB 3;  Length 1428;
  Best Local Similarity   63.9%;  Pred. No. 3.3e-28;
  Matches  216;  Conservative    0;  Mismatches  122;  Indels    0;  Gaps    0;

Qy   3859 TTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGT 3918
          ||| || || |   |||||||||  | |  ||  |  |||||||  |  | |||||  |
Db    765 TTCTGGGGATTATGTGGTCATGACTGTCTATTTTGACCTGAGCAGAAGAATGGGCTACTT 824
```

```
Qy   3919 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 3978
          || | || | |||  |||| | | |  | |      | || || ||||| || || ||
Db    825 CACCATCCAGACCTACATCCCCTGTACACTCATTGTTGTCCTATCTTGGGTGTCTTTCTG 884

Qy   3979 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 4038
          |||||| |  ||  ||| ||||||| | || ||| |||| |||||| |||| ||||| ||
Db    885 GATCAATAAGGATGCTGTTCCAGCCAGAACTTCTTTAGGAATCACCACTGTCCTGACAAT 944

Qy   4039 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 4098
          ||| ||  |  ||||| || | || |||  | ||||    ||||||||  |||||||  |
Db    945 GACTACCCTCAGCACCATTGCCCGGAAGTCTCTCCCCAAGGTCTCCTACGTCACAGCGAT 1004

Qy   4099 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 4158
          |||| ||| | |  |  | |||||| ||||   |||||  ||| || |||||| ||
Db   1005 GGATCTCTTTGTATCTGTTTGCTTCATCTTTGTCTTCTCTGCTTTGGTGGAGTATGGCAC 1064

Qy   4159 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATG 4196
          ||  | |   |  ||  ||||| || |  |  | | |
Db   1065 TCTGCATTATTTTGTCAGCAACCGGAAACCAAGCAAGG 1102


RESULT  12
MUSGABAAG2
LOCUS       MUSGABAAG2   2231 bp    mRNA            ROD       27-APR-1993
DEFINITION  Mus musculus GABA-A receptor gamma-2 subunit mRNA, complete cds.
ACCESSION   M62374
VERSION     M62374.1  GI:193403
KEYWORDS    GABA-alpha receptor gamma-2 subunit.
SOURCE      Mouse, cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2231)
  AUTHORS   Sikela,J.M., Shaw,W.D., Khan,A.S., Lin,L.-H., Leidenheimer,G. and
            Siegel,R.E.
  TITLE     A novel form of the gamma2 subunit of the GABA-A receptor:
            Functional, expresison and localization
  JOURNAL   Unpublished (1991)
FEATURES             Location/Qualifiers
     source          1. .2231
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
     CDS             348. .1772
                     /codon_start=1
                     /product="GABA-alpha receptor gamma-2 subunit"
                     /protein_id="AAA37653.1"
                     /db_xref="GI:193404"
                     /translation="MSSPNTWSIGSSVYSPVFSQKMTLWILLLLSLYPGFTSQKSDDD
                     YEDYASNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGP
                     VNAINMEYTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAH
                     WITTPNRMLRIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIV
                     YQWKRSSVEVGDTRSWRLYQFSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTI
                     QTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAM
                     DLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPLLRMFSFKAPTIDIRPR
                     SATIQMNNATHLQERDEEYGYECLDGKDCASFFCCFEDCRTGAWRHGRIHIRIAKMDS
                     YARIFFPTAFCLFNLVYWVSYLYL"
BASE COUNT      626 a    476 c    485 g    644 t
ORIGIN


  Query Match             2.3%;  Score 140.4;  DB 12;  Length 2231;
  Best Local Similarity   64.4%;  Pred. No. 1.6e-27;
  Matches  210;  Conservative    0;  Mismatches  116;  Indels    0;  Gaps    0;

Qy   3859 TTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGT 3918
          ||| |||||||   |||| ||| |  | | |||| || |||||||  |  | |||||  |
Db   1109 TTCTGGTGACTATGTGGTGATGTCTGTGTACTTCGATCTGAGCAGAAGAATGGGCTACTT 1168

Qy   3919 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 3978
          || | || |  ||  | || |   |  | | |  | | || |||||||| ||||| ||
Db   1169 CACCATCCAGACTTACATTCCCTGCACACTCATCGTGGTCCTGTCCTGGGTGTCCTTCTG 1228

Qy   3979 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 4038
          |||||| |  ||  ||| ||| ||| | || ||| |||| ||||| |||| ||||||||
Db   1229 GATCAATAAGGATGCTGTTCCTGCCAGAACATCTTTAGGAATCACTACTGTCCTGACCAT 1288

Qy   4039 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 4098
          ||| || ||  ||||| |  |  | ||    | | ||    |||||||| |||||||  |
Db   1289 GACAACTTTAAGCACCATAGCCAGAAAATCTCTGCCCAAGGTCTCCTATGTCACAGCAAT 1348

Qy   4099 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 4158
          |||| ||| | |  |  | |||||| ||||    || |  ||| || |||||| ||
Db   1349 GGATCTCTTTGTATCTGTTTGCTTCATCTTTGTGTTTTCTGCTTTGGTGGAGTATGGCAC 1408

Qy   4159 GCTCAACTTCCTGATCTACAACCAGA 4184
          ||  | |   |  ||  ||||| ||
Db   1409 CCTGCATTATTTTGTCAGCAACCGGA 1434


RESULT  13
MUSGABAAR
LOCUS       MUSGABAAR    2036 bp    mRNA            ROD       08-NOV-1993
DEFINITION  Mouse gamma-aminobutyric acid A receptor gamma-2 subunit mRNA,
            complete cds.
ACCESSION   M86572 M57522
VERSION     M86572.1  GI:193405
KEYWORDS    GABA-alpha receptor gamma-2 subunit; gamma-aminobutyric acid-A
            receptor.
SOURCE      Mus musculus (strain DBA/2J) adult brain cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2036)
  AUTHORS   Kofuji,P., Wang,J.B., Moss,S.J., Huganir,R.L. and Burt,D.R.
  TITLE     Generation of two forms of the gamma-aminobutyric acid A receptor
            gamma-2 subunit in mice by alternative splicing
  JOURNAL   J. Neurochem. 56, 713-715 (1991)
  MEDLINE   91108470
FEATURES             Location/Qualifiers
     source          1. .2036
                     /organism="Mus musculus"
                     /strain="DBA/2J"
                     /db_xref="taxon:10090"
                     /dev_stage="adult"
                     /tissue_type="brain"
     gene            177. .1577
                     /gene="GABA-A receptor gamma-2 subunit"
     sig_peptide     177. .290
                     /gene="GABA-A receptor gamma-2 subunit"
     CDS             177. .1577
                     /gene="GABA-A receptor gamma-2 subunit"
                     /codon_start=1
                     /product="gamma-aminobutyric acid A receptor gamma-2
                     subunit"
                     /protein_id="AAB59635.1"
                     /db_xref="GI:193406"
                     /translation="MSSPNTWSIGSSVYSPVFSQKMTLWILLLLSLYPGFTSQKSDDD
                     YEDYTSNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGP
                     VNAINMEYTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAH
                     WITTPNRMLRIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIV
                     YQWKRSSVEVGDTRSWRLYQFSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTI
                     QTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAM
                     DLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPAPTIDIRPRSATIQMNN
                     ATHLQERDEEYGYQCLDGKDCASFFCCFEDCRTGAWRHGRIHMRIAKMDSYARIFFPT
                     AFCLFNLVYWVSYLYL"
     mat_peptide     291. .1574
                     /gene="GABA-A receptor gamma-2 subunit"
                     /product="gamma-aminobutyric acid A receptor gamma-2
                     subunit"
     allele          321
                     /gene="GABA-A receptor gamma-2 subunit"
                     /note="found in strains DBA/2J and C57BL/6J polymorphism"
                     /replace="g"
     variation       1302^1303
                     /gene="GABA-A receptor gamma-2 subunit"
                     /replace="cttcttcggatgttttccttcaag"
```

```
BASE COUNT      597 a    422 c    443 g    574 t
ORIGIN

  Query Match             2.3%;  Score 140.4;  DB 12;  Length 2036;
  Best Local Similarity   64.4%;  Pred. No. 1.6e-27;
  Matches  210;  Conservative    0;  Mismatches  116;  Indels    0;  Gaps    0;

Qy   3859 TTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGT 3918
          ||| |||||||   |||| ||| |  | | |||| || |||||||  |  | |||||  |
Db    938 TTCTGGTGACTATGTGGTGATGTCTGTGTACTTCGATCTGAGCAGAAGAATGGGCTACTT 997

Qy   3919 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 3978
            || | ||  |  ||  | || |  |  | | |  | | || ||||||||  ||||| ||
Db    998 CACCATCCAGACTTACATTCCCTGCACACTCATCGTGGTCCTGTCCTGGGTGTCCTTCTG 1057

Qy   3979 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 4038
          |||||| |  ||  ||| ||| ||| | || ||| ||||  |||||  |||| ||||||||
Db   1058 GATCAATAAGGATGCTGTTCCTGCCAGAACATCTTTAGGAATCACTACTGTCCTGACCAT 1117

Qy   4039 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 4098
          ||| || ||  ||||| |  |  | ||  | | ||    |||||||| |||||||  |
Db   1118 GACAACTTTAAGCACCATAGCCAGAAAATCTCTGCCCAAGGTCTCCTATGTCACAGCAAT 1177

Qy   4099 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 4158
          |||| ||| | |  |  | |||||| ||||    || |  ||| || |||||| ||
Db   1178 GGATCTCTTTGTATCTGTTTGCTTCATCTTTGTGTTTTCTGCTTTGGTGGAGTATGGCAC 1237

Qy   4159 GCTCAACTTCCTGATCTACAACCAGA 4184
           ||  | |   |  ||  ||||| ||
Db   1238 CCTGCATTATTTTGTCAGCAACCGGA 1263


RESULT  14
AF090376
LOCUS       AF090376      346 bp    mRNA            ROD       15-SEP-1998
DEFINITION  Mus musculus GABA-A receptor epsilon subunit mRNA, partial cds.
ACCESSION   AF090376
VERSION     AF090376.1  GI:3600109
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Gustincich,S., Feigenspan,A., Sieghart,W. and Raviola,E.
  TITLE     GABAA receptors of dopaminergic cells of the mouse retina
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 346)
  AUTHORS   Gustincich,S., Feigenspan,A. and Raviola,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-SEP-1998) Neurobiology, Harvard Medical School, 220
            Longwood Avenue, Boston, MA 02115, USA
FEATURES             Location/Qualifiers
     source          1. .346
                     /organism="Mus musculus"
                     /strain="C57Bl/6J"
                     /db_xref="taxon:10090"
                     /tissue_type="amygdala"
     CDS             <1. .>346
                     /codon_start=2
                     /product="GABA-A receptor epsilon subunit"
                     /protein_id="AAC35563.1"
                     /db_xref="GI:3600110"
                     /translation="PLSFSSFSYDDSEMIYKWENFKLEINAKNTWKLLEFDFTGVNNK
                     TEIISTPFGDFMVMTFFFNVSRRFGFIVFQNYVPSSVTTMLSWVSFWIKIEAAAARAS
                     VGVSSVLTMATLG"
BASE COUNT       83 a     81 c     73 g    109 t
ORIGIN

  Query Match             2.3%;  Score 140;  DB 12;  Length 346;
  Best Local Similarity   84.0%;  Pred. No. 1.7e-27;
  Matches  158;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy   3863 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 3922
          ||||||||||||||||||||  | ||||||||||| ||||||||||||||||   ||| |
Db    158 GGTGACTTCATGGTCATGACATTCTTCTTCAATGTAAGCAGGCGGTTTGGCTTCATTGTC 217

Qy   3923 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 3982
          |||||||| ||||| |||||||| || ||||| ||||||||||||||| ||||| ||||||
Db    218 TTTCAAAATTATGTTCCTTCTTCTGTCACCACAATGCTCTCCTGGGTCTCCTTCTGGATC 277

Qy   3983 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 4042
          |||| |||  ||||| | ||| || ||||| ||||| |||  ||||| || |||||| ||
Db    278 AAGATAGAAGCTGCTGCTGCCAGGGCCTCTGTAGGGGTCAGTTCTGTGCTCACCATGGCC 337

Qy   4043 ACGTTGGG 4050
          ||| ||||
Db    338 ACGCTGGG 345


RESULT  15
RATGABAAI
LOCUS       RATGABAAI    1838 bp    DNA             ROD       27-APR-1993
DEFINITION  Rattus rattus GABA-A receptor gamma-2 subunit gene, complete cds.
ACCESSION   L08497
VERSION     L08497.1  GI:204217
KEYWORDS    GABA-alpha receptor gamma-2 subunit.
SOURCE      Rattus rattus (library: lambda-cDNA) brain DNA.
  ORGANISM  Rattus rattus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 1838)
  AUTHORS   Shivers,B.D., Killisch,I., Sprengel,R., Sontheimer,H., Koehler,M.,
            Schofield,P.R. and Seeburg,P.H.
  TITLE     Two novel GABA-A receptor subunits exist in distinct neuronal
            subpopulations
  JOURNAL   Neuron 3, 327-337 (1989)
  MEDLINE   90380375
REFERENCE   2  (bases 1 to 1838)
  AUTHORS   Seeburg,P.H., Wisden,W., Verdoorn,T.A., Pritchett,D., Werner,P.,
            Herb,A., Lueddens,H., Sprengel,R. and Sakmann,B.
  TITLE     The GABA-A receptor family: Molecular and functional diversity
  JOURNAL   Cold Spring Harb. Symp. Quant. Biol. 55, 29-40 (1990)
  MEDLINE   92111149
REFERENCE   3  (bases 1 to 1838)
  AUTHORS   Draguhn,A., Verdoorn,T.A., Ewert,M., Seeburg,P.H. and Sakmann,B.
  TITLE     Functional and molecular distinction between recombinant rat GABA-A
            receptor subtypes by Zn(2+)
  JOURNAL   Neuron 5, 781-788 (1990)
  MEDLINE   91097789
REFERENCE   4  (bases 1 to 1838)
  AUTHORS   Wisden,W. and Seeburg,P.H.
  TITLE     GABAA receptor channels: from subunits to functional entities
  JOURNAL   Curr. Opin. Neurobiol. 2 (3), 263-269 (1992)
  MEDLINE   92353623
REFERENCE   5  (bases 1 to 1838)
  AUTHORS   Wisden,W., Laurie,D.J., Monyer,H. and Seeburg,P.H.
  TITLE     The distribution of 13 GABA-A receptor subunit mRNAs in the rat
            brain - I. Telencephalon, diencephalon, mesencephalon
  JOURNAL   J. Neurosci. 12, 1040-1062 (1992)
  MEDLINE   92185508
REFERENCE   6  (bases 1 to 1838)
  AUTHORS   Laurie,D.J., Wisden,W. and Seeburg,P.H.
  TITLE     The distribution of 13 GABA-A receptor subunit mRNAs in the rat
            brain - II. Olfactory bulb and cerebellum
  JOURNAL   J. Neurosci. 12, 1063-1076 (1992)
  MEDLINE   92185509
FEATURES             Location/Qualifiers
     source          1. .1838
                     /organism="Rattus rattus"
                     /db_xref="taxon:10117"
                     /tissue_type="brain"
                     /tissue_lib="lambda-cDNA"
     CDS             45. .1445
```

```
                     /codon_start=1
                     /product="GABA-A receptor gamma-2 subunit"
                     /protein_id="AAC42036.1"
                     /db_xref="GI:204218"
                     /translation="MSSPNTWSTGSTVYSPVFSQKMTLWILLLLSLYPGFTSQKSDDD
                     YEDYASNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGP
                     VNAINMEYTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAH
                     WITTPNRMLRIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIV
                     YQWKRSSVEVGDTRSWRLYQFSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTI
                     QTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAM
                     DLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPAPTIDIRPRSATIQMNN
                     ATHLQERDEEYGYECLDGKDCASFFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPT
                     AFCLFNLVYWVSYLYL"
BASE COUNT      509 a    404 c    408 g    517 t
ORIGIN


  Query Match             2.3%;  Score 140;  DB 12;  Length 1838;
  Best Local Similarity   63.2%;  Pred. No. 2e-27;
  Matches  215;  Conservative    0;  Mismatches  125;  Indels    0;  Gaps    0;

Qy   3859 TTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGT 3918
          ||| |||||||   |||| ||| |  | | |||  || |||||||  |  | || ||  |
Db    806 TTCTGGTGACTATGTGGTTATGTCCGTGTACTTTGATCTGAGCAGAAGAATGGGGTACTT 865

Qy   3919 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 3978
          | || | || | |||  | || |   |  | |    | | || |||||||| ||||| ||
Db    866 TACCATCCAGACCTACATTCCCTGCACACTCATTGTGGTTCTGTCCTGGGTGTCCTTCTG 925

Qy   3979 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 4038
          |||||| |  ||  |||  || ||  | || ||| |||| |||||  |||| ||||| ||
Db    926 GATCAATAAGGATGCTGTCCCTGCAAGAACATCTTTAGGAATCACGACTGTCCTGACGAT 985

Qy   4039 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 4098
          ||||||  |  ||||| |  | || |||  | | ||    |||||||| |||||||  |
Db    986 GACCACTCTCAGCACCATAGCCCGGAAGTCTCTGCCCAAGGTCTCCTATGTCACAGCAAT 1045

Qy   4099 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 4158
          |||| |||   || |  | |||||| ||||    || |  ||| || |||||| || |
Db   1046 GGATCTCTTCGTCTCTGTTTGCTTCATCTTTGTGTTTTCAGCTTTGGTGGAGTATGGTAC 1105

Qy   4159 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCT 4198
           ||  |||   |  |   ||||| || |  |  | | | |
Db   1106 CCTGCACTATTTTGTGAGCAACCGGAAACCAAGCAAGGAT 1145


Search completed: March  9, 2000, 01:28:41
Job time: 6704 sec
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2000, 13:24:12 ; Search time 147.28 Seconds
(without alignments)
4996.021 Million cell updates/sec

Title: US-09-030-832-1
Perfect score: 6146
Sequence: 1 GTCTTATAATTGCTAAGCAC.....TCACCATCATCTGAAATGGG 6146

Scoring table: IDENTITY_NUC

Searched: 214294 seqs, 59861208 residues

Database : Issued_Patents_NA:*

Word size : 0

Number of hits that pass the threshold : 428588
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	128	2.1	1732	2	US-08-417-330A-17	Sequence 17, Appl
	2	119.6	1.9	2310	2	US-08-417-330A-15	Sequence 15, Appl
	3	112.8	1.8	1638	2	US-08-417-330A-13	Sequence 13, Appl
	4	105.6	1.7	2191	2	US-08-417-330A-11	Sequence 11, Appl
	5	99.8	1.6	1866	2	US-08-417-330A-19	Sequence 19, Appl
	6	99.6	1.6	1491	1	US-08-137-614A-3	Sequence 3, Appli
	7	99.6	1.6	1491	3	US-08-768-301-1	Sequence 1, Appli
	8	86.6	1.4	2635	3	US-08-768-301-3	Sequence 3, Appli
	9	73	1.2	1657	2	US-08-554-659-1	Sequence 1, Appli
	10	72.8	1.2	1542	1	US-08-249-112-1	Sequence 1, Appli
	11	72.8	1.2	1542	6	PCT-US95-06556-1	Sequence 1, Appli
	12	72	1.2	7218	1	US-08-232-463-14	Sequence 14, Appl
	13	71.4	1.2	1657	2	US-08-554-659-3	Sequence 3, Appli
	14	66.6	1.1	2066	5	US-08-072-064-3	Sequence 3, Appli
	15	66.6	1.1	2066	5	US-08-072-064-5	Sequence 5, Appli
	16	65	1.1	2066	5	US-08-072-064-2	Sequence 2, Appli
	17	65	1.1	1970	5	US-08-072-064-9	Sequence 9, Appli
	18	65	1.1	2059	6	PCT-US92-08558-2	Sequence 2, Appli
	19	65	1.1	1970	6	PCT-US92-08558-3	Sequence 3, Appli
	20	63.4	1.0	2066	5	US-08-072-064-7	Sequence 7, Appli
	21	62.2	1.0	3958	2	US-08-435-933-5	Sequence 5, Appli
	22	62.2	1.0	3958	6	PCT-US96-06035-5	Sequence 5, Appli
	23	61	1.0	1650	1	US-08-459-100A-1	Sequence 1, Appli
	24	61	1.0	1650	6	PCT-US94-09589-1	Sequence 1, Appli
	25	57.8	0.9	1479	1	US-08-249-112-2	Sequence 2, Appli
	26	57.8	0.9	1479	6	PCT-US95-06556-2	Sequence 2, Appli
c	27	47.6	0.8	7218	1	US-08-232-463-14	Sequence 14, Appl
	28	39.2	0.6	152	2	US-08-435-933-4	Sequence 4, Appli
	29	39.2	0.6	152	6	PCT-US96-06035-4	Sequence 4, Appli
	30	37.4	0.6	575	2	US-08-554-659-11	Sequence 11, Appl
	31	36.6	0.6	8779	3	US-08-750-703-4	Sequence 4, Appli
c	32	35	0.6	4032	1	US-08-107-748-3	Sequence 3, Appli
c	33	35	0.6	4032	1	US-08-245-809-4	Sequence 4, Appli
c	34	35	0.6	4032	6	PCT-US92-01385-3	Sequence 3, Appli
	35	34.6	0.6	56516	4	US-08-996-306-1	Sequence 1, Appli
	36	34.4	0.6	2254	2	US-08-153-848-27	Sequence 27, Appl
	37	34.4	0.6	1161	2	US-08-153-848-31	Sequence 31, Appl
	38	34.4	0.6	2254	6	PCT-US93-11153-27	Sequence 27, Appl
	39	34.4	0.6	1161	6	PCT-US93-11153-31	Sequence 31, Appl
c	40	33.2	0.5	2397	7	5258288-2	Patent No. 5258288
c	41	33	0.5	2791	4	US-09-016-000-8	Sequence 8, Appli
c	42	32.8	0.5	790	7	5194596-8	Patent No. 5194596
c	43	32.8	0.5	789	7	5219739-8	Patent No. 5219739
	44	32.6	0.5	128	2	US-08-554-659-7	Sequence 7, Appli
	45	32.6	0.5	3238	6	PCT-US94-10080-5	Sequence 5, Appli

ALIGNMENTS

```
RESULT 1
US-08-417-330A-17
; Sequence 17, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1732 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  27...1385
;      OTHER INFORMATION:
US-08-417-330A-17


  Query Match                 2.1%;  Score 128;  DB 2;  Length 1732;
```

```
  Best Local Similarity   61.9%;  Pred. No. 5.1e-29;
  Matches  203;  Conservative    0;  Mismatches  125;  Indels    0;  Gaps    0;

Qy   3861 CAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTG 3920
          ||||||| | | |  | |||||  ||| |||| |  ||   |||  | | |||||  |
Db    697 CAGGTGAATACGTTATAATGACAGTTTACTTCCACTTGCAAAGGAAGATGGGCTACTTCA 756

Qy   3921 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 3980
            | || |  ||    ||||      ||||    || || |||  ||| || || ||||
Db    757 TGATACAGATATACACTCCTTGCATTATGACAGTCATTCTTTCCCAGGTGTCTTTCTGGA 816

Qy   3981 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 4040
          | || |  ||||| |  ||||  | ||   ||| |||||||| ||||| | || ||||
Db    817 TTAATAAGGAGTCCGTCCCAGCAAGAACTGTTCTTGGGATCACCACTGTTTTAACTATGA 876

Qy   4041 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGG 4100
          |||| ||| ||| |  | | ||  |   ||| ||  || || |||  ||| ||| |||
Db    877 CCACTTTGAGCATCAGTGCCCGGCACTCTTTGCCAAAAGTGTCATATGCCACTGCCATGG 936

Qy   4101 ATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGC 4160
          |||  |  || ||  | ||||| |  |||  |||||  |||||  | ||||| || |
Db    937 ATTGGTTCATAGCTGTTTGCTTTGCATTCGTCTTCTCTGCTCTTATCGAGTTCGCAGCTG 996

Qy   4161 TCAACTTCCTGATCTACAACCAGACAAA 4188
          |||||| | | | | |    |||||| |
Db    997 TCAACTACTTTACCAATCTTCAGACACA 1024


RESULT   2
US-08-417-330A-15
; Sequence 15, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2310 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  298...1683
;      OTHER INFORMATION:
US-08-417-330A-15


  Query Match             1.9%;  Score 119.6;  DB 2;  Length 2310;
  Best Local Similarity   61.0%;  Pred. No. 2.4e-26;
  Matches  194;  Conservative    0;  Mismatches  124;  Indels    0;  Gaps    0;

Qy   3861 CAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTG 3920
          |||| || | ||   |||||||   |  |||| |  |||  |||  | |||||||  |||
Db   1019 CAGGCGAATACACAATCATGACAGCTCACTTCCACCTGAAAAGGAAGATTGGCTACTTTG 1078

Qy   3921 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 3980
            | | || | |||  | || |       |||||  |||  | ||   ||| ||||||||||
Db   1079 TCATCCAGACCTACCTTCCCTGCATAATGACCGTGATCTTATCACAGGTGTCCTTTTGGC 1138

Qy   3981 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 4040
          | ||    || || |  |||||| ||||   | | ||| ||||| | || ||||||||||
Db   1139 TGAACCGGGAATCAGTCCCAGCCAGGACAGTTTTTGGGGTCACCACGGTGCTGACCATGA 1198

Qy   4041 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGG 4100
          | ||  |  ||| |    |  | ||   | | ||    ||  ||||   ||| ||| |||
Db   1199 CGACCCTCAGCATCAGCGCCAGGAACTCTCTGCCCAAAGTGGCCTACGCCACCGCCATGG 1258

Qy   4101 ATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGC 4160
          | |  |  || ||  | ||||  | ||||  |||||  || ||| | ||||||||   |
Db   1259 ACTGGTTCATAGCTGTGTGCTATGCCTTCGTCTTCTCGGCGCTGATAGAGTTTGCCACGG 1318

Qy   4161 TCAACTTCCTGATCTACA 4178
          |||| | | | | | | |
Db   1319 TCAATTACTTTACCAAGA 1336


RESULT   3
US-08-417-330A-13
; Sequence 13, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
```

```
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1638 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  87...1562
;      OTHER INFORMATION:
US-08-417-330A-13


  Query Match             1.8%;  Score 112.8;  DB 2;  Length 1638;
  Best Local Similarity   59.3%;  Pred. No. 2.3e-24;
  Matches  192;  Conservative    0;  Mismatches  132;  Indels    0;  Gaps    0;

Qy   3853 GTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGG 3912
          || |  | |||| || |   | |||||||| |    |||| || | |   |     ||||
Db    854 GTCTAGTACAGGAGAATATGTCGTCATGACAACCCACTTCCATCTCAAGCGAAAAATTGG 913

Qy   3913 CTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTC 3972
          |||  |||   | || | |||  | || | |  | ||||    || || ||    || ||
Db    914 CTACTTTGTGATCCAGACCTACTTGCCATGTATCATGACTGTCATTCTGTCACAAGTGTC 973

Qy   3973 CTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCT 4032
            || ||| |||| | |||||||| ||| ||||| ||     | ||  ||||| |||| ||
Db    974 GTTCTGGCTCAACAGAGAGTCTGTTCCTGCCCGTACAGTCTTTGGTGTCACCACTGTGCT 1033

Qy   4033 GACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCAC 4092
          ||||||||||| ||| | | |  | |  | ||    || ||    ||  | |||   ||
Db   1034 TACCATGACCACCTTGAGTATCAGTGCCAGAAATTCCTTACCTAAAGTGGCATATGCGAC 1093

Qy   4093 AGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTT 4152
          |||  |||| |   |  || ||| |||| |  | |||    || |  || ||| | || ||
Db   1094 GGCCATGGACTGGTTCATAGCCGTCTGTTATGCCTTTGTATTTTCTGCACTGATTGAATT 1153

Qy   4153 TGCTGTGCTCAACTTCCTGATCTA 4176
          |||     ||||||   | | | |
Db   1154 TGCCACTGTCAACTATTTCACCAA 1177


RESULT   4
US-08-417-330A-11
; Sequence 11, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2191 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  214...1566
;      OTHER INFORMATION:
US-08-417-330A-11


  Query Match             1.7%;  Score 105.6;  DB 2;  Length 2191;
  Best Local Similarity   58.1%;  Pred. No. 4.6e-22;
  Matches  186;  Conservative    0;  Mismatches  134;  Indels    0;  Gaps    0;

Qy   3859 TTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGT 3918
          | |||||||  |   |  || |||||    |   ||| |  |||  ||     |||| ||| |
Db    912 TACAGGTGAATATACTGTAATGACAGCTCATTTCCACCTGAAAAGAAAAATTGGGTATTT 971

Qy   3919 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 3978
          ||   |||||| |||| | ||||    | ||||    || ||||||   ||||| || ||
Db    972 TGTGATTCAAACCTATCTGCCTTGCATCATGACTGTCATTCTCTCCCAAGTTTCATTCTG 1031

Qy   3979 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 4038
          | | || | ||| ||||  || ||  | ||     | ||  | ||  |||| || || ||
Db   1032 GCTTAACAGAGAATCTGTGCCTGCAAGAACTGTGTTTGGAGTAACAACTGTCCTAACAAT 1091

Qy   4039 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 4098
          ||| ||  |  ||| |  | |||| ||   | ||||    ||  | |||   || ||| |
Db   1092 GACAACTCTAAGCATCAGTGCTCGGAATTCTCTCCCCAAAGTGGCTTATGCAACTGCCAT 1151

Qy   4099 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 4158
          ||| |  | ||| ||  | || |  |  ||    |||| || ||  | || |||||
Db   1152 GGACTGGTTTATTGCTGTTTGTTATGCATTTGTGTTCTCTGCCCTAATTGAATTTGCAAC 1211

Qy   4159 GCTCAACTTCCTGATCTACA 4178
            | || | | | | | | |
Db   1212 TGTTAATTACTTCACCAAAA 1231


RESULT   5
US-08-417-330A-19
; Sequence 19, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
```

```
;       STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;       CITY:  RAHWAY
;       STATE:  NJ
;       COUNTRY:  US
;       ZIP:  07065-0900
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/417,330A
;       FILING DATE:  05-APR-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  HAND, MARK
;       REGISTRATION NUMBER:  36,545
;       REFERENCE/DOCKET NUMBER:  T1109IA
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  908-594-3905
;       TELEFAX:  908-594-4720
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1866 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  Coding Sequence
;       LOCATION:  225...1646
;       OTHER INFORMATION:
US-08-417-330A-19


  Query Match           1.6%;  Score 99.8;  DB 2;  Length 1866;
  Best Local Similarity  56.6%;  Pred. No. 2.5e-20;
  Matches  185;  Conservative    0;  Mismatches  142;  Indels    0;  Gaps    0;

Qy   3849 TTTTGTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGT 3908
          || | | |    |||||  ||         |  |  |  ||| ||  | |  ||
Db    889 TTGTTTTTTCCACAGGTTCCTATCCCAGGTTATCCCTCAGCTTTAAGCTTAAGAGAAACA 948

Qy   3909 TTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGG 3968
          |||||||  ||  | | ||||  ||  | |||||   | |||  || || ||||||||||
Db    949 TTGGCTACTTTATCCTGCAAACATACATGCCTTCCATCCTGATTACCATCCTCTCCTGGG 1008

Qy   3969 TTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTG 4028
          | ||||| |||||  ||    ||  || |  | ||  ||    |  |||| |||||  |||
Db   1009 TCTCCTTCTGGATTAATTACGATGCTTCAGCTGCAAGGGTGGCATTAGGAATCACAACTG 1068

Qy   4029 TTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATA 4088
          | || || ||||||||  |   ||||      ||  | | | ||||      || |||||
Db   1069 TCCTCACAATGACCACAATCAACACCCACCTCCGGGAAACTCTCCCTAAAATCCCCTATG 1128

Qy   4089 TCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGG 4148
          | |  ||| | ||  | ||  |       ||||| ||||||   |||   || ||  |||
Db   1129 TGAAGGCCATTGACATGTACCTGATGGGGTGCTTTGTCTTCGTTTTCATGGCCCTTCTGG 1188

Qy   4149 AGTTTGCTGTGCTCAACTTCCTGATCT 4175
          | | |||  |  |||||| | |  |||
Db   1189 AATATGCCCTAGTCAACTACATCTTCT 1215


RESULT   6
US-08-137-614A-3
; Sequence 3, Application US/08137614A
; Patent No. 5487976
;  GENERAL INFORMATION:
;     APPLICANT:  Soderlund, David M.
;     APPLICANT:  Knipple, Douglas C.
;     APPLICANT:  Henderson, Joseph E.
;     TITLE OF INVENTION:  Gene Encoding An Insect
;     TITLE OF INVENTION:  Gamma-Aminobutyric Acid (GABA) Receptor Subunit
;     NUMBER OF SEQUENCES:  31
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;       STREET:  Clinton Square, P.O. Box 1051
;       CITY:  Rochester
;       STATE:  New York
;       COUNTRY:  USA
;       ZIP:  14603
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/137,614A
;       FILING DATE:  15-OCT-1993
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Timian, Susan J.
;       REGISTRATION NUMBER:  34,103
;       REFERENCE/DOCKET NUMBER:  19603/120
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (716)263-1636
;       TELEFAX:  (716)263-1600
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1491 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-137-614A-3


  Query Match           1.6%;  Score 99.6;  DB 1;  Length 1491;
  Best Local Similarity  57.8%;  Pred. No. 2.5e-20;
  Matches  177;  Conservative    0;  Mismatches  129;  Indels    0;  Gaps    0;

Qy   3861 CAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTG 3920
          | || | ||    |  | |  || | |  |||||  ||    ||    | || ||  |||
Db    719 CTGGAGTCTATCAGCGCCTCTCGCTCTCATTCAAACTGCAACGGAATATCGGATACTTTG 778

Qy   3921 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 3980
            || ||||  ||| | ||         ||| |   |||||  || ||||| || || ||||
Db    779 TATTCCAAACTTATCTGCCCAGCATTCTGATCGTAATGCTGTCGTGGGTCTCGTTCTGGA 838

Qy   3981 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 4040
          | ||    ||| |  |   ||||||    |  | || ||||||  | || || ||||||||
Db    839 TTAACCACGAGGCGACGAGTGCCCGGGTTGCATTGGGCATCACCACGGTGCTCACCATGA 898

Qy   4041 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGG 4100
          ||||  |  ||||   |  ||| |       | |||||  | || ||| | |  ||  | |
Db    899 CCACCATTAGCACGGGTGTTCGCAGCTCACTGCCGCGCATATCGTATGTGAAGGCGATCG 958

Qy   4101 ATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGC 4160
          |  | ||| | | |||  |||||||| |||   |||   || || |||||  |  ||||
Db    959 ACATTTATCTGGTCATGTGCTTCGTTTTCGTGTTCGCAGCCCTCTTGGAATACGCTGCCG 1018

Qy   4161 TCAACT 4166
          | ||||
Db   1019 TTAACT 1024


RESULT   7
US-08-768-301-1
; Sequence 1, Application US/08768301
; Patent No. 5854002
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  Tomalski, Michael D.
;    APPLICANT:  Gant, Daniel B.
;    TITLE OF INVENTION:  METHOD OF IDENTIFYING COMPOUNDS THAT BIND
;    TITLE OF INVENTION:  TO THE INSECT GABA RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brumbaugh, Graves, Donohue & Raymond
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  10112-0228
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/768,301
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacLeod, Janet M
;      REGISTRATION NUMBER:  35,263
;      REFERENCE/DOCKET NUMBER:  A30693
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-408-2500
;      TELEFAX:  212-765-2519
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
US-08-768-301-1


  Query Match             1.6%;  Score 99.6;  DB 3;  Length 1491;
  Best Local Similarity   57.8%;  Pred. No. 2.5e-20;
  Matches  177;  Conservative    0;  Mismatches  129;  Indels    0;  Gaps    0;

Qy   3861 CAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTG 3920
          | || | ||    |  | |  || | |  |||||  ||    ||    | || ||  |||
Db    719 CTGGAGTCTATCAGCGCCTCTCGCTCTCATTCAAACTGCAACGGAATATCGGATACTTTG 778

Qy   3921 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 3980
            || ||||  ||| | ||        ||| |   ||||| || ||||| || || ||||
Db    779 TATTCCAAACTTATCTGCCCAGCATTCTGATCGTAATGCTGTCGTGGGTCTCGTTCTGGA 838

Qy   3981 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 4040
          | ||    ||| |  |    ||||||    |  | || ||||||| | || || |||||||
Db    839 TTAACCACGAGGCGACGAGTGCCCGGGTTGCATTGGGCATCACCACGGTGCTCACCATGA 898

Qy   4041 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGG 4100
          ||||  |  ||||   |  ||| |      | |||||  | || ||| | |  ||  | |
Db    899 CCACCATTAGCACGGGTGTTCGCAGCTCACTGCCGCGCATATCGTATGTGAAGGCGATCG 958

Qy   4101 ATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGC 4160
          |  | ||| | | ||| |||||||| |||   |||   || || ||||| |  ||||
Db    959 ACATTTATCTGGTCATGTGCTTCGTTTTCGTGTTCGCAGCCCTCTTGGAATACGCTGCCG 1018

Qy   4161 TCAACT 4166
          | ||||
Db   1019 TTAACT 1024
```

```
RESULT   8
US-08-768-301-3
; Sequence 3, Application US/08768301
; Patent No. 5854002
;  GENERAL INFORMATION:
;    APPLICANT:  Tomalski, Michael D.
;    APPLICANT:  Gant, Daniel B.
;    TITLE OF INVENTION:  METHOD OF IDENTIFYING COMPOUNDS THAT BIND
;    TITLE OF INVENTION:  TO THE INSECT GABA RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brumbaugh, Graves, Donohue & Raymond
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  10112-0228
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/768,301
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacLeod, Janet M
;      REGISTRATION NUMBER:  35,263
;      REFERENCE/DOCKET NUMBER:  A30693
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-408-2500
;      TELEFAX:  212-765-2519
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2635 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
US-08-768-301-3


  Query Match             1.4%;  Score 86.6;  DB 3;  Length 2635;
  Best Local Similarity   54.2%;  Pred. No. 3.6e-16;
  Matches  176;  Conservative    0;  Mismatches  149;  Indels    0;  Gaps    0;

Qy   3856 TCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTA 3915
          || | |    || | |    |  ||| | |   |||| |  ||    | |   | ||| |
Db   1477 TCATCCGTCGGAGTACTCCATGTTGATGGTAAACTTCCACCTGCAGCGTCACATGGGCAA 1536

Qy   3916 TGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTT 3975
            |      | ||    || |  || |  | | ||      | | |||   ||||| |||||
Db   1537 CTTCCTGATCCAGGTGTACGGTCCCTGCTGCCTGCTGGTGGTCCTCAGTTGGGTGTCCTT 1596

Qy   3976 TTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGAC 4035
            ||| | ||    ||| |  || | |  |||    || || ||||||||  | || |||||
Db   1597 CTGGCTGAACCGCGAGGCCACTGCTGATCGGGTTTCCCTCGGGATCACTACCGTGCTGAC 1656

Qy   4036 CATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGC 4095
            ||||||    | ||        |||| | | || | ||    || ||||||  ||| ||
Db   1657 GATGACCTTTCTCGGACTGGAGGCTCGCACGGATCTGCCCAAGGTGTCCTATCCCACGGC 1716
```

```
Qy   4096 CTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGC 4155
          | |||| ||||   |   | |||  |||| |||   |||   | |  |  || |||||||
Db   1717 CCTGGACTTCTTCGTGTTCCTCTCGTTCGGCTTTATCTTTGCCACAATCCTGCAGTTTGC 1776

Qy   4156 TGTGCTCAACTTCCTGATCTACAAC 4180
           ||| |  ||| |   | | |  ||
Db   1777 CGTGGTGCACTACTACACCAAGTAC 1801
```

RESULT 9
US-08-554-659-1
; Sequence 1, Application US/08554659
; Patent No. 5767261
; GENERAL INFORMATION:
; APPLICANT: Wingate, Vincent
; APPLICANT: Wolff, Mark
; TITLE OF INVENTION: LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,659
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9732
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1657 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 115..1581
US-08-554-659-1

Query Match 1.2%; Score 73; DB 2; Length 1657;
Best Local Similarity 54.7%; Pred. No. 4e-12;
Matches 145; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

```
Qy   3907 GTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTG 3966
          | | || ||   |    |||| |  ||| | || |||  | | |     ||  | || ||
Db    864 GATGGGATACTATTTAATTCAGATTTATATTCCGTCTGGCCTAATTGTCATTATATCTTG 923

Qy   3967 GGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTC 4026
          ||| || |||||| | ||   | | |  | || ||  ||   || |||||  |||| |
Db    924 GGTATCATTTTGGTTGAATCGAAATGCGACACCTGCAAGGGTATCACTAGGTGTCACAAC 983

Qy   4027 TGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTA 4086
          |||  |||| ||||| ||| |     | |   |   |  | | ||     |||| ||
Db    984 TGTATTGACGATGACGACGCTCATGTCGTCCACGAATGCGGCTCTGCCCAAGATCTCATA 1043

Qy   4087 TATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTT 4146
```

```
          | |||   || | ||| ||||| | |  |  || |||||| |   ||||  |  | | |
Db   1044 TGTCAAGTCCATCGATGTCTATCTGGGAACTTGTTTCGTCATGGTCTTCACCAGTTTACT 1103

Qy   4147 GGAGTTTGCTGTGCTCAACTTCCTG 4171
           || | |||   | |   ||   ||
Db   1104 AGAATATGCCACGGTTGGCTATATG 1128
```

RESULT 10
US-08-249-112-1
; Sequence 1, Application US/08249112
; Patent No. 5527703
; GENERAL INFORMATION:
; APPLICANT: Cully, Doris F.
; APPLICANT: Arena, Joseph P.
; APPLICANT: Liu, Ken K.
; APPLICANT: Vassilatis, Demetrios
; TITLE OF INVENTION: DNA ENCODING GLUTAMATE GATED CHLORIDE
; TITLE OF INVENTION: CHANNELS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wallen, John W.
; STREET: 126 E. Lincoln Ave., P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,112
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 19194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-249-112-1

Query Match 1.2%; Score 72.8; DB 1; Length 1542;
Best Local Similarity 55.0%; Pred. No. 4.4e-12;
Matches 143; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

```
Qy   3924 TTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCA 3983
          | |||  |||  |||| || | | ||       ||  | ||||||||||| |||||| |
Db    886 TCCAACTCTACATCCCGTCATGCATGCTAGTCATCGTATCCTGGGTTTCATTTTGGTTTG 945

Qy   3984 AGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCA 4043
          |   |    |    || || ||   | | || ||  ||||| |  | || || |||||
Db    946 ATCGAACTGCAATCCCGGCTCGTGTCACCCTCGGAGTCACCACGCTGCTTACAATGACAG 1005

Qy   4044 CGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATT 4103
          |         ||  |     |   | || | || ||||||||||  ||  | |||
Db   1006 CTCAATCAGCCGGTATCAATTCACAACTACCTCCAGTTTCCTATATCAAGGCGATTGATG 1065

Qy   4104 TCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCA 4163
          |||  || |    ||  |   |||  |||||||  ||||||||||||  || | |
Db   1066 TCTGGATTGGTGCATGTATGACATTCATTTTCTGCGCGTTGTTGGAGTTTGCATTGGTAA 1125
```

```
Qy   4164 ACTTCCTGATCTACAACCAG 4183
          |     |     |||| |||
Db   1126 ATCATATAGCTAACAAGCAG 1145


RESULT  11
PCT-US95-06556-1
; Sequence 1, Application PC/TUS9506556
;  GENERAL INFORMATION:
;    APPLICANT:  Cully, Doris F.
;    APPLICANT:  Arena, Joseph P.
;    APPLICANT:  Liu, Ken K.
;    APPLICANT:  Vassilatis, Demetrios
;    TITLE OF INVENTION:  DNA ENCODING GLUTAMATE GATED CHLORIDE
;    TITLE OF INVENTION:  CHANNELS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wallen, John W.
;      STREET:  126 E. Lincoln Ave., P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06556
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/249,112
;      FILING DATE:  25-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wallen, John W.
;      REGISTRATION NUMBER:  35,403
;      REFERENCE/DOCKET NUMBER:  19194
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-3905
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1542 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US95-06556-1


  Query Match             1.2%;  Score 72.8;  DB 6;  Length 1542;
  Best Local Similarity   55.0%;  Pred. No. 4.4e-12;
  Matches  143;  Conservative    0;  Mismatches  117;  Indels    0;  Gaps    0;

Qy   3924 TTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCA 3983
          | |||  |||  |||| || | | ||      ||  | ||||||||||| ||||||
Db    886 TCCAACTCTACATCCCGTCATGCATGCTAGTCATCGTATCCTGGGTTTCATTTTGGTTTG 945

Qy   3984 AGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCA 4043
          |  |    |    || || ||   | | || ||  ||||| |  | || || |||||
Db    946 ATCGAACTGCAATCCCGGCTCGTGTCACCCTCGGAGTCACCACGCTGCTTACAATGACAG 1005

Qy   4044 CGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATT 4103
          |        ||  |     |    |  | || |  || ||||||||||  ||  | |||
Db   1006 CTCAATCAGCCGGTATCAATTCACAACTACCTCCAGTTTCCTATATCAAGGCGATTGATG 1065

Qy   4104 TCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCA 4163
          |||  || |     ||  |    |||  |||||||  ||||||||||||  || | |
Db   1066 TCTGGATTGGTGCATGTATGACATTCATTTTCTGCGCGTTGTTGGAGTTTGCATTGGTAA 1125

Qy   4164 ACTTCCTGATCTACAACCAG 4183
          |     |     |||| |||
Db   1126 ATCATATAGCTAACAAGCAG 1145


RESULT  12
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14


  Query Match             1.2%;  Score 72;  DB 1;  Length 7218;
  Best Local Similarity   2.4%;  Pred. No. 2.2e-11;
  Matches    9;  Conservative  239;  Mismatches  134;  Indels    0;  Gaps    0;

Qy   5101 GGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCT 5160
          ||||   | |||:::::::::::  ::   :: :: : :::::  :::::::::::: ::
Db   1055 GGAGCTTGCGATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1114

Qy   5161 ACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCA 5220
           ::::::::::: :   :   :   : ::  : :: :::::::                 :
Db   1115 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1174

Qy   5221 GCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTC 5280
           :       ::: :::    :  : :::::::::::: :: :: :  : ::::::::::
Db   1175 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1234

Qy   5281 CTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCCAATGGGTATC 5340
          ::: ::  :::: :::::: ::: : :: ::  :::  : :::::: :::  :   : ::
Db   1235 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1294
```

```
Qy   5341 TATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTC 5400
          : ::::: : : :  :: : :  : :: :::::: :::: : : :: ::::::::::::::
Db   1295 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1354

Qy   5401 TTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGG 5460
          :::  ::::: :  :::::::: :  :::::::  :  ::::::::  ::::  :::
Db   1355 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1414

Qy   5461 CACTAGGCCTTGGTGACTTCCT 5482
          : ::   ::::  :  :::: |
Db   1415 YYYYYYYYYYYYYYYYYYYYGT 1436
```

```
RESULT  13
US-08-554-659-3
; Sequence 3, Application US/08554659
; Patent No. 5767261
;  GENERAL INFORMATION:
;    APPLICANT:  Wingate, Vincent
;    APPLICANT:  Wolff, Mark
;    TITLE OF INVENTION:  LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
;    TITLE OF INVENTION:  AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/554,659
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9732
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1657 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  115..1581
US-08-554-659-3
```

```
  Query Match             1.2%;  Score 71.4;  DB 2;  Length 1657;
  Best Local Similarity   54.3%;  Pred. No. 1.2e-11;
  Matches  144;  Conservative    0;  Mismatches  121;  Indels    0;  Gaps    0;

Qy   3907 GTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTG 3966
          | | || ||   |    |||| |  ||| | || ||| | | |     ||  | || ||
Db    864 GATGGGATACTATTTAATTCAGATTTATATTCCGTCTGGCCTAATTGTCATTATATCTTG 923

Qy   3967 GGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTC 4026
          ||| || |||||| | ||   | |  | | || ||  ||    | |||||  |||| |
Db    924 GGTATCATTTTGGTTGAATCGAAATGCGACACCTGCAAGGGTAGCACTAGGTGTCACAAC 983

Qy   4027 TGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTA 4086
          |||  |||| ||||| ||| |     | |   |   |  | | ||     |||| ||
Db    984 TGTATTGACGATGACGACGCTCATGTCGTCCACGAATGCGGCTCTGCCCAAGATCTCATA 1043

Qy   4087 TATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTT 4146
          | |||   || | ||| ||||| | |  |  || |||||| |   |||| |  | | |
Db   1044 TGTCAAGTCCATCGATGTCTATCTGGGAACTTGTTTCGTCATGGTCTTCACCAGTTTACT 1103

Qy   4147 GGAGTTTGCTGTGCTCAACTTCCTG 4171
           || | |||   | |   ||   ||
Db   1104 AGAATATGCCACGGTTGGCTATATG 1128
```

```
RESULT  14
US-08-072-064-3
; Sequence 3, Application US/08072064
; Patent No. 6008046
;  GENERAL INFORMATION:
;    APPLICANT:  FFRENCH-CONSTANT, RICHARD H.
;    APPLICANT:  JACKSON, MEYER B.
;    TITLE OF INVENTION:  DRUG AND PESTICIDE SCREENING
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER G. CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/072,064
;      FILING DATE:  19930602
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 770,881
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  OPHD-00574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2066 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
US-08-072-064-3
```

```
  Query Match             1.1%;  Score 66.6;  DB 5;  Length 2066;
  Best Local Similarity   53.2%;  Pred. No. 4.3e-10;
  Matches  141;  Conservative    0;  Mismatches  124;  Indels    0;  Gaps    0;

Qy   3907 GTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTG 3966
          | | |||||         | |||| |||  | || |||    |||  |    |  | || ||
Db    892 GATGGGCTACTACCTTATACAAATCTACATACCCTCTGGACTGATCGTTGTTATATCATG 951

Qy   3967 GGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTC 4026
          ||| || ||||||| ||||      |  |  | || || ||    || || ||  | ||  |
Db    952 GGTATCATTTTGGCTCAATCGCAATGCAACGCCGGCGCGTGTGTCGCTCGGTGTGACAAC 1011

Qy   4027 TGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTA 4086
          ||  |||| ||||||||| |||     | |   |   |        | ||     | || ||
Db   1012 CGTGTTGACAATGACCACTTTGATGTCGTCAACAAATGCAGCGCTGCCAAAGATTTCGTA 1071
```

```
Qy   4087 TATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTT 4146
          ||| | |  | ||  ||||| | |  |  |||||||| |   |||   |  |||  |
Db   1072 CGTCAAATCGATTGACGTCTATCTGGGAACATGCTTCGTTATGGTCTTTGCCAGTCTACT 1131

Qy   4147 GGAGTTTGCTGTGCTCAACTTCCTG 4171
          ||| |  ||   | ||  || | ||
Db   1132 GGAATACGCCACGGTCGGCTACATG 1156


RESULT  15
US-08-072-064-5
; Sequence 5, Application US/08072064
; Patent No. 6008046
;  GENERAL INFORMATION:
;    APPLICANT:  FFRENCH-CONSTANT, RICHARD H.
;    APPLICANT:  JACKSON, MEYER B.
;    TITLE OF INVENTION:  DRUG AND PESTICIDE SCREENING
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER G. CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/072,064
;      FILING DATE:  19930602
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 770,881
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  OPHD-00574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2066 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
US-08-072-064-5


  Query Match             1.1%;  Score 66.6;  DB 5;  Length 2066;
  Best Local Similarity   53.2%;  Pred. No. 4.3e-10;
  Matches  141;  Conservative    0;  Mismatches  124;  Indels    0;  Gaps    0;

Qy   3907 GTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTG 3966
          | | |||||        | |||| |||  | || |||    ||| |    |  | || ||
Db    892 GATGGGCTACTACCTTATACAAATCTACATACCCTCTGGACTGATCGTTGTTATATCATG 951

Qy   3967 GGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTC 4026
          ||| || |||||| ||||     |  |  | || || ||    || || ||  | ||  |
Db    952 GGTATCATTTTGGCTCAATCGCAATGCAACGCCGGCGCGTGTGTCGCTCGGTGTGACAAC 1011

Qy   4027 TGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTA 4086
           ||  |||| |||||||| |||    | |   |   |       | ||     | || ||
Db   1012 CGTGTTGACAATGACCACTTTGATGTCGTCAACAAATGCAGCGCTGCCAAAGATTTCGTA 1071

Qy   4087 TATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTT 4146
            ||| | |  | ||  ||||| | |  |  |||||||  |   |||   |  |||  |
```

```
Db   1072 CGTCAAATCGATTGACGTCTATCTGGGAACATGCTTCGTTATGGTCTTTGCCAGTCTACT 1131

Qy   4147 GGAGTTTGCTGTGCTCAACTTCCTG 4171
          ||| |  ||   | ||  || | ||
Db   1132 GGAATACGCCACGGTCGGCTACATG 1156


Search completed:  March  9, 2000, 13:38:51
Job time:  879 sec
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2000, 22:35:01 ; Search time 235.59 Seconds
(without alignments)
6526.935 Million cell updates/sec

Title: US-09-030-832-1
Perfect score: 6146
Sequence: 1 GTCTTATAATTGCTAAGCAC.....TCACCATCATCTGAAATGGG 6146

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5035.8	81.9	10697	1	V11778	GABA-A receptor ep
2	2202.8	35.8	3123	1	V11776	GABA-A receptor ep
3	2202.8	35.8	3026	1	V11777	Variant of GABA-A
4	744.8	12.1	1552	1	V36319	Human GABA recepto
5	153	2.5	187	1	T21715	Human gene signatu
6	132.4	2.2	1565	1	T02334	GABA-A receptor ga
7	128	2.1	1408	1	Q33130	GABA-A receptor al
8	128	2.1	1408	1	Q69142	Human GABA recepto
9	125.6	2.0	1707	1	T28988	Human GABA-A recep
10	119.6	1.9	2310	1	Q33129	GABA-A receptor al
11	119.6	1.9	2310	1	Q69141	Human GABA recepto
12	112.8	1.8	1638	1	Q33128	GABA-A receptor al
13	112.8	1.8	1638	1	Q69140	Human GABA recepto
14	105.6	1.7	2189	1	Q33127	GABA-A receptor al
15	105.6	1.7	2189	1	Q69139	Human GABA recepto
16	99.8	1.6	1866	1	Q33131	GABA-A receptor be
17	99.8	1.6	1866	1	Q69143	Human GABA recepto
18	99.6	1.6	1491	1	Q99330	GABA receptor subu
19	99.6	1.6	1491	1	V84685	Insect GABA recept
20	95.6	1.6	1884	1	V83111	Human GABA-A recep
21	95.6	1.6	1884	1	V83112	Human GABA-A recep
22	86.6	1.4	2635	1	V84686	Insect GABA recept
23	85.6	1.4	1555	1	T28989	Human GABA-A recep
24	74.8	1.2	1368	1	X24372	Cat flea glutamate
25	74.8	1.2	1297	1	X24373	Cat flea glutamate
26	73	1.2	1657	1	V55007	GABA gated chlorid
27	73	1.2	1844	1	V64372	GABA-gated chlorid
28	72.8	1.2	1542	1	T09695	Caenorhabditis ele
29	71.4	1.2	1657	1	V55008	GABA gated chlorid
30	68.2	1.1	669	1	V64374	GABA-gated chlorid
31	67.8	1.1	1519	1	V64373	GABA-gated chlorid
32	67.4	1.1	1650	1	T10500	Human GABA-A recep
33	67.4	1.1	1650	1	T84630	Human GABA-A recep
34	65	1.1	2059	1	Q40045	Sequence of cDNA N
35	65	1.1	1823	1	X16065	DNA sequence of Lu
36	62.2	1.0	3958	1	T43596	Glutamate-gated ch
37	57.8	0.9	1479	1	T09696	Caenorhabditis ele
38	45	0.7	45	1	V36324	Human GABA recepto
39	43.4	0.7	45	1	V36325	Human GABA recepto
c 40	40.2	0.7	110000	1	X20248_01	Continuation (2 of
41	39.2	0.6	152	1	T43599	Glutamate-gated ch
42	37.4	0.6	575	1	V55016	Fragment of GABA g
43	37.2	0.6	1293	1	T94539	Tobacco cinnamoyl
44	37	0.6	110000	1	V21209_10	Continuation (11 o
c 45	36.8	0.6	50000	1	X23517	Human kidney amino

ALIGNMENTS

RESULT 1
V11778
ID V11778 standard; DNA; 10697 BP.
AC V11778;
DT 25-SEP-1998 (first entry)
DE GABA-A receptor epsilon sub-unit related genomic sequence.
KW ss; GABA-A receptor; diagnosis; therapy; drug screening.
OS Mammalia.
FH Key Location/Qualifiers
FT exon 1. .110
FT /*tag= a
FT /number= 1
FT intron 111. .1217
FT /*tag= b
FT /number= 1
FT exon 1218. .1435
FT /*tag= c
FT /number= 2
FT intron 1436. .1883
FT /*tag= d
FT /number= 2
FT exon 1884. .2172
FT /*tag= e
FT /number= 3
FT intron 2173. .3169
FT /*tag= f
FT /number= 3
FT exon 3170. .3252
FT /*tag= g
FT /number= 4
FT intron 3253. .4559
FT /*tag= h
FT /number= 4
FT exon 4560. .4697
FT /*tag= i
FT /number= 5
FT intron 4698. .7962
FT /*tag= j
FT /number= 5
FT exon 7963. .8115
FT /*tag= k
FT /number= 6
FT intron 8116. .8255
FT /*tag= l
FT /number= 6
FT exon 8256. .8455
FT /*tag= m
FT /number= 7
FT intron 8456. .8738
FT /*tag= n
FT /number= 7
FT exon 8739. .10697
FT /*tag= o
FT /number= 8
PN DE19644501-A1.
PD 30-APR-1998.
PF 25-OCT-1996; 044501.
PR 25-OCT-1996; DE-044501.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR WPI; 98-252096/23.
PT Protein related to GABA-A receptor sub-unit epsilon - useful for

PT diagnosis, therapy or drug screening
PS Disclosure; Fig 3; 12pp; German.
CC The GABA-A receptor sub-unit epsilon related protein is used for the
CC diagnosis and/or therapy of related disorders. It can also be used to
CC screen for substances that modulate the activity of the protein.
SQ Sequence 10697 BP; 2524 A; 2704 C; 2471 G; 2991 T;

Query Match 81.9%; Score 5035.8; DB 1; Length 10697;
Best Local Similarity 92.2%; Pred. No. 0;
Matches 5531; Conservative 3; Mismatches 16; Indels 448; Gaps 4;

```
Qy    572 TAGGTGACCTGAATGAGGAGCCAAGGGACCTCCCCAGGGTAGCTCCCAGAGCAACCCTGG 631
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4695 TTGGTGACCTGAATGAGGAGCCAAGGGACCTCCCCAGGGTAGCTCCCAGAGCAACCCTGG 4754

Qy    632 AAACACTCTTCACACATCCTGACCAAGTTCAGGGCAGTGAAGGCACTGCCCTCATCGTTT 691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4755 AAACACTCTTCACACATCCTGACCAAGTTCAGGGCAGTGAAGGCACTGCCCTCATCGTTT 4814

Qy    692 CCAGAATGTGGATGGAGCCAGTCACCCAACCAGCCATTTGTCGTGAGAGGCATCTTGTTC 751
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4815 CCAGAATGTGGATGGAGCCAGTCACCCAACCAGCCATTTGTCGTGAGAGGCATCTTGTTC 4874

Qy    752 TGCTACCATGTGACTAGGCAGAAAATCTGCTTTTGTTTCATTTATTGAGTCAGTCTCTGG 811
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4875 TGCTACCATGTGACTAGGCAGAAAATCTGCTTTTGTTTCATTTATTGAGTCAGTCTCTGG 4934

Qy    812 ATGAGGGAAAGCTCATGCTCATGTGGCTAGAGCTTTGCTTGCACAGTATTAGGCAGGGGC 871
          |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4935 ATGAGGGAARGCTCATGCTCATGTGGCTAGAGCTTTGCTTGCACAGTATTAGGCAGGGGC 4994

Qy    872 AGAGGGCTGGGCTACCTTAAAAATACTTGCCCTTTTTCTTGGGGACTCTGGGGAAGCGGT 931
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   4995 AGAGGGCTGGGCTACCTAAAAAATACTTGCCCTTTTTCTTGGGGACTCTGGGGAAGCGGT 5054

Qy    932 TTTACTACCTTTGACTTGGGAGCCTTGCTCTTCTGCCAGCTAACCATGGGCCTGCCTCTT 991
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5055 TTTACTACCTTTGACTTGGGAGCCTTGCTCTTCTGCCAGCTAACCATGGGCCTGCCTCTT 5114

Qy    992 GGTTTTCTGCACCTCAGCTTTTCCCGGATAGGTGGGGACCCATCATCAAAAGTGACAGAG 1051
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5115 GGTTTTCTGCACCTCAGCTTTTCCCGGATAGGTGGGGACCCATCATCAAAAGTGACAGAG 5174

Qy   1052 AAGATAAGGCCCAGGGGCTTTCAAGTCACTAGTGGTTCCGTTTAGTAGATGATTGTGCAT 1111
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5175 AAGATAAGGCCCAGGGGCTTTCAAGTCACTAGTGGTTCCGTTTAGTAGATGATTGTGCAT 5234

Qy   1112 TGTTTCAAAATGGTGCCCTAGTGACTACAAAGCCCCAGAGCCAGCATCATCATCAAAGCA 1171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5235 TGTTTCAAAATGGTGCCCTAGTGACTACAAAGCCCCAGAGCCAGCATCATCATCAAAGCA 5294

Qy   1172 ATGACAGTAGGTAAGCACCAGACCTCCTTGGGAGTGAGGAGGATTCTTGAGGAGAAAAGA 1231
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5295 ATGACAGTAGGTAAGCACCAGACCTCCTTGGGAGTGAGGAGGATTCTTGAGGAGAAAAGA 5354

Qy   1232 GGTCTTCTTTCTCCTCTGCTGGAGACTAGTTGATCTGGAGACGTGGTTCCTTCAATGTCA 1291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5355 GGTCTTCTTTCTCCTCTGCTGGAGACTAGTTGATCTGGAGACGTGGTTCCTTCAATGTCA 5414

Qy   1292 GAGTTATCTTTGGGACTGGTCTCAAACTCTTCCAGTTGGGCCCTGGGGCAGGTCTCTCCA 1351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5415 GAGTTATCTTTGGGACTGGTCTCAAACTCTTCCAGTTGGGCCCTGGGGCAGGTCTCTCCA 5474

Qy   1352 TCTGGAGCATACTTACGTGCTCGGCGATTAAGGGTTCAGAATGCAGTGGTAGCCTGCTAC 1411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5475 TCTGGAGCATACTTACGTGCTCGGCGATTAAGGGTTCAGAATGCAGTGGTAGCCTGCTAC 5534

Qy   1412 TCTGGCCATCTTGGACCTTGATCCAGAGAATCTCTGCTTCAGGAGCTTCTAAGAGAGTCC 1471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5535 TCTGGCCATCTTGGACCTTGATCCAGAGAATCTCTGCTTCAGGAGCTTCTAAGAGAGTCC 5594

Qy   1472 AGCCCTGCCTCCAGAGAGAGGCTTGCCCTTCACTGATGGCTGTGGAGCCTCTGATGGAAT 1531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5595 AGCCCTGCCTCCAGAGAGAGGCTTGCCCTTCACTGATGGCTGTGGAGCCTCTGATGGAAT 5654

Qy   1532 ATTATTGCTGGTCAGGAATTCACTGTCTTACAAGGAGGTTTCCTTCTTCTCTAGACAGTT 1591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5655 ATTATTGCTGGTCAGGAATTCACTGTCTTACAAGGAGGTTTCCTTCTTCTCTAGACAGTT 5714

Qy   1592 CTGTTCATCAAAAAACTCTCCCTGTTCTTCTGAAATTGGAGTCTCTGGAAGTTCCACACA 1651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5715 CTGTTCATCAAAAAACTCTCCCTGTTCTTCTGAAATTGGAGTCTCTGGAAGTTCCACACA 5774

Qy   1652 TTAAGCTTAGTTCTTTTTCCTTGGAACTGTCCAGGTTACATTAGTCCAGCCACTGTTTCA 1711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5775 TTAAGCTTAGTTCTTTTTCCTTGGAACTGTCCAGGTTACATTAGTCCAGCCACTGTTTCA 5834

Qy   1712 CAGGACCGAGATTAAACGATCAACATCATCATTCCCGGCATGGATCATAGTCTGTTGTAG 1771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5835 CAGGACCGAGATTAAACGATCAACATCATCATTCCCGGCATGGATCATAGTCTGTTGTAG 5894

Qy   1772 TCTACATAGCCCTAGTTTATTTTTCTTCCCTTATTCTTCAAAGCTTTGGGTCCATTCATT 1831
          |||||||||||||||||||||||||||||||||||||||| |  ||||||||||||||
Db   5895 TCTACATAGCCCTAGTTTATTTTTCTTCCCTTATTCTTCAAAGGTGGGGGTCCATTCATT 5954

Qy   1832 CTTCTAGTCCCAGTCCTCTGGACATGGTCTATTTAATTGTGTCCCTCTGACACTGCAGTG 1891
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   5955 CTTCTAGTCCCAGTCCTCTGGACATGGTCTATTTAATTGTGTCCCTCTGACACTGCAATG 6014

Qy   1892 ACCAACCATGATCTGGTCAAAGAGGATAAGAGTTTGAGCAGAAAACCATCTTTAGCATAT 1951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6015 ACCAACCATGATCTGGTCAAAGAGGATAAGAGTTTGAGCAGAAAACCATCTTTAGCATAT 6074

Qy   1952 ATTTTTTTGCTTTGGTTCATCAGCCCCAGATATATTGTTTTCCTTACCCGTGCTTCTCTC 2011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6075 ATTTTTTTGCTTTGGTTCATCAGCCCCAGATATATTGTTTTCCTTACCCGTGCTTCTCTC 6134

Qy   2012 ACTCCTCAAGAAGAAGAAAGTGTGTGTTAGCATCTTTCTCTTGTCCTTCAAGACAAATTG 2071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6135 ACTCCTCAAGAAGAAGAAAGTGTGTGTTAGCATCTTTCTCTTGTCCTTCAAGACAAATTG 6194

Qy   2072 GCATCTCTTGACGAGCGGAGAAGGTTCTTTTTTGGCCAGAATAAATAAAATTAAAATAGA 2131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6195 GCATCTCTTGACGAGCGGAGAAGGTTCTTTTTTGGCCAGAATAAATAAAATTAAAATAGA 6254

Qy   2132 ATCATCCAACAGAATAATAAATCTTCGTGCAACAAGAATATATTATATAAACCCAGCAAT 2191
          ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db   6255 ATCATCCAACAGAATAATAAATCTTCGTGCAACAAGAATATATTATATARACCCAGCAAT 6314

Qy   2192 TTTGCAGGGCCTGGGTATAACTAATTAGAAGTGTCTTAAATTGCAGTCAAGATCCCACGG 2251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6315 TTTGCAGGGCCTGGGTATAACTAATTAGAAGTGTCTTAAATTGCAGTCAAGATCCCACGG 6374

Qy   2252 CAAGAGGACTTTTGATAAATACATTCTGGCCAGTAGGCAAGTGCGAGGGTGGTCCGTGCA 2311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6375 CAAGAGGACTTTTGATAAATACATTCTGGCCAGTAGGCAAGTGCGAGGGTGGTCCGTGCA 6434

Qy   2312 GCAGCTCTGGAGGAGTTCTATCCCAAAGCTATACTCAACACACAGGTTTCCCACTGACAA 2371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   6435 GCAGCTCTGGAGGAGTTCTATCCCAAAGCTATACTCAACACACAGGTTTCCCACTGACNA 6494

Qy   2372 CAGGTCGCTCCCTTGCCTTCTTCCAGAAGAATCTGAGAAGCTTTGCTCCTTGAGTTTCAG 2431
          |||:||||                          ||||||||||||||||||||||||||
Db   6495 CAGSTCGC----------------------CTGAGAAGCTTTGCTCCTTGAGTTTCAG 6530

Qy   2432 TGCTGCCAAGGTGAGTACGAAAGGCTGCTCTTCTCATTCAGCTCCAGCCCACCCAGACCT 2491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6531 TGCTGCCAAGGTGAGTACGAAAGGCTGCTCTTCTCATTCAGCTCCAGCCCACCCAGACCT 6590

Qy   2492 GCTGGGCAGTTGATCCACTTTCCAAAATAGGAGGACACACGGACAGGTTAGTGTTCTGGT 2551
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   6591 GCTGGGCAGTTGATCCACTTTCCCAAATAGGAGGACACACGGACAGGTTAGTGTTCTGGT 6650

Qy   2552 CTGCTTTACAAAGCTGTTGCCTGACAGGAGCAAGAGTTGCTGAGTGTCTGCTGGGTTCCA 2611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   6651 CTGCTTTACAAAGCTGTTGCCTGACAGGAGCAAGAGTTGCTGAGTGTCTGCTGGGTTCCA 6710

Qy   2612 GGCTGTTCTGAGCTTGGATGGGCAGGGGCTAAGCCACAGGGCCTGCATGAGCCCTGCCTT 2671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6711 GGCTGTTCTGAGCTTGGATGGGCAGGGGCTAAGCCACAGGGCCTGCATGAGCCCTGCCTT 6770

Qy   2672 GAAGGGACTTAAAAGACGACCTAATTATAGGCCTAGGAATTTTACAGTATTGCAACTGCA 2731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6771 GAAGGGACTTAAAAGACGACCTAATTATAGGCCTAGGAATTTTACAGTATTGCAACTGCA 6830

Qy   2732 ATGTGATGCTGAAAGTGGAAAATGATGTCCTGGGCTCAGAGAAAAGCCCACACCAGCCTG 2791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6831 ATGTGATGCTGAAAGTGGAAAATGATGTCCTGGGCTCAGAGAAAAGCCCACACCAGCCTG 6890

Qy   2792 GGAGTCATGATAGCAGCAGAGTGCTTGGGGAGGGTGTGTCAGAGCATAAAGCAGCATGAA 2851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6891 GGAGTCATGATAGCAGCAGAGTGCTTGGGGAGGGTGTGTCAGAGCATAAAGCAGCATGAA 6950

Qy   2852 TGCTACAAAAGAAGATGCCAACTAGAGATATAGGTTGTCATCAGGTCCCGGAGGAGCCAT 2911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6951 TGCTACAAAAGAAGATGCCAACTAGAGATATAGGTTGTCATCAGGTCCCGGAGGAGCCAT 7010

Qy   2912 GACCGTCTAGCTGAGAGCCATGACCAAGGACACAATGTCCAAGTGACTGTGAGGACCTCA 2971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7011 GACCGTCTAGCTGAGAGCCATGACCAAGGACACAATGTCCAAGTGACTGTGAGGACCTCA 7070

Qy   2972 GTCTGCCCTGTGGATGTGTATGCCACAGACCTGACTTCTGGAGGGCTGACTGAAATGTTC 3031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7071 GTCTGCCCTGTGGATGTGTATGCCACAGACCTGACTTCTGGAGGGCTGACTGAAATGTTC 7130

Qy   3032 ATTTTAAGCTTTTTCTTCTCTTTCCCTGAAACACTCAGTTTGGGTTAGGGGTCATAGACT 3091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7131 ATTTTAAGCTTTTTCTTCTCTTTCCCTGAAACACTCAGTTTGGGTTAGGGGTCATAGACT 7190

Qy   3092 AAGACCAAAGAGTCCAGGGTTAGAATCTTGGTGTAAAATTGCAGGCCATCTCAGGAAATC 3151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7191 AAGACCAAAGAGTCCAGGGTTAGAATCTTGGTGTAAAATTGCAGGCCATCTCAGGAAATC 7250

Qy   3152 TGTGAGCAGATGGGATTGGCTTTGGGTAAGGTGCGTGTGGAAAATGTCAGTGGGAGCCGG 3211
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   7251 TGTGAGCAGATGGGAATGGCTTTGGGTAAGGTGCGTGTGGAAAATGTCAGTGGGAGCCGG 7310

Qy   3212 GTCATGGTGGGCCTTTAGCATCAGATTCCAGAGTGCAGATAGTCTGTATAGCTCATGTGA 3271
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   7311 GTCATGGTGGGCCTTTAGCATCAGATTCCAGAATGCAGATAGTCTGTATAGCTCATGTGA 7370

Qy   3272 AACAGGGAGCCACCAAAACTTTGGGGAGCAGGCTAGTGCCGGTTTTGACCACCTGTGGAG 3331
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   7371 AACAGGGAGCCACCAAAACTTTGGGGAGCAGGCTAGTGCCGGTCTTGACCACCTGTGGAG 7430

Qy   3332 CAGTGCTCACTCACGAAGGCATTTTGCCATCACATGAATGTGCAGAAAGGAGGCCAAAAG 3391
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   7431 CAGTGCTCACTCACGAAGGCATTTTGGCATCACATGAATGTGCAGAAAGGAGGCCAAAAG 7490

Qy   3392 CATTCTGTGCTTCTCCACCACAGCACAGACTTCCCTAGTCTCATTTGCTGAGAGTAGACA 3451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7491 CATTCTGTGCTTCTCCACCACAGCACAGACTTCCCTAGTCTCATTTGCTGAGAGTAGACA 7550

Qy   3452 TTCTGAGGGCCAGCAGTGCAGGTGTGATGTGCCTCAGAGGGTATGAAGCCCTTAGTCAGC 3511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7551 TTCTGAGGGCCAGCAGTGCAGGTGTGATGTGCCTCAGAGGGTATGAAGCCCTTAGTCAGC 7610

Qy   3512 CATCTGGATATCAGCTGCGTGGGCATGATATCTAGAAGGCTAATTGATTTTTTCACTTTC 3571
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7611 CATCTGGATATCAGCTGCGTGGGCATGATATCTAGAAGGCTAATTGATTTTTTCACTTTC 7670

Qy   3572 ACCTGACTCTCTTGCCAACCTGCAGAGACAGACATTGGGTGTAGGACAGTGAACTGAGAA 3631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7671 ACCTGACTCTCTTGCCAACCTGCAGAGACAGACATTGGGTGTAGGACAGTGAACTGAGAA 7730

Qy   3632 GGAAGCTATTAAGATTCTGGCCTTGGCTTAGCTCTCAACTGGCCATTGGTCTTGCAGTAA 3691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7731 GGAAGCTATTAAGATTCTGGCCTTGGCTTAGCTCTCAACTGGCCATTGGTCTTGCAGTAA 7790
```

```
Qy   3692 GTCTTTTTTCTGGGCTTCTTCTGGTCCTATTTGTATGTATTGCATTGTCACATCATGCCT 3751
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7791 GTCTTTTTTCTGGGCTTCTTCTGGTCCTATTTGTATGTATTGCATTGTCACATCATGCCT 7850

Qy   3752 CTATCCTAGGGAATACTGTGAGCTGAAAAATGAGACCCTTACTGTTCACGTCCTGCTAAG 3811
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7851 CTATCCTAGGGAATACTGTGAGCTGAAAAATGAGACCCTTACTGTTCACGTCCTGCTAAG 7910

Qy   3812 GGGGACCGTCGTGTCAGCACTGTAATGCAGTGATGTTTTTTGTGTCTTTCAGGTGACTTC 3871
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7911 GGGGACCGTCGTGTCAGCACTGTAATGCAGTGATGTTTTTTGTGTCTTTCAGGTGACTTC 7970

Qy   3872 ATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAAC 3931
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7971 ATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAAC 8030

Qy   3932 TATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAG 3991
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8031 TATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAG 8090

Qy   3992 TCTGCTCCAGCCCGGACCTCTCT---------------------------------------- 4015
          |||||||||||||||||||||||
Db   8091 TCTGCTCCAGCCCGGACCTCTCTAGGTAAGAGGAGAAACAGGTATACGCATAGGCACATG 8150

Qy   4015 ---------------------------------------------------------------- 4015

Db   8151 GCTGGGAGTTGGCTGGGCCAGGGCAGAGTTGCCTTGTCATGGAGTCTTTTAACCAATGTC 8210

Qy   4015 ----------------------------------------------AGGGATCACCTCTGTTC 4031
                                                         |||||||||||||||||
Db   8211 GCACATAGGTCAGGAGCTGAGCCCATCACTCTTGTGCTCTTGCAGGGATCACCTCTGTTC 8270

Qy   4032 TGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCA 4091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8271 TGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCA 8330

Qy   4092 CAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGT 4151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8331 CAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGT 8390

Qy   4152 TTGCTGTGCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCC 4211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8391 TTGCTGTGCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCC 8450

Qy   4212 GCCAT---------------------------------------------------------- 4217
          |||||
Db   8451 GCCATGTATGAGCTGGGTATGGGAGTGGTGGCAAGGCTTTGGAGTGTAGAGACATGCTAG 8510

Qy   4217 ---------------------------------------------------------------- 4217

Db   8511 CAAGGGTACTGGGGATATGGCACATGGGTGGTCAGCTTGCTGAGTGATAGAATGTTACCC 8570

Qy   4217 ---------------------------------------------------------------- 4217

Db   8571 AGGGTGGTGGCGGGGTTGAATCAACTTCCTGATGTAATGGTGAGAAGTTGGAGGAGAGAA 8630

Qy   4217 ---------------------------------------------------------------- 4217

Db   8631 GCCAAGATATGGTGTGCCAAAGACAGTTTCCAGAAAATCCGGAGGCAGCACTTAGACTTG 8690

Qy   4217 ----------------------------------------------CCTCGTATCAAT 4228
                                                         ||||||||||||
Db   8691 GGTTATCTTCCCTTGACTTTTCCCCACTTCTTTCCTTGTCCATTTTAGCCTCGTATCAAT 8750

Qy   4229 AGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAA 4288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8751 AGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAA 8810

Qy   4289 GCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGC 4348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8811 GCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGC 8870
```

```
Qy   4349 TCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAG 4408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8871 TCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAG 8930

Qy   4409 CTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGT 4468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8931 CTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGT 8990

Qy   4469 GAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTAC 4528
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   8991 GAGGGCAGTACCTGGCAGCAGGCCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTAC 9050

Qy   4529 TCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGC 4588
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   9051 TCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTTTTTTGC 9110

Qy   4589 CTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCAGGAGGT 4648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9111 CTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCAGGAGGT 9170

Qy   4649 CCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGCGACTAGAGT 4708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9171 CCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGGAGCGACTAGAGT 9230

Qy   4709 TTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCCTCTC 4768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9231 TTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCCTCTC 9290

Qy   4769 CCCTACCTGGCCCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAATAAATGG 4828
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   9291 CCCTACCTGGCCCATTCACTGAGTTTTCTCAGCAGACCATTTCAAATTATTAATAAATGG 9350

Qy   4829 GCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACAGCCACT 4888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9351 GCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACAGCCACT 9410

Qy   4889 TAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCCAACAAT 4948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9411 TAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCCAACAAT 9470

Qy   4949 GCTGACCACCAGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTAGTGCTT 5008
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   9471 GCTGACCACCAGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGCAGTGCTT 9530

Qy   5009 TCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATACCTGGC 5068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9531 TCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATACCTGGC 9590

Qy   5069 ACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTTTGGTCA 5128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9591 ACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTTTGGTCA 9650

Qy   5129 GATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGATAGACAC 5188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9651 GATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGATAGACAC 9710

Qy   5189 TGGCATTATCCCTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACAGCATTC 5248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9711 TGGCATTATCCCTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACAGCATTC 9770

Qy   5249 CTCTCTCTCTGCTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTCTGCACT 5308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9771 CTCTCTCTCTGCTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTCTGCACT 9830

Qy   5309 ACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGTAACTAC 5368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9831 ACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGTAACTAC 9890

Qy   5369 TCCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACT 5428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9891 TCCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACT 9950

Qy   5429 TTCCCAGTGACTTCCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCTGGGGCC 5488
          |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   9951 TTCCCAGTGACTTCCCCTAGCCCTGA-CCAGGCACTAGGCCTTGGTGACTTCCTGGGGCC 10009

Qy   5489 AAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACC 5548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10010 AAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACC 10069

Qy   5549 CAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCAC 5608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10070 CAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCAC 10129

Qy   5609 TGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTA 5668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10130 TGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTA 10189

Qy   5669 TGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGAT 5728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10190 TGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGAT 10249

Qy   5729 AGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAG 5788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10250 AGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAG 10309

Qy   5789 TCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACC 5848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10310 TCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACC 10369

Qy   5849 TTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTC 5908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10370 TTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTC 10429

Qy   5909 TGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGC 5968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10430 TGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGC 10489

Qy   5969 CTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAA 6028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10490 CTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAA 10549

Qy   6029 TGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGT 6088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10550 TGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGT 10609

Qy   6089 TGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGG 6146
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10610 TGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGG 10667
```

RESULT 2
V11776
ID V11776 standard; cDNA; 3123 BP.
AC V11776;
DT 25-SEP-1998 (first entry)
DE GABA-A receptor epsilon sub-unit related gene.
KW ss; GABA-A receptor; diagnosis; therapy; drug screening.
OS Mammalia.
FH Key Location/Qualifiers
FT CDS 55. .1573
FT /*tag= a
FT /product= "GABA-A receptor epsilon sub-unit related
FT protein"
PN DE19644501-A1.
PD 30-APR-1998.
PF 25-OCT-1996; 044501.
PR 25-OCT-1996; DE-044501.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR WPI; 98-252096/23.
DR P-PSDB; W59048.
PT Protein related to GABA-A receptor sub-unit epsilon - useful for
PT diagnosis, therapy or drug screening
PS Example 1; Fig 1; 12pp; German.
CC The GABA-A receptor sub-unit epsilon related protein is used for the

```
CC   diagnosis and/or therapy of related disorders.  It can also be used to
CC   screen for substances that modulate the activity of the protein.
SQ   Sequence   3123 BP;    710 A;    877 C;    686 G;    849 T;

  Query Match           35.8%;  Score 2202.8;  DB 1;  Length 3123;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 2253;  Conservative    0;  Mismatches    2;  Indels   29;  Gaps    2;

Qy   3863 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 3922
Db    838 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 897

Qy   3923 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 3982
Db    898 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 957

Qy   3983 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 4042
Db    958 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 1017

Qy   4043 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGAT 4102
Db   1018 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGAT 1077

Qy   4103 TTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTC 4162
Db   1078 TTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTC 1137

Qy   4163 AACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGT 4222
Db   1138 AACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGT 1197

Qy   4223 ATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACAT 4282
Db   1198 ATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACAT 1257

Qy   4283 CAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCG 4342
Db   1258 CAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCG 1317

Qy   4343 TCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGC 4402
Db   1318 TCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGC 1377

Qy   4403 TCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCC 4462
Db   1378 TCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCC 1437

Qy   4463 GATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGAT 4522
Db   1438 GATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGAT 1497

Qy   4523 AACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTT 4582
Db   1498 AACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTT 1557

Qy   4583 GTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCA 4642
Db   1558 GTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCA 1617

Qy   4643 GGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGCGAC 4702
Db   1618 GGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGGAGCGAC 1677

Qy   4703 TAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCC 4762
Db   1678 TAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCC 1737

Qy   4763 CCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAAT 4822
Db   1738 CCTCTCCCCTACCTGGCCCATTCACTGAGTTTTCTCAGCAGACCATTTCAAATTATTAAT 1797

Qy   4823 AAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACA 4882
Db   1798 AAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACA 1857

Qy   4883 GCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCC 4942
Db   1858 GCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCC 1917

Qy   4943 AACAATGCTGACCACCAGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTA 5002
Db   1918 AACAATGCTGACCACCAGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGCA 1977

Qy   5003 GTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATA 5062
Db   1978 GTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATA 2037

Qy   5063 CCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTT 5122
Db   2038 CCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTT 2097

Qy   5123 TGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGAT 5182
Db   2098 TGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGAT 2157

Qy   5183 AGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACA 5242
Db   2158 AGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACA 2217

Qy   5243 GCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTC 5302
Db   2218 GCATTCCTCT----------------------------CTTGCTGGCTCCATCTTTCGTC 2249

Qy   5303 TGCACTACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGT 5362
Db   2250 TGCACTACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGT 2309

Qy   5363 AACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCT 5422
Db   2310 AACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCT 2369

Qy   5423 GTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCT 5482
Db   2370 GTAACTTTCCCAGTGACTTCCCCTAGCCCTGA-CCAGGCACTAGGCCTTGGTGACTTCCT 2428

Qy   5483 GGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTG 5542
Db   2429 GGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTG 2488

Qy   5543 CCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCA 5602
Db   2489 CCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCA 2548

Qy   5603 GTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAA 5662
Db   2549 GTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAA 2608

Qy   5663 TTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTT 5722
Db   2609 TTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTT 2668

Qy   5723 CATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAAC 5782
Db   2669 CATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAAC 2728

Qy   5783 CCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACT 5842
Db   2729 CCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACT 2788

Qy   5843 GTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGT 5902
Db   2789 GTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGT 2848

Qy   5903 CACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTT 5962
```

```
Db   2849 CACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTT 2908

Qy   5963 CTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCA 6022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2909 CTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCA 2968

Qy   6023 GTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTA 6082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2969 GTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTA 3028

Qy   6083 ATTTGTTGGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAA 6142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3029 ATTTGTTGGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAA 3088

Qy   6143 TGGG 6146
          ||||
Db   3089 TGGG 3092
```

```
RESULT   3
V11777
ID   V11777 standard; DNA; 3026 BP.
AC   V11777;
DT   25-SEP-1998  (first entry)
DE   Variant of GABA-A receptor epsilon sub-unit related gene.
KW   ss; GABA-A receptor; diagnosis; therapy; drug screening.
OS   Mammalia.
FH   Key             Location/Qualifiers
FT   CDS             55. .1479
FT                   /*tag= a
FT                   /product= "Variant of GABA-A receptor epsilon sub-unit
FT                            related protein"
PN   DE19644501-A1.
PD   30-APR-1998.
PF   25-OCT-1996; 044501.
PR   25-OCT-1996; DE-044501.
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI   Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR   WPI; 98-252096/23.
DR   P-PSDB; W59048.
PT   Protein related to GABA-A receptor sub-unit epsilon - useful for
PT   diagnosis, therapy or drug screening
PS   Disclosure; Fig 2; 12pp; German.
CC   The GABA-A receptor sub-unit epsilon related protein is used for the
CC   diagnosis and/or therapy of related disorders.  It can also be used to
CC   screen for substances that modulate the activity of the protein.
SQ   Sequence   3026 BP;    689 A;    853 C;    663 G;    821 T;
```

```
  Query Match             35.8%;  Score 2202.8;  DB 1;  Length 3026;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 2253;  Conservative    0;  Mismatches    2;  Indels   29;  Gaps    2;

Qy   3863 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 3922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    742 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 801

Qy   3923 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 3982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    802 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 861

Qy   3983 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 4042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    862 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 921

Qy   4043 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGAT 4102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    922 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGAT 981

Qy   4103 TTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTC 4162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    982 TTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTC 1041
```

```
Qy   4163 AACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGT 4222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1042 AACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGT 1101

Qy   4223 ATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACAT 4282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1102 ATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACAT 1161

Qy   4283 CAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCG 4342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1162 CAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCG 1221

Qy   4343 TCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGC 4402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1222 TCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGC 1281

Qy   4403 TCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCC 4462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1282 TCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCC 1341

Qy   4463 GATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGAT 4522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1342 GATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGAT 1401

Qy   4523 AACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTT 4582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1402 AACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTT 1461

Qy   4583 GTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCA 4642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1462 GTTTGCCTTAACTTGTAGGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCA 1521

Qy   4643 GGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGCGAC 4702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1522 GGAGGTCCAAGCCCCTTGCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGCGAC 1581

Qy   4703 TAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCC 4762
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1582 TAGAGTTTTTCCTGCCCCATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCC 1641

Qy   4763 CCTCTCCCCTACCTGGCCCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAAT 4822
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   1642 CCTCTCCCCTACCTGGCCCATTCACTGAGTTTTCTCAGCAGACCATTTCAAATTATTAAT 1701

Qy   4823 AAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACA 4882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1702 AAATGGGCCACCTCCCTCTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACA 1761

Qy   4883 GCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCC 4942
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1762 GCCACTTAGTGATCAGCTCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCC 1821

Qy   4943 AACAATGCTGACCACCAGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTA 5002
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   1822 AACAATGCTGACCACCAGACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGCA 1881

Qy   5003 GTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATA 5062
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1882 GTGCTTTCGGCCCAGTTCTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATA 1941

Qy   5063 CCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTT 5122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1942 CCTGGCACCTCATTAAGATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTT 2001

Qy   5123 TGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGAT 5182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2002 TGGTCAGATTATTATGTTCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGAT 2061

Qy   5183 AGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACA 5242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2062 AGACACTGGCATTATCCCTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACA 2121
```

```
Qy   5243 GCATTCCTCTCTCTCTGCTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTC 5302
          ||||||||||                              ||||||||||||||||||||||
Db   2122 GCATTCCTCT--------------------------CTTGCTGGCTCCATCTTTCGTC 2153

Qy   5303 TGCACTACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGT 5362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2154 TGCACTACCAATTCAATGCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGT 2213

Qy   5363 AACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCT 5422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2214 AACTACTCCCTGCTTTATATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCT 2273

Qy   5423 GTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCT 5482
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   2274 GTAACTTTCCCAGTGACTTCCCCTAGCCCTGA-CCAGGCACTAGGCCTTGGTGACTTCCT 2332

Qy   5483 GGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTG 5542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2333 GGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTG 2392

Qy   5543 CCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCA 5602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2393 CCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCA 2452

Qy   5603 GTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAA 5662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2453 GTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAA 2512

Qy   5663 TTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTT 5722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2513 TTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTT 2572

Qy   5723 CATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAAC 5782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2573 CATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAAC 2632

Qy   5783 CCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACT 5842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2633 CCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACT 2692

Qy   5843 GTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGT 5902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2693 GTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGT 2752

Qy   5903 CACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTT 5962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2753 CACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTT 2812

Qy   5963 CTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCA 6022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2813 CTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCA 2872

Qy   6023 GTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTA 6082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2873 GTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTA 2932

Qy   6083 ATTTGTTGGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAA 6142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2933 ATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAA 2992

Qy   6143 TGGG 6146
          ||||
Db   2993 TGGG 2996
```

```
RESULT   4
V36319
ID   V36319 standard; cDNA; 1552 BP.
AC   V36319;
DT   12-OCT-1998  (first entry)
DE   Human GABA receptor epsilon subunit cDNA.
KW   GABA receptor; gamma-amino butyric acid receptor; human;
KW   appetite; cognition; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             18. .1538
FT                   /*tag= a
PN   WO9823742-A1.
PD   04-JUN-1998.
PF   18-NOV-1997; G03159.
PR   03-OCT-1997; GB-020995.
PR   25-NOV-1996; GB-024442.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Whiting PJ;
DR   WPI; 98-322722/28.
DR   P-PSDB; W61045.
PT   New isolated GABA receptor subunit, epsilon - used to develop
PT   products for the screening and design of drugs, e.g. for modulating
PT   appetite behaviours, hormonal interactions and cognition
PS   Claim 5; Fig 1; 37pp; English.
CC   This cDNA sequence codes for a novel class of subunit (see W61045),
CC   classified as epsilon, within the human GABA receptor gene family.
CC   It was generated from human brain cDNA by PCR using primers (see
CC   V36322-23) derived from the 5' untranslated region (UTR) of an
CC   anchored PCR product (see V36320-21) and from the 3'UTR of EST
CC   R49718 (obtained from an EST database search using a GABA-A
CC   receptor polypeptide).  A stably co-transfected eukaryotic cell
CC   line capable of expressing the GABA epsilon receptor subunit, at
CC   least one alpha receptor subunit and at least one beta receptor
CC   subunit is claimed.  A recombinant expression vector, and protein
CC   and membrane preparations of the GABA receptor obtained from the
CC   co-transfected cells are also claimed.  The new GABA-A receptor
CC   epsilon subunit and products can be used in the screening and
CC   design of drugs which act upon the GABA receptor.  The ligands or
CC   drug candidates identified may be used as therapeutic agents, e.g.
CC   for the modulation of appetite behaviours, hormonal interactions
CC   and cognition.  They can also be used for the study of structure,
CC   pharmacology and function of the various GABA receptor subtypes.
SQ   Sequence   1552 BP;    344 A;    443 C;    349 G;    416 T;
```

```
  Query Match           12.1%;  Score 744.8;  DB 1;  Length 1552;
  Best Local Similarity   99.7%;  Pred. No. 3.5e-219;
  Matches  746;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   3863 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 3922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    801 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 860

Qy   3923 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 3982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 920

Qy   3983 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 4042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    921 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 980

Qy   4043 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGAT 4102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    981 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGAT 1040

Qy   4103 TTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTC 4162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1041 TTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTC 1100

Qy   4163 AACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGT 4222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1101 AACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGT 1160

Qy   4223 ATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACAT 4282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161 ATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACAT 1220

Qy   4283 CAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCG 4342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221 CAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCG 1280
```

```
Qy   4343 TCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGC 4402
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1281 TCTTGCTCTGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGC 1340

Qy   4403 TCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCC 4462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341 TCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCC 1400

Qy   4463 GATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGAT 4522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1401 GATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGAT 1460

Qy   4523 AACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTT 4582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1461 AACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTT 1520

Qy   4583 GTTTGCCTTAACTTGTAGGTACCAGCTG 4610
          ||||||||||||||||||||||||||| |
Db   1521 GTTTGCCTTAACTTGTAGGTACCAGCGG 1548
```

RESULT 5
T21715
ID T21715 standard; cDNA to mRNA; 187 BP.
AC T21715;
DT 31-JUL-1996 (first entry)
DE Human gene signature HUMGS03162.
KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
OS Homo sapiens.
PN WO9514772-A1.
PD 01-JUN-1995.
PF 11-NOV-1994; J01916.
PR 12-NOV-1993; JP-355504.
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
PI Matsubara K, Okubo K;
DR WPI; 95-206931/27.
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues
PS Claim 1; Page 951; 2245pp; Japanese.
CC A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in T19001-T26837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.
SQ Sequence 187 BP; 53 A; 32 C; 44 G; 57 T;

Query Match 2.5%; Score 153; DB 1; Length 187;
Best Local Similarity 99.4%; Pred. No. 3.4e-37;
Matches 153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy   5993 GATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCT 6052
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db      1 GATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGNCATGCCCCAATGCT 60

Qy   6053 TCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCT 6112
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCT 120

Qy   6113 CCATCTACTTTTTGTCACCATCATCTGAAATGGG 6146
          |||||||||||||||||||||||||||||||||
Db    121 CCATCTACTTTTTGTCACCATCATCTGAAATGGG 154
```

RESULT 6
T02334
ID T02334 standard; cDNA; 1565 BP.
AC T02334;
DT 02-FEB-1996 (first entry)
DE GABA-A receptor gamma-3 subunit cDNA.
KW GABA-A receptor; gamma-aminobutyric acid receptor; gamma-3 subunit;
KW ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 33. .1436
FT /*tag= a
PN WO9529234-A1.
PD 02-NOV-1995.
PF 12-APR-1995; G00834.
PR 22-APR-1994; GB-008064.
PA (MERI) MERCK SHARP & DOHME LTD.
PI Whiting PJ;
DR WPI; 95-382983/49.
DR P-PSDB; R83968.
PT New cell line expressing human GABA-A receptor sub-units - useful in
PT drug screening and design
PS Claim 5; Page 18-20; 30pp; English.
CC A rat GABA-A receptor gamma-3 subunit cDNA probe was used to screen
CC a human foetal brain cDNA library. The single isolated clone
CC lacked the 5' and 3' ends of the gamma-3 subunit coding region.
CC These were obtd. by further PCR using primers based on the
CC truncated sequence, giving a complete cDNA sequence (T02334).
CC This can be used to express gamma-3 in transfected eukaryotic
CC (pref. rodent fibroblast) cell lines for prodn. of hybrid GABA-A
CC receptors having novel subunit compositions.
SQ Sequence 1565 BP; 430 A; 397 C; 339 G; 399 T;

Query Match 2.2%; Score 132.4; DB 1; Length 1565;
Best Local Similarity 64.2%; Pred. No. 3.5e-30;
Matches 199; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

```
Qy   3859 TTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGT 3918
          | ||||||| |   | |||||||| || |  ||  |  |||| |   |  | || ||  |
Db    740 TGCAGGTGATTATGTTGTCATGACTATATATTTTGAATTGAGTACAAGAATGGGATACTT 799

Qy   3919 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 3978
            || |||| |  ||  | || | |    ||||   | |  | ||||||||| || |||||
Db    800 CACCATTCAGACATACATTCCCTGTATACTGACTGTGGTTTTATCCTGGGTGTCATTTTG 859

Qy   3979 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 4038
          |||||| | |||  || | |||||  | ||  |  |||| |||||| | || ||||||||
Db    860 GATCAAAAAAGATGCTACGCCAGCAAGAACAGCATTAGGCATCACCACGGTGCTGACCAT 919

Qy   4039 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 4098
          ||||||  || ||||| |  |  | |||   || || || || |||||  | || ||| |
Db    920 GACCACCCTGAGCACCATCGCCAGGAAGTCCTTGCCACGCGTGTCCTACGTGACCGCCAT 979

Qy   4099 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 4158
          |||  | | | |  |  | |||||| | ||   |||| ||| ||| |||||| |||
Db    980 GGACCTTTTTGTGACTGTGTGCTTCCTGTTTGTCTTCGCCGCGCTGATGGAGTATGCCAC 1039

Qy   4159 GCTCAACTTC 4168
          |||||||
Db   1040 CCTCAACTAC 1049
```

RESULT 7
Q33130
ID Q33130 standard; DNA; 1408 BP.

```
AC   Q33130;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-6 subunit gene.
KW   Primer; human; alpha-6; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             27. .1388
FT                   /*tag= a
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   P-PSDB; R31187.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Claim 8; Fig 5; 43pp; English.
CC   The sequence given encodes the human alpha-6 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Rat alpha-6 cDNA was used as a probe
CC   and a human alpha-6 cDNA clone was isolated from a cerebellum cDNA
CC   library.  No full length cDNA's were isolated. To obtain a full length
CC   cDNA 3 clones were joined together using convenient restriction sites.
CC   GABA-A receptor comprises a multimeric protein of molecular size
CC   230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   1408 BP;    392 A;    321 C;    300 G;    395 T;

  Query Match             2.1%;  Score 128;  DB 1;  Length 1408;
  Best Local Similarity   61.9%;  Pred. No. 7.4e-29;
  Matches  203;  Conservative    0;  Mismatches  125;  Indels    0;  Gaps    0;

Qy   3861 CAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTG 3920
            ||||||| | | |  | |||||  ||| |||| |  ||   |||  | | |||||  |
Db    697 CAGGTGAATACGTTATAATGACAGTTTACTTCCACTTGCAAAGGAAGATGGGCTACTTCA 756

Qy   3921 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 3980
             | || |  ||    ||||      ||||    || || |||  ||| || || ||||
Db    757 TGATACAGATATACACTCCTTGCATTATGACAGTCATTCTTTCCCAGGTGTCTTTCTGGA 816

Qy   3981 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 4040
             | || |  ||||| |  |||||  | ||   ||| ||||||||| ||||| | || ||||
Db    817 TTAATAAGGAGTCCGTCCCAGCAAGAACTGTTCTTGGGATCACCACTGTTTTAACTATGA 876

Qy   4041 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGG 4100
            |||| ||| ||| |  | | ||  |   ||| ||    || || |||  ||| ||| |||
Db    877 CCACTTTGAGCATCAGTGCCCGGCACTCTTTGCCAAAAGTGTCATATGCCACTGCCATGG 936

Qy   4101 ATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGC 4160
            |||  |  || ||  | ||||| |  |||  |||||  |||||  | ||||| || |
Db    937 ATTGGTTCATAGCTGTTTGCTTTGCATTCGTCTTCTCTGCTCTTATCGAGTTCGCAGCTG 996

Qy   4161 TCAACTTCCTGATCTACAACCAGACAAA 4188
            |||||| | | | | |    ||||||  |
Db    997 TCAACTACTTTACCAATCTTCAGACACA 1024
```

```
RESULT   8
Q69142
ID   Q69142 standard; DNA; 1408 BP.
AC   Q69142;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha6 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             27. .1388
FT                   /*tag= a
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   P-PSDB; R59865.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.5; 79pp; English.
CC   This receptor DNA may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   1408 BP;    392 A;    321 C;    300 G;    395 T;

  Query Match             2.1%;  Score 128;  DB 1;  Length 1408;
  Best Local Similarity   61.9%;  Pred. No. 7.4e-29;
  Matches  203;  Conservative    0;  Mismatches  125;  Indels    0;  Gaps    0;

Qy   3861 CAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTG 3920
            ||||||| | | |  | |||||  ||| |||| |  ||   |||  | | |||||  |
Db    697 CAGGTGAATACGTTATAATGACAGTTTACTTCCACTTGCAAAGGAAGATGGGCTACTTCA 756

Qy   3921 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 3980
             | || |  ||    ||||      ||||    || || |||  ||| || || ||||
Db    757 TGATACAGATATACACTCCTTGCATTATGACAGTCATTCTTTCCCAGGTGTCTTTCTGGA 816

Qy   3981 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 4040
             | || |  ||||| |  |||||  | ||   ||| ||||||||| ||||| | || ||||
Db    817 TTAATAAGGAGTCCGTCCCAGCAAGAACTGTTCTTGGGATCACCACTGTTTTAACTATGA 876

Qy   4041 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGG 4100
            |||| ||| ||| |  | | ||  |   ||| ||    || || |||  ||| ||| |||
Db    877 CCACTTTGAGCATCAGTGCCCGGCACTCTTTGCCAAAAGTGTCATATGCCACTGCCATGG 936

Qy   4101 ATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGC 4160
            |||  |  || ||  | ||||| |  |||  |||||  |||||  | ||||| || |
Db    937 ATTGGTTCATAGCTGTTTGCTTTGCATTCGTCTTCTCTGCTCTTATCGAGTTCGCAGCTG 996

Qy   4161 TCAACTTCCTGATCTACAACCAGACAAA 4188
            |||||| | | | | |    ||||||  |
Db    997 TCAACTACTTTACCAATCTTCAGACACA 1024
```

```
RESULT   9
T28988
ID   T28988 standard; cDNA; 1707 BP.
AC   T28988;
DT   06-JAN-1997  (first entry)
DE   Human GABA-A receptor alpha 4 subunit cDNA.
KW   GABA-A receptor; gamma-aminobutyric acid; alpha-4 subunit; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             39. .1703
FT                   /*tag= a
PN   WO9610637-A1.
```

```
PD   11-APR-1996.
PF   29-SEP-1995; G02323.
PR   01-OCT-1994; GB-020010.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Le Bourdelles B,  Whiting PJ;
DR   WPI; 96-209359/21.
DR   P-PSDB; R97298.
PT   DNA encoding alpha-4 and delta subunit(s) of the human GABAa
PT   receptor  - also stably co-transfected eukaryotic cells expressing
PT   receptors contg. these subunit(s), used for screening and designing
PT   drugs
PS   Claim 9; Fig 2; 45pp; English.
CC   A cDNA clone (T28988) codes for the alpha-4 subunit (R97298) of the
CC   human GABA-A receptor.  It was isolated from human brain thalamus
CC   cDNA using primers (see also T28994-95) based on the 5' and 3'
CC   untranslated regions of a partial cDNA clone.  The cDNA can be
CC   incorporated into a vector and used to direct expression of the
CC   alpha-4 subunit in transfected cells, partic. rodent fibroblasts.
CC   Co-transfected host cells capable of expressing the alpha-4, delta
CC   (see also R97299) and beta subunits can be used to screen or design
CC   drugs that act on GABA-A receptors.
SQ   Sequence   1707 BP;    490 A;    373 C;    368 G;    476 T;


  Query Match             2.0%;  Score 125.6;  DB 1;  Length 1707;
  Best Local Similarity   61.1%;  Pred. No. 4.7e-28;
  Matches  203;  Conservative    0;  Mismatches  129;  Indels    0;  Gaps    0;

Qy   3858 TTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATG 3917
           || | ||||| |  || || |||||| ||| |||| |  | ||  ||  | | || |||
Db    754 TTACGGGTGAATATATTGTTATGACGGTTTACTTCCACCTCAGACGGAAGATGGGTTATT 813

Qy   3918 TTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTT 3977
           ||    |||| | |||| | || |      ||||   ||| || ||    ||||| ||||
Db    814 TTATGATTCAGACCTATATTCCGTGCATTATGACAGTGATTCTTTCTCAAGTTTCATTTT 873

Qy   3978 GGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCA 4037
           |||| || | ||| || | ||| ||  |||||    | || || ||  |||| || ||||
Db    874 GGATAAATAAAGAATCAGTTCCCGCTAGGACCGTATTTGGAATAACAACTGTCCTCACCA 933

Qy   4038 TGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCT 4097
           |||||||  |  ||| |  | | ||  |   ||| ||    || ||||||   || |||
Db    934 TGACCACACTAAGCATCAGTGCACGACATTCTTTGCCCAAAGTGTCCTATGCTACCGCCA 993

Qy   4098 TGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTG 4157
           |||| |  |  || ||  ||||||| |  ||    || |  || ||  | ||||||||||
Db    994 TGGACTGGTTCATAGCTGTCTGCTTTGCTTTTGTATTTTCGGCCCTTATCGAGTTTGCTG 1053

Qy   4158 TGCTCAACTTCCTGATCTACAACCAGACAAAA 4189
             ||||||   | | | | |  || |   ||
Db   1054 CTGTCAACTATTTCACCAATATTCAAATGGAA 1085


RESULT  10
Q33129
ID   Q33129 standard; DNA; 2310 BP.
AC   Q33129;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-5 subunit gene.
KW   Primer; human; alpha-5; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             298. .1686
FT                   /*tag=  a
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   P-PSDB; R31186.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Claim 7; Fig 4; 43pp; English.
CC   The sequence given encodes the human alpha-5 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Rat alpha-5 cDNA was used as a probe
CC   and a human alpha-5 cDNA clone was isolated from a hippocampal cDNA
CC   library.  GABA-A receptor comprises a multimeric protein of molecular
CC   size 230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   2310 BP;    655 A;    582 C;    512 G;    561 T;


  Query Match             1.9%;  Score 119.6;  DB 1;  Length 2310;
  Best Local Similarity   61.0%;  Pred. No. 4.1e-26;
  Matches  194;  Conservative    0;  Mismatches  124;  Indels    0;  Gaps    0;

Qy   3861 CAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTG 3920
           |||| || | ||   |||||||   |  |||| |  |||  |||  | |||||||  |||
Db   1019 CAGGCGAATACACAATCATGACAGCTCACTTCCACCTGAAAAGGAAGATTGGCTACTTTG 1078

Qy   3921 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 3980
             | | || | |||  | || |      |||||  |||  | ||   ||| |||||||||
Db   1079 TCATCCAGACCTACCTTCCCTGCATAATGACCGTGATCTTATCACAGGTGTCCTTTTGGC 1138

Qy   3981 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 4040
           | ||    || || |  |||||| ||||   | | ||| ||||| | || ||||||||||
Db   1139 TGAACCGGGAATCAGTCCCAGCCAGGACAGTTTTTGGGGTCACCACGGTGCTGACCATGA 1198

Qy   4041 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGG 4100
           | ||  |  ||| |    |  | ||   | | ||    ||  ||||   ||| ||| |||
Db   1199 CGACCCTCAGCATCAGCGCCAGGAACTCTCTGCCCAAAGTGGCCTACGCCACCGCCATGG 1258

Qy   4101 ATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGC 4160
           | |  |  || ||  | ||||  | ||||  |||||  || ||| | ||||||||   |
Db   1259 ACTGGTTCATAGCTGTGTGCTATGCCTTCGTCTTCTCGGCGCTGATAGAGTTTGCCACGG 1318

Qy   4161 TCAACTTCCTGATCTACA 4178
           |||| | | | | | | |
Db   1319 TCAATTACTTTACCAAGA 1336


RESULT  11
Q69141
ID   Q69141 standard; DNA; 2310 BP.
AC   Q69141;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha5 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             298. .1687
FT                   /*tag=  a
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
```

```
DR   WPI; 94-234213/28.
DR   P-PSDB; R59864.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.4; 79pp; English.
CC   This receptor DNA may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   2310 BP;    654 A;    583 C;    513 G;    560 T;

  Query Match             1.9%;  Score 119.6;  DB 1;  Length 2310;
  Best Local Similarity   61.0%;  Pred. No. 4.1e-26;
  Matches  194;  Conservative    0;  Mismatches  124;  Indels    0;  Gaps    0;

Qy    3861 CAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTG 3920
           |||| || | ||   |||||||   | |||| |  |||  |||  | |||||||  |||
Db    1019 CAGGCGAATACACAATCATGACAGCTCACTTCCACCTGAAAAGGAAGATTGGCTACTTTG 1078

Qy    3921 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 3980
           | | || | |||  | || |      |||||  |||  | ||   ||| ||||||||||
Db    1079 TCATCCAGACCTACCTTCCCTGCATAATGACCGTGATCTTATCACAGGTGTCCTTTTGGC 1138

Qy    3981 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 4040
           | ||    || || |  |||||| ||||   | | ||| ||||| | || ||||||||||
Db    1139 TGAACCGGGAATCAGTCCCAGCCAGGACAGTTTTTGGGGTCACCACGGTGCTGACCATGA 1198

Qy    4041 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGG 4100
           | ||  |  |||  |     |  | ||   | | ||    ||  ||||   ||| ||| |||
Db    1199 CGACCCTCAGCATCAGCGCCAGGAACTCTCTGCCCAAAGTGGCCTACGCCACCGCCATGG 1258

Qy    4101 ATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGC 4160
           |  |  |  || ||  | ||||  | ||||  |||||  || ||| | ||||||||   |
Db    1259 ACTGGTTCATAGCTGTGTGCTATGCCTTCGTCTTCTCGGCGCTGATAGAGTTTGCCACGG 1318

Qy    4161 TCAACTTCCTGATCTACA 4178
           |||| | | | | | | |
Db    1319 TCAATTACTTTACCAAGA 1336


RESULT  12
Q33128
ID   Q33128 standard; DNA; 1638 BP.
AC   Q33128;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-3 subunit gene.
KW   Primer; human; alpha-3; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             87. .1565
FT                   /*tag=  a
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   P-PSDB; R31185.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Claim 6; Fig 3; 43pp; English.
CC   The sequence given encodes the human alpha-3 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Bovine alpha-3 cDNA was used as a
CC   probe and an alpha-3 cDNA clone was isolated from a human foetal
CC   brain cDNA library, which was missing approx. 100 bp of the 5' end.
CC   This missing fragment was isolated by PCR.  The two fragments were
CC   ligated together to give a full length alpha-3 cDNA.    GABA-A
CC   receptor comprises a multimeric protein of molecular size 230-370 kD
CC   with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   1638 BP;    430 A;    436 C;    365 G;    407 T;

  Query Match             1.8%;  Score 112.8;  DB 1;  Length 1638;
  Best Local Similarity   59.3%;  Pred. No. 4e-24;
  Matches  192;  Conservative    0;  Mismatches  132;  Indels    0;  Gaps    0;

Qy    3853 GTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGG 3912
           || |  | |||| || |   | ||||||| |    |||| || | |   |     ||||
Db     854 GTCTAGTACAGGAGAATATGTCGTCATGACAACCCACTTCCATCTCAAGCGAAAAATTGG 913

Qy    3913 CTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTC 3972
           |||  |||   | || | |||  | || | |  | ||||    || || ||    || ||
Db     914 CTACTTTGTGATCCAGACCTACTTGCCATGTATCATGACTGTCATTCTGTCACAAGTGTC 973

Qy    3973 CTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCT 4032
           || ||| |||| | |||||||| ||| ||||| ||     | ||  ||||| |||| ||
Db     974 GTTCTGGCTCAACAGAGAGTCTGTTCCTGCCCGTACAGTCTTTGGTGTCACCACTGTGCT 1033

Qy    4033 GACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCAC 4092
           ||||||||||| ||| | | |  | |  | ||    || ||    ||  | |||   ||
Db    1034 TACCATGACCACCTTGAGTATCAGTGCCAGAAATTCCTTACCTAAAGTGGCATATGCGAC 1093

Qy    4093 AGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTT 4152
           ||| |||| |  |  || ||| |||| |  | |||    || |  || ||| | || ||
Db    1094 GGCCATGGACTGGTTCATAGCCGTCTGTTATGCCTTTGTATTTTCTGCACTGATTGAATT 1153

Qy    4153 TGCTGTGCTCAACTTCCTGATCTA 4176
           |||     ||||||   | | | |
Db    1154 TGCCACTGTCAACTATTTCACCAA 1177


RESULT  13
Q69140
ID   Q69140 standard; DNA; 1638 BP.
AC   Q69140;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha3 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             87. .1562
FT                   /*tag=  a
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   P-PSDB; R59863.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.3; 79pp; English.
CC   This receptor DNA may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
```

```
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   1638 BP;    430 A;    437 C;    364 G;    407 T;


  Query Match             1.8%;  Score 112.8;  DB 1;  Length 1638;
  Best Local Similarity   59.3%;  Pred. No. 4e-24;
  Matches  192;  Conservative    0;  Mismatches  132;  Indels    0;  Gaps    0;

Qy   3853 GTGTCTTTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGG 3912
           || |  | |||| || |   | |||||||| |    |||| || | |   |     ||||
Db    854 GTCTAGTACAGGAGAATATGTCGTCATGACAACCCACTTCCATCTCAAGCGAAAAATTGG 913

Qy   3913 CTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTC 3972
           |||  |||   | || | |||  | || | |  | ||||    || || ||    || ||
Db    914 CTACTTTGTGATCCAGACCTACTTGCCATGTATCATGACTGTCATTCTGTCACAAGTGTC 973

Qy   3973 CTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCT 4032
           || ||| |||| | |||||||| ||| ||||| ||     | ||  ||||| |||| ||
Db    974 GTTCTGGCTCAACAGAGAGTCTGTTCCTGCCCGTACAGTCTTTGGTGTCACCACTGTGCT 1033

Qy   4033 GACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCAC 4092
           |||||||||||| ||| | | |  | |  | ||    || ||    ||  | |||   ||
Db   1034 TACCATGACCACCTTGAGTATCAGTGCCAGAAATTCCTTACCTAAAGTGGCATATGCGAC 1093

Qy   4093 AGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTT 4152
           ||| |||| |  |  || ||| |||| |  | |||    || |  || ||| | || ||
Db   1094 GGCCATGGACTGGTTCATAGCCGTCTGTTATGCCTTTGTATTTTCTGCACTGATTGAATT 1153

Qy   4153 TGCTGTGCTCAACTTCCTGATCTA 4176
           |||     ||||||   | | | |
Db   1154 TGCCACTGTCAACTATTTCACCAA 1177


RESULT  14
Q33127
ID   Q33127 standard; DNA; 2189 BP.
AC   Q33127;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-2 subunit gene.
KW   Primer; human; alpha-3; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             214. .1569
FT                   /*tag=  a
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   P-PSDB; R31184.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Claim 5; Fig 2; 43pp; English.
CC   The sequence given encodes the human alpha-2 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Bovine alpha-2 cDNA was used as a
CC   probe and an alpha-2 cDNA clone was isolated from a human foetal
CC   brain cDNA library. GABA-A receptor comprises a multimeric protein
CC   of molecular size 230-270 kD with specific binding sites for various
CC   drugs including benzodiazepines, barbiturates, and beta-carbolines,
CC   in addition to the agonist ligand GABA.  The receptor is composed of
CC   several distinct types of subunit, which are divided into four classes
CC   (alpha, beta, gamma and delta) based on sequence homology.  To date
CC   six types of alpha, three types of beta, two types of gamma and one
CC   type of delta subunit have been identified.  It has been found that
CC   in addition to an alpha and a beta subunit, either gamma-1 or gamma-2
CC   is also required to confer benzodiazipine sensitivity.  The benzo-
CC   diazepine pharmacology of the receptor is largely dependent on the
CC   identity of the alpha and gamma subunits present.  Receptors
CC   containing a delta subunit do not appear to bind benzodiazepines.
SQ   Sequence   2189 BP;    640 A;    466 C;    418 G;    665 T;


  Query Match             1.7%;  Score 105.6;  DB 1;  Length 2189;
  Best Local Similarity   58.1%;  Pred. No. 8.3e-22;
  Matches  186;  Conservative    0;  Mismatches  134;  Indels    0;  Gaps    0;

Qy   3859 TTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGT 3918
           | |||||||  |  |  || |||||   |   ||| |  |||  ||     |||| ||| |
Db    912 TACAGGTGAATATACTGTAATGACAGCTCATTTCCACCTGAAAAGAAAAATTGGGTATTT 971

Qy   3919 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 3978
           ||   |||||| |||| | ||||    | ||||    || ||||||   ||||| || ||
Db    972 TGTGATTCAAACCTATCTGCCTTGCATCATGACTGTCATTCTCTCCCAAGTTTCATTCTG 1031

Qy   3979 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 4038
           | | || | ||| ||||   || ||  | ||     | ||  | ||  |||| || || ||
Db   1032 GCTTAACAGAGAATCTGTGCCTGCAAGAACTGTGTTTGGAGTAACAACTGTCCTAACAAT 1091

Qy   4039 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 4098
           ||| ||  |  ||| |  | |||| ||   | ||||    ||  | |||   || ||| |
Db   1092 GACAACTCTAAGCATCAGTGCTCGGAATTCTCTCCCCAAAGTGGCTTATGCAACTGCCAT 1151

Qy   4099 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 4158
           ||| |  | ||| ||  | || |  |  ||    ||||  || ||  | || |||||
Db   1152 GGACTGGTTTATTGCTGTTTGTTATGCATTTGTGTTCTCTGCCCTAATTGAATTTGCAAC 1211

Qy   4159 GCTCAACTTCCTGATCTACA 4178
             | || | | | | | | |
Db   1212 TGTTAATTACTTCACCAAAA 1231


RESULT  15
Q69139
ID   Q69139 standard; DNA; 2189 BP.
AC   Q69139;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha2 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             214. .1566
FT                   /*tag=  a
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   P-PSDB; R59862.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.2; 79pp; English.
CC   This receptor DNA may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   2189 BP;    640 A;    466 C;    418 G;    665 T;


  Query Match             1.7%;  Score 105.6;  DB 1;  Length 2189;
  Best Local Similarity   58.1%;  Pred. No. 8.3e-22;
  Matches  186;  Conservative    0;  Mismatches  134;  Indels    0;  Gaps    0;

Qy   3859 TTCAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGT 3918
           | |||||||  |  |  || |||||   |   ||| |  |||  ||     |||| ||| |
```

```
Db     912 TACAGGTGAATATACTGTAATGACAGCTCATTTCCACCTGAAAAGAAAAATTGGGTATTT 971

Qy    3919 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 3978
           ||   |||||| |||| | ||||    | ||||    || ||||||   ||||| || ||
Db     972 TGTGATTCAAACCTATCTGCCTTGCATCATGACTGTCATTCTCTCCCAAGTTTCATTCTG 1031

Qy    3979 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 4038
           | | || | ||| |||| || ||  | ||     | ||  | ||  |||| || || ||
Db    1032 GCTTAACAGAGAATCTGTGCCTGCAAGAACTGTGTTTGGAGTAACAACTGTCCTAACAAT 1091

Qy    4039 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 4098
           ||| ||  |  ||| |  | |||| ||   | ||||    ||  | |||   || ||| |
Db    1092 GACAACTCTAAGCATCAGTGCTCGGAATTCTCTCCCCAAAGTGGCTTATGCAACTGCCAT 1151

Qy    4099 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 4158
           ||| |  | ||| ||  | || |  |  ||    |||| || ||  | || |||||
Db    1152 GGACTGGTTTATTGCTGTTTGTTATGCATTTGTGTTCTCTGCCCTAATTGAATTTGCAAC 1211

Qy    4159 GCTCAACTTCCTGATCTACA 4178
             | || | | | | | | |
Db    1212 TGTTAATTACTTCACCAAAA 1231


Search completed: March  9, 2000, 22:43:31
Job time: 510 sec
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2000, 01:06:52 ; Search time 3156.82 Seconds
(without alignments)
7350.825 Million cell updates/sec

Title: US-09-030-832-1
Perfect score: 6146
Sequence: 1 GTCTTATAATTGCTAAGCAC.....TCACCATCATCTGAAATGGG 6146

Scoring table: IDENTITY_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

Number of hits that pass the threshold : 9077268

1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*
44: gb_est25:*
45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_gss1:*
80: gb_gss2:*
81: gb_gss3:*
82: gb_gss4:*
83: em_gss1:*
84: em_gss2:*
85: em_gss3:*
86: em_gss4:*
87: gb_gss5:*
88: gb_gss6:*
89: gb_gss7:*
90: gb_gss8:*
91: gb_gss9:*
92: em_gss5:*
93: em_gss6:*
94: em_gss7:*
95: em_gss8:*
96: em_gss9:*
97: em_gss10:*
98: em_gss11:*
99: gb_gss10:*
100: gb_gss11:*
101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	464	7.5	475	82	AQ702366	AQ702366 HS_5431_A
c	2	458	7.5	501	63	AI963395	AI963395 wt62f07.x
c	3	456	7.4	486	46	AI432632	AI432632 tg31g10.x
c	4	446.4	7.3	477	45	AI332325	AI332325 qp97g08.x
c	5	445	7.2	476	45	AI334197	AI334197 qp92d09.x
c	6	429	7.0	460	45	AI334196	AI334196 qp92d07.x
c	7	429	7.0	460	46	AI400573	AI400573 tg88b09.x

c	8	401.6	6.5	464	63	AW009693	AW009693 ws86b05.x
c	9	401	6.5	434	64	AW070871	AW070871 xa05c11.x
	10	398.4	6.5	404	28	C17786	C17786 C17786 Huma
c	11	398	6.5	433	38	AA776409	AA776409 zj50e04.s
c	12	394	6.4	429	44	AI276837	AI276837 ql67f08.x
c	13	390.4	6.4	474	63	AW014213	AW014213 UI-H-BI0-
	14	388.4	6.3	500	24	H63934	H63934 yr54h01.r1
c	15	386.4	6.3	418	37	AA677867	AA677867 zi13e03.s
	16	357.2	5.8	479	22	R64082	R64082 yi22g06.r1
	17	345.2	5.6	389	24	H83086	H83086 yq46f02.r1
	18	334.8	5.4	387	23	R91732	R91732 yp98f02.r1
c	19	333.4	5.4	403	37	AA682288	AA682288 zj85g12.s
c	20	330	5.4	371	37	AA704433	AA704433 zj22h01.s
c	21	320.4	5.2	363	41	AI040493	AI040493 ox14e03.s
c	22	318	5.2	366	20	T27014	T27014 NIBT136C07
	23	317.2	5.2	386	21	T78142	T78142 yc98d07.r1
	24	315	5.1	346	32	AA347290	AA347290 EST53563
c	25	314.4	5.1	485	24	H63532	H63532 yr54h01.s1
	26	301.4	4.9	303	31	AA299532	AA299532 EST12052
c	27	294	4.8	337	50	AI682740	AI682740 wc65f01.x
	28	291	4.7	477	21	R07942	R07942 yf16g04.r1
	29	282	4.6	293	28	C17228	C17228 C17228 Clon
c	30	281	4.6	311	40	AA954089	AA954089 on62h10.s
	31	280.4	4.6	522	22	R49718	R49718 yg71c11.r1
c	32	262.2	4.3	450	22	R49719	R49719 yg71c11.s1
c	33	251.2	4.1	317	21	R07883	R07883 yf16g04.s1
	34	246.2	4.0	465	22	R35778	R35778 yh90f03.r1
c	35	227.6	3.7	291	43	AI168466	AI168466 oo10f05.x
c	36	218.6	3.6	274	23	H25140	H25140 yl43f11.s1
c	37	218.4	3.6	260	36	AA634042	AA634042 ac74d11.s
c	38	215.4	3.5	259	62	AI924717	AI924717 wn74g12.x
	39	210.4	3.4	223	20	T27015	T27015 NIBT136C07R
	40	184	3.0	201	31	AA321214	AA321214 EST23669
c	41	182	3.0	212	44	AI279924	AI279924 qx57g03.x
c	42	179.6	2.9	400	22	R35667	R35667 yh90f03.s1
c	43	177	2.9	202	37	AA677292	AA677292 zj61e08.s
c	44	171	2.8	177	32	AA347289	AA347289 EST53562
c	45	168	2.7	206	32	AA368252	AA368252 EST79500

ALIGNMENTS

```
RESULT   1
AQ702366/c
LOCUS       AQ702366      475 bp    DNA             GSS       07-JUL-1999
DEFINITION  HS_5431_A1_E07_T7A RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=1007 Col=13 Row=I, genomic survey sequence.
ACCESSION   AQ702366
VERSION     AQ702366.1  GI:5411792
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 475)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 1007  row: I  column: 13
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 475.
FEATURES             Location/Qualifiers
     source          1. .475
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=1007 Col=13 Row=I"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
BASE COUNT      129 a    127 c    107 g    110 t      2 others
ORIGIN


  Query Match             7.5%;  Score 464;  DB 82;  Length 475;
  Best Local Similarity   98.5%;  Pred. No. 1.1e-126;
  Matches  467;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy   1073 CAAGTCACTAGTGGTTCCGTTTAGTAGATGATTGTGCATTGTTTCAAAATGGTGCCCTAG 1132
           |||||||||||||||| |||||||||||||||||||||||||||||| ||||||| |||
Db    475 CAAGTCACTAGTGGTTCGGTTTAGTAGATGATTGTGCATTGTTTCAAANTGGTGCCNTAG 416

Qy   1133 TGACTACAAAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAG 1192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    415 TGACTACAAAGCCCCAGAGCCAGCATCATCATCAAAGCAATGACAGTAGGTAAGCACCAG 356

Qy   1193 ACCTCCTTGGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTG 1252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    355 ACCTCCTTGGGAGTGAGGAGGATTCTTGAGGAGAAAAGAGGTCTTCTTTCTCCTCTGCTG 296

Qy   1253 GAGACTAGTTGATCTGGAGACGTGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTC 1312
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    295 GAGACTAGTTGATCTGGAGACATGGTTCCTTCAATGTCAGAGTTATCTTTGGGACTGGTC 236

Qy   1313 TCAAACTCTTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCT 1372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    235 TCAAACTCTTCCAGTTGGGCCCTGGGGCAGGTCTCTCCATCTGGAGCATACTTACGTGCT 176

Qy   1373 CGGCGATTAAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGA 1432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    175 CGGCGATTAAGGGTTCAGAATGCAGTGGTAGCCTGCTACTCTGGCCATCTTGGACCTTGA 116

Qy   1433 TCCAGAGAATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGG 1492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    115 TCCAGAGAATCTCTGCTTCAGGAGCTTCTAAGAGAGTCCAGCCCTGCCTCCAGAGAGAGG 56

Qy   1493 CTTGCCCTTCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGCTGGTCAG 1546
           |||||||||||||||||||||||||||||||||||||||||||||||||||||   |||||
Db     55 CTTGCCCTTCACTGATGGCTGTGGAGCCTCTGATGGAATATTATTGAGAGTCAG 2


RESULT   2
AI963395/c
LOCUS       AI963395      501 bp    mRNA            EST       20-AUG-1999
DEFINITION  wt62f07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2512069 3',
            mRNA sequence.
ACCESSION   AI963395
VERSION     AI963395.1  GI:5756108
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 501)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
```

```
COMMENT     On Dec 20, 1995 this sequence version replaced gi:1135445.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Life Technologies catalog #: 11548-013
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco
            High quality sequence stop: 420.
FEATURES             Location/Qualifiers
     source          1. .501
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2512069"
                     /clone_lib="NCI_CGAP_Pan1"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.72 kb. Life Technologies catalog #:
                     11548-013"
BASE COUNT      141 a    113 c    114 g    133 t
ORIGIN


  Query Match             7.5%;  Score 458;  DB 63;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-125;
  Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   5689 AGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGG 5748
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    501 AGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGG 442

Qy   5749 GCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACT 5808
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    441 GCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACT 382

Qy   5809 GTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGG 5868
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381 GTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGG 322

Qy   5869 CTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAA 5928
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 CTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAA 262

Qy   5929 GGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCC 5988
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 GGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCC 202

Qy   5989 CCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAA 6048
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 CCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAA 142

Qy   6049 TGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGGTGGATAGGGTGGG 6108
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 TGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGGTGGATAGGGTGGG 82

Qy   6109 GTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGG 6146
           ||||||||||||||||||||||||||||||||||||
Db     81 GTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGG 44


RESULT   3
AI432632/c
LOCUS       AI432632      486 bp    mRNA            EST       30-MAR-1999
DEFINITION  tg31g10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2110434 3',
            mRNA sequence.
ACCESSION   AI432632
VERSION     AI432632.1  GI:4283251
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 486)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2949103.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Insert Length: 1551   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 462.
FEATURES             Location/Qualifiers
     source          1. .486
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2110434"
                     /clone_lib="NCI_CGAP_Pr28"
                     /sex="male"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Plasmid DNA from the
                     normalized library NCI_CGAP_Pr22 was prepared, and ss
                     circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     985608-986759, 1101192-1101959, and 1217928-1220615).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
BASE COUNT      141 a    112 c    114 g    119 t
ORIGIN


  Query Match             7.4%;  Score 456;  DB 46;  Length 486;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-124;
  Matches  456;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   5691 CACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGC 5750
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 CACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGC 427

Qy   5751 AGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGT 5810
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 AGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGT 367

Qy   5811 GGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCT 5870
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 GGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCT 307

Qy   5871 AGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGG 5930
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 AGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGG 247

Qy   5931 CCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCC 5990
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 CCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCC 187

Qy   5991 AAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATG 6050
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    186 AAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATG 127

Qy   6051 CTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGT 6110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 CTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGT 67

Qy   6111 CTCCATCTACTTTTTGTCACCATCATCTGAAATGGG 6146
          |||||||||||||||||||||||||||||||||
Db     66 CTCCATCTACTTTTTGTCACCATCATCTGAAATGGG 31


RESULT   4
AI332325/c
LOCUS       AI332325      477 bp    mRNA            EST       13-FEB-1999
DEFINITION  qp97g08.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
            IMAGE:1931006 3', mRNA sequence.
ACCESSION   AI332325
VERSION     AI332325.1  GI:4068884
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 477)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1877761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 855   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 445.
FEATURES             Location/Qualifiers
     source          1. .477
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1931006"
                     /clone_lib="Soares_fetal_lung_NbHL19W"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCAATTTTTTTTTTTTTTTT-3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. This library was constructed
                     from the same fetus as the fetal heart library, Soares
                     fetal heart NbHH19W."
BASE COUNT      138 a    111 c    110 g    118 t
ORIGIN


  Query Match             7.3%;  Score 446.4;  DB 45;  Length 477;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-121;
  Matches  447;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   5699 ACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCT 5758
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    477 ACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCT 418

Qy   5759 TATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCA 5818
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    417 TATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCA 358

Qy   5819 CTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCT 5878
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    357 CTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCT 298

Qy   5879 CAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAAT 5938
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    297 CAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAAT 238

Qy   5939 GGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAA 5998
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    237 GGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAA 178

Qy   5999 ATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATA 6058
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    177 ATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATA 118

Qy   6059 TGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCT 6118
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    117 TGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCT 58

Qy   6119 ACTTTTTGTCACCATCATCTGAAATGGG 6146
          |||||||||||| ||||||||||||||||
Db     57 ACTTTTTGTCACTATCATCTGAAATGGG 30


RESULT   5
AI334197/c
LOCUS       AI334197      476 bp    mRNA            EST       13-FEB-1999
DEFINITION  qp92d09.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
            IMAGE:1930481 3', mRNA sequence.
ACCESSION   AI334197
VERSION     AI334197.1  GI:4070756
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 19, 1998 this sequence version replaced gi:2045081.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 997   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 458.
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1930481"
                     /clone_lib="Soares_fetal_lung_NbHL19W"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCAATTTTTTTTTTTTTTTT-3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. This library was constructed
                     from the same fetus as the fetal heart library, Soares
                     fetal heart NbHH19W."
BASE COUNT      137 a    111 c    111 g    117 t
ORIGIN
```

```
  Query Match             7.2%;  Score 445;  DB 45;  Length 476;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-121;
  Matches  445;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    5702 AGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTAT 5761
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     476 AGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTAT 417

Qy    5762 CCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTG 5821
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     416 CCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTG 357

Qy    5822 GAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAG 5881
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     356 GAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAG 297

Qy    5882 TTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGC 5941
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     296 TTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGC 237

Qy    5942 GACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATC 6001
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     236 GACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATC 177

Qy    6002 TCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGC 6061
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     176 TCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGC 117

Qy    6062 TAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTACT 6121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     116 TAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTACT 57

Qy    6122 TTTTGTCACCATCATCTGAAATGGG 6146
           |||||||||||||||||||||||||
Db      56 TTTTGTCACCATCATCTGAAATGGG 32


RESULT   6
AI334196/c
LOCUS       AI334196      460 bp    mRNA            EST       13-FEB-1999
DEFINITION  qp92d07.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
            IMAGE:1930477 3', mRNA sequence.
ACCESSION   AI334196
VERSION     AI334196.1  GI:4070755
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 460)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 19, 1998 this sequence version replaced gi:2045079.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1507   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 436.
FEATURES             Location/Qualifiers
     source          1. .460
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1930477"
                     /clone_lib="Soares_fetal_lung_NbHL19W"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCAATTTTTTTTTTTTTTTT-3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. This library was constructed
                     from the same fetus as the fetal heart library, Soares
                     fetal heart NbHH19W."
BASE COUNT      130 a    105 c    110 g    115 t
ORIGIN


  Query Match             7.0%;  Score 429;  DB 45;  Length 460;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-116;
  Matches  429;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    5718 AGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATG 5777
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     460 AGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATG 401

Qy    5778 AAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGC 5837
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     400 AAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGC 341

Qy    5838 CCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCT 5897
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     340 CCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCT 281

Qy    5898 TCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTC 5957
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     280 TCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTC 221

Qy    5958 AATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTA 6017
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     220 AATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTA 161

Qy    6018 ACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGT 6077
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     160 ACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGT 101

Qy    6078 CTGTAATTTGTTGGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATC 6137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100 CTGTAATTTGTTGGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATC 41

Qy    6138 TGAAATGGG 6146
           |||||||||
Db      40 TGAAATGGG 32


RESULT   7
AI400573/c
LOCUS       AI400573      460 bp    mRNA            EST       30-MAR-1999
DEFINITION  tg88b09.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2115833
            3', mRNA sequence.
ACCESSION   AI400573
VERSION     AI400573.1  GI:4243660
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 460)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Apr 7, 1998 this sequence version replaced gi:3034543.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
```

```
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 562   Std Error: 0.00
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .460
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2115833"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      129 a    106 c    110 g    114 t      1 others
ORIGIN


  Query Match             7.0%;  Score 429;  DB 46;  Length 460;
  Best Local Similarity   99.8%;  Pred. No. 2.8e-116;
  Matches  429;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   5717 GAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGAT 5776
           ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    460 GAGCTTCATGATAGCCNTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGAT 401

Qy   5777 GAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAG 5836
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    400 GAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAG 341

Qy   5837 CCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTC 5896
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    340 CCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTC 281

Qy   5897 TTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCT 5956
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    280 TTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCT 221

Qy   5957 CAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGT 6016
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    220 CAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGT 161

Qy   6017 AACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTG 6076
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    160 AACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTG 101

Qy   6077 TCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCAT 6136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    100 TCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCAT 41

Qy   6137 CTGAAATGGG 6146
           ||||||||||
Db     40 CTGAAATGGG 31


RESULT   8
AW009693/c
LOCUS       AW009693      464 bp    mRNA            EST       10-SEP-1999
DEFINITION  ws86b05.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504817 3',
            mRNA sequence.
ACCESSION   AW009693
VERSION     AW009693.1  GI:5858471
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 464)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Mar 16, 1998 this sequence version replaced gi:2961718.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
            M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arraying: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco
            High quality sequence stop: 366.
FEATURES             Location/Qualifiers
     source          1. .464
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2504817"
                     /clone_lib="NCI_CGAP_Co3"
                     /sex="pooled"
                     /tissue_type="colon"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from 12 pooled bulk tumor samples and primed
                     with a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector. Library went through one round of
                     normalization. "
BASE COUNT      134 a    102 c    101 g    127 t
ORIGIN


  Query Match             6.5%;  Score 401.6;  DB 63;  Length 464;
  Best Local Similarity   97.8%;  Pred. No. 4.2e-108;
  Matches  407;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   5731 CCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTC 5790
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    464 CCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTC 405

Qy   5791 ACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTT 5850
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    404 ACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTT 345

Qy   5851 CTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTG 5910
           |||||||||||||||||||||||||||||||||||||||| | || |||||||| ||
Db    344 TTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTTTTTTTTGTCACCTTTG 285

Qy   5911 CTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCT 5970
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    284 CTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCT 225

Qy   5971 GAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATG 6030
           |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    224 GAGGTGCTCAGACTGCCCCCAAGATCAAATCTTTCCTGGCTGTAGTAACCCAGTGGAATG 165

Qy   6031 AATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTG 6090
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    164 AATTTGGACATGCCCCAATGCTTTTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTG 105
```

```
Qy   6091 GGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGG 6146
          ||||||||||||||||||||||||||||||||||| ||||||| |||||||||
Db    104 GGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCCCCATCATTTGAAATGGG 49


RESULT  9
AW070871/c
LOCUS       AW070871      434 bp    mRNA            EST       13-OCT-1999
DEFINITION  xa05c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:2567444 3', mRNA sequence.
ACCESSION   AW070871
VERSION     AW070871.1  GI:6025869
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 434)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jul 9, 1999 this sequence version replaced gi:5434981.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
   source            1. .434
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2567444"
                     /clone_lib="Soares_NFL_T_GBC_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo. "
BASE COUNT      119 a    100 c    104 g    111 t
ORIGIN


  Query Match             6.5%;  Score 401;  DB 64;  Length 434;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-108;
  Matches  401;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   5746 AGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGG 5805
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434 AGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGG 375

Qy   5806 ACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATA 5865
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 ACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATA 315

Qy   5866 GGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGG 5925
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 GGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGG 255

Qy   5926 CAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTG 5985
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 CAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTG 195

Qy   5986 CCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCC 6045
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 CCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCC 135

Qy   6046 CAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGT 6105
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 CAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGT 75

Qy   6106 GGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGG 6146
          ||||||||||||||||||||||||||||||||||||||||
Db     74 GGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGG 34


RESULT  10
C17786
LOCUS       C17786        404 bp    mRNA            EST       02-OCT-1996
DEFINITION  C17786 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone
            GEN-552F09 5', mRNA sequence.
ACCESSION   C17786
VERSION     C17786.1  GI:1579389
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 404)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1404821.
            Contact: Tsutomu Fujiwara
            Otsuka GEN Research Institute
            Otsuka Pharmaceutical Co.,Ltd
            463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
            Tel: 0886-65-2888
            Fax: 0886-37-1035.
FEATURES             Location/Qualifiers
     source          1. .404
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="GEN-552F09"
                     /clone_lib="Human placenta cDNA (TFujiwara)"
                     /tissue_type="placenta"
BASE COUNT       93 a    118 c     79 g    114 t
ORIGIN


  Query Match             6.5%;  Score 398.4;  DB 28;  Length 404;
  Best Local Similarity   99.8%;  Pred. No. 3.4e-107;
  Matches  399;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   5384 CCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCC 5443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCC 60

Qy   5444 CCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAA 5503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAA 120

Qy   5504 CTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCG 5563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCG 180

Qy   5564 GAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGC 5623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGC 240

Qy   5624 ACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTT 5683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTT 300
```

```
Qy   5684 GGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCT 5743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCT 360

Qy   5744 TTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACC 5783
          |||||||||||||||||||||||||||||||||||| ||
Db    361 TTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAACCC 400


RESULT  11
AA776409/c
LOCUS       AA776409      433 bp    mRNA            EST       05-FEB-1998
DEFINITION  zj50e04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:453726 3', mRNA sequence.
ACCESSION   AA776409
VERSION     AA776409.1  GI:2835743
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 17, 1998 this sequence version replaced gi:2044660.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 379.
FEATURES             Location/Qualifiers
     source          1. .433
                     /organism="Homo sapiens"
                     /db_xref="GDB:1390082"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:453726"
                     /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.  1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      119 a     98 c    105 g    111 t
ORIGIN


  Query Match             6.5%;  Score 398;  DB 38;  Length 433;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-107;
  Matches  398;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   5749 GCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACT 5808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    433 GCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACT 374

Qy   5809 GTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGG 5868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    373 GTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGG 314

Qy   5869 CTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAA 5928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    313 CTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAA 254

Qy   5929 GGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCC 5988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    253 GGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCC 194

Qy   5989 CCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAA 6048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    193 CCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAA 134

Qy   6049 TGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGGTGGATAGGGTGGG 6108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    133 TGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGGTGGATAGGGTGGG 74

Qy   6109 GTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGG 6146
          |||||||||||||||||||||||||||||||||||||
Db     73 GTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGG 36


RESULT  12
AI276837/c
LOCUS       AI276837      429 bp    mRNA            EST       29-JAN-1999
DEFINITION  ql67f08.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1877415
            3', mRNA sequence.
ACCESSION   AI276837
VERSION     AI276837.1  GI:3899111
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 429)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 19, 1998 this sequence version replaced gi:2286330.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 575  Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 422.
FEATURES             Location/Qualifiers
     source          1. .429
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1877415"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      119 a     96 c    103 g    111 t
ORIGIN
```

```
  Query Match             6.4%;  Score 394;  DB 44;  Length 429;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-106;
  Matches  394;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    5753 GATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGG 5812
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     429 GATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGG 370

Qy    5813 ATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAG 5872
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     369 ATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAG 310

Qy    5873 ACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCC 5932
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     309 ACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCC 250

Qy    5933 CAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAA 5992
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     249 CAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAA 190

Qy    5993 GATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCT 6052
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     189 GATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCT 130

Qy    6053 TCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCT 6112
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     129 TCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCT 70

Qy    6113 CCATCTACTTTTTGTCACCATCATCTGAAATGGG 6146
           ||||||||||||||||||||||||||||||||||
Db      69 CCATCTACTTTTTGTCACCATCATCTGAAATGGG 36


RESULT  13
AW014213/c
LOCUS       AW014213      474 bp    mRNA            EST       10-SEP-1999
DEFINITION  UI-H-BI0-aak-a-03-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone
            IMAGE:2709412 3', mRNA sequence.
ACCESSION   AW014213
VERSION     AW014213.1  GI:5862970
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 474)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137517.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: NCI-CGAP clone distribution
            information can be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html The following repetitive
            elements were found in this cDNA sequence: 417-470, >MIR#SINE/MIR
            Seq primer: M13 Forward
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .474
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2709412"
                     /clone_lib="NCI_CGAP_Sub1"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NCI_CGAP_Sub1 library is a subtracted library derived from
                     BI.  BI constitutes a mixture of 21 normalized or
                     subtracted NCI_CGAP  libraries: NCI_CGAP_Co4,
                     NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10,
                     NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12,
                     NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2,
                     NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1, NCI_CGAP_Lei2,
                     NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
                     NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6, NCI_CGAP_Brn25.
                      These 21 libraries were pooled and a single-stranded DNA
                     preparation of the resulting mixture was used as a tracer
                     in a subtractive hybridization with a driver whose
                     composition is detailed below: NCI_CGAP_Kid3 pool 1 LLAM
                     3334-3337, 3682-3683, 3798-3803   (IMAGE CloneIDs
                     1322376-1323911, 1456008-1456775, 1500552-1502855)
                     NCI_CGAP_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
                      (IMAGE CloneIDs 1323912-1325831, 1471368-1472903,
                     1492104-1493255) NCI_CGAP_Lu5 pool 1 LLAM 3575-3582,
                     3851-3854   (IMAGE CloneIDs 1414920-1417991,
                     1520904-1522439)  NCI_CGAP_GC4 pool 1 LLAM 3164-3167,
                     3716-3720, 3733-3735   (IMAGE CloneIDs 1257096-1258631,
                     1469064-1470983, 1475592-1476743) NCI_CGAP_Pr22 pool 1
                     LLAM 2457-2459, 2758-2759, 3062-3068   (IMAGE CloneIDs
                     985608-986759, 1101192-1101959, 1217928-1220615)
                     NCI_CGAP_Co10 pool 1 LLAM 2644-2653, 2871-2872   (IMAGE
                     CloneIDs 1057416-1061255, 1144584-1145351)  The resulting
                     subtracted library contained 530,000 recombinants.
                     Subtraction was performed as previously described
                     [Bonaldo,  Lennon & Soares (1996): Normalization and
                     Subtraction: Two Approaches  To Facilitate Gene Discovery.
                     Genome Research 6, 791-806.
                     TAG_LIB=NCI_CGAP_Co10
                     TAG_TISSUE=colon
                     TAG_SEQ=AAACG"
BASE COUNT      121 a    116 c    113 g    124 t
ORIGIN


  Query Match             6.4%;  Score 390.4;  DB 63;  Length 474;
  Best Local Similarity   98.5%;  Pred. No. 9.2e-105;
  Matches  394;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    5747 GGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGA 5806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     465 GGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGA 406

Qy    5807 CTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAG 5866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     405 CTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAG 346

Qy    5867 GGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGC 5926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     345 GGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGC 286

Qy    5927 AAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGC 5986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     285 AAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGC 226

Qy    5987 CCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCC 6046
           ||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db     225 CCCCAAGATCGGATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCC 166

Qy    6047 AATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTG 6106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     165 AATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTG 106

Qy    6107 GGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGG 6146
           |||||  ||||  ||||||  ||||||||||| |||||||||
Db     105 GGGTCACCATGTACTTTCTGTCACCATCATGTGAAATGGG 66


RESULT  14
H63934
```

```
LOCUS       H63934         500 bp    mRNA            EST       11-OCT-1995
DEFINITION  yr54h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:209137 5', mRNA sequence.
ACCESSION   H63934
VERSION     H63934.1  GI:1018735
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 500)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 877
            High quality sequence stops: 379
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 877   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 379.
FEATURES             Location/Qualifiers
     source          1. .500
                     /organism="Homo sapiens"
                     /db_xref="GDB:3781978"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:209137"
                     /clone_lib="Soares fetal liver spleen 1NFLS"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Pac I - oligo(dT) primer
                     [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      120 a    126 c    110 g    139 t      5 others
ORIGIN
```

```
  Query Match             6.3%;  Score 388.4;  DB 24;  Length 500;
  Best Local Similarity   93.8%;  Pred. No. 3.8e-104;
  Matches  438;  Conservative    0;  Mismatches   22;  Indels    7;  Gaps    3;

Qy   5411 GTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGGCACTAGGCCT 5470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGGCACTAGGCCT 60

Qy   5471 TGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGC 5530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGC 120

Qy   5531 CATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGG 5590
          |||||||||||||||||||| |    ||||||||||||||||||||||||||||||||
Db    121 CATTGATTGGTGCCCACCCAGGGAAGCTGGTCGGAGTTCTATCACTTGCTTGACCCCTGG 180

Qy   5591 ACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCA 5650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    181 ACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCA 240

Qy   5651 AATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTC 5710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTC 300

Qy   5711 TGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTT 5770
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTT 360

Qy   5771 GCAGATGAAAACCCTGAGTCACAGATT---TCTGTGGGACTGTGGATCTCACTGGAAGCT 5827
          |||||||||||||||||||||||||||   | || ||      ||||||||||||||||
Db    361 GCAGATGAAAACCCTGAGTCACAGATTTTCTGTGGGGACTGTGGGATCTCACTGGAAGCT 420

Qy   5828 A-TCCAAGAGCCCACTG---TCACCTTCTAGACCACATGATAGGGCT 5870
          | ||||||||||||||    |    |   |||||||||||||| |
Db    421 ATTCCAAGAGCCCACTGGTCACCTTNTTAGGACCACATGATAGGGGT 467
```

```
RESULT  15
AA677867/c
LOCUS       AA677867      418 bp    mRNA            EST       19-DEC-1997
DEFINITION  zi13e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:430684 3', mRNA sequence.
ACCESSION   AA677867
VERSION     AA677867.1  GI:2658389
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 418)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     On Nov 6, 1997 this sequence version replaced gi:931632.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .418
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:430684"
                     /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.   1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      117 a     94 c    102 g    105 t
ORIGIN
```

```
  Query Match             6.3%;  Score 386.4;  DB 37;  Length 418;
```

```
  Best Local Similarity   99.7%;  Pred. No. 1.3e-103;
  Matches  387;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    5759 TATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCA 5818
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     418 TATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCA 359

Qy    5819 CTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCT 5878
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     358 CTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCT 299

Qy    5879 CAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAAT 5938
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     298 CAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTTGCAAGGCCCAGAAT 239

Qy    5939 GGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAA 5998
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 GGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAA 179

Qy    5999 ATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATA 6058
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     178 ATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATA 119

Qy    6059 TGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCT 6118
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     118 TGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCT 59

Qy    6119 ACTTTTTGTCACCATCATCTGAAATGGG 6146
           ||||||||||||||||||||||||||||
Db      58 ACTTTTTGTCACCATCATCTGAAATGGG 31


Search completed: March 11, 2000, 02:00:13
Job time: 3201 sec
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 10, 2000, 10:50:12 ; Search time 586.21 Seconds
(without alignments)
-9444.151 Million cell updates/sec

Title: US-09-412-600-1
Perfect score: 1332
Sequence: 1 gaggagcctacggtttggca.....aaaaaaaaaaaaaaaaaaaa 1332

Scoring table: IDENTITY_NUC

Searched: 4799332 seqs, -2078174120 residues

Database : Pending_Patents_NA:*

Word size : 0

Number of hits that pass the threshold : 9598654

1: /cgn2_6/ptodata/2/pna/PCTUS9_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US081A_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US081B_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US081C_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US081D_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US082A_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US082B_COMB.seq:*
10: /cgn2_6/ptodata/2/pna/US082C_COMB.seq:*
11: /cgn2_6/ptodata/2/pna/US083A_COMB.seq:*
12: /cgn2_6/ptodata/2/pna/US083B_COMB.seq:*
13: /cgn2_6/ptodata/2/pna/US084A_COMB.seq:*
14: /cgn2_6/ptodata/2/pna/US084B_COMB.seq:*
15: /cgn2_6/ptodata/2/pna/US084C_COMB.seq:*
16: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*
17: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*
18: /cgn2_6/ptodata/2/pna/US087A_COMB.seq:*
19: /cgn2_6/ptodata/2/pna/US087B_COMB.seq:*
20: /cgn2_6/ptodata/2/pna/US087C_COMB.seq:*
21: /cgn2_6/ptodata/2/pna/US088A_COMB.seq:*
22: /cgn2_6/ptodata/2/pna/US088B_COMB.seq:*
23: /cgn2_6/ptodata/2/pna/US088C_COMB.seq:*
24: /cgn2_6/ptodata/2/pna/US088D_COMB.seq:*
25: /cgn2_6/ptodata/2/pna/US089A_COMB.seq:*
26: /cgn2_6/ptodata/2/pna/US089B_COMB.seq:*
27: /cgn2_6/ptodata/2/pna/US089C_COMB.seq:*
28: /cgn2_6/ptodata/2/pna/US089D_COMB.seq:*
29: /cgn2_6/ptodata/2/pna/US089E_COMB.seq:*
30: /cgn2_6/ptodata/2/pna/US089F_COMB.seq:*
31: /cgn2_6/ptodata/2/pna/US089G_COMB.seq:*
32: /cgn2_6/ptodata/2/pna/US089H_COMB.seq:*
33: /cgn2_6/ptodata/2/pna/US089I_COMB.seq:*
34: /cgn2_6/ptodata/2/pna/US090A_COMB.seq:*
35: /cgn2_6/ptodata/2/pna/US090B_COMB.seq:*
36: /cgn2_6/ptodata/2/pna/US090C_COMB.seq:*
37: /cgn2_6/ptodata/2/pna/US090D_COMB.seq:*
38: /cgn2_6/ptodata/2/pna/US090E_COMB.seq:*
39: /cgn2_6/ptodata/2/pna/US091A_COMB.seq:*
40: /cgn2_6/ptodata/2/pna/US091B_COMB.seq:*
41: /cgn2_6/ptodata/2/pna/US091C_COMB.seq:*
42: /cgn2_6/ptodata/2/pna/US092A_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US092B_COMB.seq:*
44: /cgn2_6/ptodata/2/pna/US092C_COMB.seq:*
45: /cgn2_6/ptodata/2/pna/US092D_COMB.seq:*
46: /cgn2_6/ptodata/2/pna/US092E_COMB.seq:*
47: /cgn2_6/ptodata/2/pna/US093A_COMB.seq:*
48: /cgn2_6/ptodata/2/pna/US093B_COMB.seq:*
49: /cgn2_6/ptodata/2/pna/US093C_COMB.seq:*
50: /cgn2_6/ptodata/2/pna/US093D_COMB.seq:*
51: /cgn2_6/ptodata/2/pna/US093E_COMB.seq:*
52: /cgn2_6/ptodata/2/pna/US093F_COMB.seq:*
53: /cgn2_6/ptodata/2/pna/US094A_COMB.seq:*
54: /cgn2_6/ptodata/2/pna/US094B_COMB.seq:*
55: /cgn2_6/ptodata/2/pna/US6000_COMB.seq:*
56: /cgn2_6/ptodata/2/pna/US6001A_COMB.seq:*
57: /cgn2_6/ptodata/2/pna/US6001B_COMB.seq:*
58: /cgn2_6/ptodata/2/pna/US6002A_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6002B_COMB.seq:*
60: /cgn2_6/ptodata/2/pna/US6002C_COMB.seq:*
61: /cgn2_6/ptodata/2/pna/US6003A_COMB.seq:*
62: /cgn2_6/ptodata/2/pna/US6003B_COMB.seq:*
63: /cgn2_6/ptodata/2/pna/US6004A_COMB.seq:*
64: /cgn2_6/ptodata/2/pna/US6004B_COMB.seq:*
65: /cgn2_6/ptodata/2/pna/US6004C_COMB.seq:*
66: /cgn2_6/ptodata/2/pna/US6005_COMB.seq:*
67: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
68: /cgn2_6/ptodata/2/pna/US6007_COMB.seq:*
69: /cgn2_6/ptodata/2/pna/US6008A_COMB.seq:*
70: /cgn2_6/ptodata/2/pna/US6008B_COMB.seq:*
71: /cgn2_6/ptodata/2/pna/US6008C_COMB.seq:*
72: /cgn2_6/ptodata/2/pna/US6009A_COMB.seq:*
73: /cgn2_6/ptodata/2/pna/US6009B_COMB.seq:*
74: /cgn2_6/ptodata/2/pna/US6010A_COMB.seq:*
75: /cgn2_6/ptodata/2/pna/US6010B_COMB.seq:*
76: /cgn2_6/ptodata/2/pna/US6011A_COMB.seq:*
77: /cgn2_6/ptodata/2/pna/US6011B_COMB.seq:*
78: /cgn2_6/ptodata/2/pna/US6012A_COMB.seq:*
79: /cgn2_6/ptodata/2/pna/US6012B_COMB.seq:*
80: /cgn2_6/ptodata/2/pna/US6013A_COMB.seq:*
81: /cgn2_6/ptodata/2/pna/US6013B_COMB.seq:*
82: /cgn2_6/ptodata/2/pna/US6014A_COMB.seq:*
83: /cgn2_6/ptodata/2/pna/US6014B_COMB.seq:*
84: /cgn2_6/ptodata/2/pna/US6014C_COMB.seq:*
85: /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*
86: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:*
87: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:*
88: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
89: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
90: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
91: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
92: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1332	100.0	1332	53	US-09-412-600-1	Sequence 1, Appli
2	963.2	72.3	1933	53	US-09-412-600-3	Sequence 3, Appli
3	513.6	38.6	538	79	US-60-125-818-7041	Sequence 7041, Ap
4	513.2	38.5	564	80	US-60-130-174-968	Sequence 968, App
5	486.6	36.5	562	80	US-60-130-174-1974	Sequence 1974, Ap
c 6	465	34.9	489	79	US-60-125-818-7499	Sequence 7499, Ap
7	449.4	33.7	549	79	US-60-125-818-9582	Sequence 9582, Ap
8	381.2	28.6	418	79	US-60-125-818-3076	Sequence 3076, Ap
9	371.6	27.9	395	79	US-60-125-818-6049	Sequence 6049, Ap
10	364	27.3	380	71	US-60-089-524-1471	Sequence 1471, Ap
11	353.6	26.5	362	52	US-09-391-630-9354	Sequence 9354, Ap
12	353.6	26.5	362	83	US-60-144-084-8742	Sequence 8742, Ap
13	346.6	26.0	1205	3	US-08-054-920-3	Sequence 3, Appli
14	345.8	26.0	371	71	US-60-089-524-2117	Sequence 2117, Ap
c 15	344.4	25.9	593	80	US-60-130-174-1975	Sequence 1975, Ap
16	337.8	25.4	1233	3	US-08-054-920-1	Sequence 1, Appli
17	336	25.2	1226	3	US-08-054-920-5	Sequence 5, Appli
18	328.8	24.7	1119	3	US-08-054-920-9	Sequence 9, Appli
19	320.2	24.0	335	83	US-60-144-084-34683	Sequence 34683, A
20	318.8	23.9	483	71	US-60-089-524-1043	Sequence 1043, Ap

21	318.4	23.9	1159	3	US-08-054-920-7	Sequence 7, Appli
22	313.8	23.6	329	83	US-60-144-084-11647	Sequence 11647, A
23	310.4	23.3	397	71	US-60-089-524-3910	Sequence 3910, Ap
24	301	22.6	419	80	US-60-130-174-911	Sequence 911, App
25	283.2	21.3	405	82	US-60-141-135-2870	Sequence 2870, Ap
26	275.8	20.7	460	79	US-60-125-816-4785	Sequence 4785, Ap
27	274.4	20.6	282	47	US-09-306-349-15849	Sequence 15849, A
28	264.8	19.9	268	47	US-09-306-349-17703	Sequence 17703, A
29	256.2	19.2	369	52	US-09-391-630-8083	Sequence 8083, Ap
30	256.2	19.2	369	83	US-60-144-084-7858	Sequence 7858, Ap
31	253.2	19.0	258	47	US-09-306-349-13390	Sequence 13390, A
32	252.6	19.0	434	79	US-60-125-816-4787	Sequence 4787, Ap
33	252.2	18.9	269	47	US-09-306-349-8268	Sequence 8268, Ap
34	246.4	18.5	248	45	US-09-283-466-32340	Sequence 32340, A
35	244.2	18.3	250	83	US-60-144-084-31271	Sequence 31271, A
36	244	18.3	269	52	US-09-391-630-8685	Sequence 8685, Ap
37	244	18.3	269	83	US-60-144-084-27628	Sequence 27628, A
38	243.8	18.3	249	45	US-09-283-466-39444	Sequence 39444, A
39	242.4	18.2	279	47	US-09-306-349-21705	Sequence 21705, A
40	242	18.2	251	83	US-60-144-084-15514	Sequence 15514, A
41	240.8	18.1	244	47	US-09-306-349-8130	Sequence 8130, Ap
42	236.6	17.8	333	83	US-60-144-084-11267	Sequence 11267, A
43	234.6	17.6	271	47	US-09-306-349-9030	Sequence 9030, Ap
44	234.2	17.6	265	47	US-09-306-349-10362	Sequence 10362, A
45	232.8	17.5	236	47	US-09-306-349-13168	Sequence 13168, A

ALIGNMENTS

```
RESULT   1
US-09-412-600-1
; Sequence 1, Application US/09412600
; GENERAL INFORMATION:
;  APPLICANT: ARAHIRA, MASAOMI
;  APPLICANT: FUKAZAWA, CHIKAFUSA
;  TITLE OF INVENTION: CDNA ENCODING PLANT-DERIVED EPOXIDE HYDROLASE, GENE
;  TITLE OF INVENTION: ENCODING SAME AND TRANSFORMANT
;  FILE REFERENCE: 8361-0009-0
;  CURRENT APPLICATION NUMBER: US/09/412,600
;  CURRENT FILING DATE: 1999-10-06
;  EARLIER APPLICATION NUMBER: JP21183/1999
;  EARLIER FILING DATE: 1999-01-29
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1332
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (73)..(1098)
US-09-412-600-1


  Query Match           100.0%;  Score 1332;  DB 53;  Length 1332;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1332;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 gaggagcctacggtttggcattgagtgtgaaacaggctaataaatgtgagtggttcaccg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 gaggagcctacggtttggcattgagtgtgaaacaggctaataaatgtgagtggttcaccg 60

Qy      61 ccgcaacttccaatgtgcgagcacttactcgtctcactgtcttgctatatttgggtgaga 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ccgcaacttccaatgtgcgagcacttactcgtctcactgtcttgctatatttgggtgaga 120

Qy     121 acacagaggatagtggagttcaacgagatggagcaaataaggcacagaacagttgaagtg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 acacagaggatagtggagttcaacgagatggagcaaataaggcacagaacagttgaagtg 180

Qy     181 aatggcataaaaatgcatgttgcagagaaaggagagggtccagtggtgttgttcctccac 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 aatggcataaaaatgcatgttgcagagaaaggagagggtccagtggtgttgttcctccac 240

Qy     241 ggcttccctgagctctggtactcatggcgccatcagattctctctctcagctccctcggc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ggcttccctgagctctggtactcatggcgccatcagattctctctctcagctccctcggc 300

Qy     301 taccgcgccgtcgctcccgatctccgtggctacggtgacaccgaggcaccaccttcaatc 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 taccgcgccgtcgctcccgatctccgtggctacggtgacaccgaggcaccaccttcaatc 360

Qy     361 agcagctacaactgcttccacatagtgggtgatctcgttgcgcttattgactctctgggt 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 agcagctacaactgcttccacatagtgggtgatctcgttgcgcttattgactctctgggt 420

Qy     421 gtccaacaagtgttccttgtggctcatgactggggagccatcataggttggtatctatgc 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 gtccaacaagtgttccttgtggctcatgactggggagccatcataggttggtatctatgc 480

Qy     481 atgtttcgccctgacaaagttaaggcctatgtctgcctcagtgtccctctcctccgcaga 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 atgtttcgccctgacaaagttaaggcctatgtctgcctcagtgtccctctcctccgcaga 540

Qy     541 gacccaaacatcagaacggtggatggcatgcgtgctttgtatggagacgactactatgtc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 gacccaaacatcagaacggtggatggcatgcgtgctttgtatggagacgactactatgtc 600

Qy     601 tgcagatttcagaaaccaggggaaatggaggctcagatggctgaagttggcactgagtat 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 tgcagatttcagaaaccaggggaaatggaggctcagatggctgaagttggcactgagtat 660

Qy     661 gttctcaaaaacatccttacaactcgcaatcctggtcctccaattcttcccaagggaagg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 gttctcaaaaacatccttacaactcgcaatcctggtcctccaattcttcccaagggaagg 720

Qy     721 tttcaattcaatccagaaatgcccaacaccttgccctcttggctcacagaagaagatctc 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 tttcaattcaatccagaaatgcccaacaccttgccctcttggctcacagaagaagatctc 780

Qy     781 gcctattatgtctccaaatttgagaaaaccggattcactggacccttgaactactacaga 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 gcctattatgtctccaaatttgagaaaaccggattcactggacccttgaactactacaga 840

Qy     841 aatttcaacttaaattgggagttgacggcaccatggacaggagggccaatcaaggtgccc 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 aatttcaacttaaattgggagttgacggcaccatggacaggagggccaatcaaggtgccc 900

Qy     901 gtaaaatacataacaggtgagttggacatggtatacaactcgctgaacttgaaggagtat 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 gtaaaatacataacaggtgagttggacatggtatacaactcgctgaacttgaaggagtat 960

Qy     961 atccacggcggagggttcaagcaagatgtgccaaatttagaacaagtgattgtgcagaaa 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 atccacggcggagggttcaagcaagatgtgccaaatttagaacaagtgattgtgcagaaa 1020

Qy    1021 ggagtggctcacttcaataatcaagaagcagcagaggaaatcgataattacatatacgat 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 ggagtggctcacttcaataatcaagaagcagcagaggaaatcgataattacatatacgat 1080

Qy    1081 tttatcaaaaagttctgatcttgtccaaaaacgaattcaaccagatataaagtcgcagct 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 tttatcaaaaagttctgatcttgtccaaaaacgaattcaaccagatataaagtcgcagct 1140

Qy    1141 gaagtgaaagggtgttataattgcgcttttgttttgatatttaaggtatcgagatctttt 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 gaagtgaaagggtgttataattgcgcttttgttttgatatttaaggtatcgagatctttt 1200

Qy    1201 ttatgggcaggattcatcaactgcagaaaacctccataccatcaaccttcctatgcctgt 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ttatgggcaggattcatcaactgcagaaaacctccataccatcaaccttcctatgcctgt 1260

Qy    1261 ttgtattaattaactgataataatactgtatggtttggtacttgctaaataaaaaaaaaa 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 ttgtattaattaactgataataatactgtatggtttggtacttgctaaataaaaaaaaaa 1320
```

```
Qy   1321 aaaaaaaaaaaa 1332
          ||||||||||||
Db   1321 aaaaaaaaaaaa 1332
```

RESULT 2
US-09-412-600-3
; Sequence 3, Application US/09412600
; GENERAL INFORMATION:
; APPLICANT: ARAHIRA, MASAOMI
; APPLICANT: FUKAZAWA, CHIKAFUSA
; TITLE OF INVENTION: CDNA ENCODING PLANT-DERIVED EPOXIDE HYDROLASE, GENE
; TITLE OF INVENTION: ENCODING SAME AND TRANSFORMANT
; FILE REFERENCE: 8361-0009-0
; CURRENT APPLICATION NUMBER: US/09/412,600
; CURRENT FILING DATE: 1999-10-06
; EARLIER APPLICATION NUMBER: JP21183/1999
; EARLIER FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1933
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (271)..(810)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (979)..(1218)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1368)..(1613)
US-09-412-600-3

Query Match 72.3%; Score 963.2; DB 53; Length 1933;
Best Local Similarity 80.1%; Pred. No. 3.7e-280;
Matches 1305; Conservative 0; Mismatches 8; Indels 317; Gaps 2;

```
Qy      1 gaggagcctacggtttggcattgagtgtgaaacaggctaataaatgtgagtggttcaccg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    199 gaggagcctacggtttggcattgagtgtgaaacaggctaataaatgtgagtggttcaccg 258

Qy     61 ccgcaacttccaatgtgcgagcacttactcgtctcactgtcttgctatatttgggtgaga 120
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 ccgcaacttcaaatgtgcgagcacttactcgtctcactgtcttgctatatttgggtgaga 318

Qy    121 acacagaggatagtggagttcaacgagatggagcaaataaggcacagaacagttgaagtg 180
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    319 acacagaggatagtggagttcaacgagatggagcaaataaagcacagaacagttgaagtg 378

Qy    181 aatggcataaaaatgcatgttgcagagaaaggagagggtccagtggtgttgttcctccac 240
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    379 aatggcataaaaatgcatggtgcagagaaaggagagggtccagtggtgttgttcctccac 438

Qy    241 ggcttccctgagctctggtactcatggcgccatcagattctctctctcagctccctcggc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    439 ggcttccctgagctctggtactcatggcgccatcagattctctctctcagctccctcggc 498

Qy    301 taccgcgccgtcgctcccgatctccgtggctacggtgacaccgaggcaccaccttcaatc 360
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    499 taccgcgccgtcgctcccgatctccgtggctacggtgacaccgaagcaccaccttcaatc 558

Qy    361 agcagctacaactgcttccacatagtgggtgatctcgttgcgcttattgactctctgggt 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 agcagctacaactgcttccacatagtgggtgatctcgttgcgcttattgactctctgggt 618

Qy    421 gtccaacaagtgttccttgtggctcatgactggggagccatcataggttggtatctatgc 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 gtccaacaagtgttccttgtggctcatgactggggagccatcataggttggtatctatgc 678

Qy    481 atgtttcgccctgacaaagttaaggcctatgtctgcctcagtgtccctctcctccgcaga 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 atgtttcgccctgacaaagttaaggcctatgtctgcctcagtgtccctctcctccgcaga 738

Qy    541 gacccaaacatcagaacggtggatggcatgcgtgctttgtatggagacgactactatgtc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 gacccaaacatcagaacggtggatggcatgcgtgctttgtatggagacgactactatgtc 798

Qy    601 tgcagattt---------------------------------------------------- 610
          |||||||||
Db    799 tgcagatttcaggtttattaattaattctctcattttgcttatttttatcccacccttgt 858

Qy    610 ---------------------------------------------------------- 610

Db    859 ttttctttctctttctaattaactttgcacgaaatttaatttgtttctgtgaaatggggt 918

Qy    610 ----------------------------------------------------------cag 612
                                                                     |||
Db    919 cggaagattgtagtaccagatgcgaattattgtttttaaaccgtgtgtgtgtaactgcag 978

Qy    613 aaaccaggggaaatggaggctcagatggctgaagttggcactgagtatgttctcaaaaac 672
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    979 aaaccaggggaaatggaggctcagatggctgaagttggcactgagtatgttctcgaaaac 1038

Qy    673 atccttacaactcgcaatcctggtcctccaattcttcccaagggaaggtttcaattcaat 732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 atccttacaactcgcaatcctggtcctccaattcttcccaagggaaggtttcaattcaat 1098

Qy    733 ccagaaatgcccaacaccttgccctcttggctcacagaagaagatctcgcctattatgtc 792
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1099 ccagaaatgcccaacaccttgccctcttggctcacagaagaagatctcgcctattatgtc 1158

Qy    793 tccaaatttgagaaaaccggattcactggacccttgaactactacagaaatttcaactt- 852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 tccaaatttgagaaaaccggattcactggacccttgaactactacagaaatttcaacttg 1218

Qy    852 ---------------------------------------------------------- 852

Db   1219 taatttcttgattctccgtatttgcccgggataattgttttccactgctctaagttaatg 1278

Qy    852 ---------------------------------------------------------- 852

Db   1279 tttctttcttgggaaaatatttgttcaacatgacgggatcccaataaaaaaagaccatta 1338

Qy    852 ----------------------------aaattgggagttgacggcaccatggacaggag 883
                                       ||||||||||||||||||||||||||||||||
Db   1339 attaattaattattgtatgtatttgcagaaattgggagttgacggcaccatggacaggag 1398

Qy    884 ggccaatcaaggtgcccgtaaaatacataacaggtgagttggacatggtatacaactcgc 943
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1399 ggcaaatcaaggtgcccgtaaaatacataacaggtgagttggacatggtatacaactcgc 1458

Qy    944 tgaacttgaaggagtatatccacggcggagggttcaagcaagatgtgccaaatttagaac 1003
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1459 tgaacttgaaggagtatatccacggcggagggttcaagcaagatgtgccaaatttagaac 1518

Qy   1004 aagtgattgtgcagaaaggagtggctcacttcaataatcaagaagcagcagaggaaatcg 1063
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1519 aagtgattgtgcagaaaggagtggctcacttcaataatcaagaagcagcagaggaaatcg 1578

Qy   1064 ataattacatatacgattttatcaaaaagttctgatcttgtccaaaaacgaattcaacca 1123
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1579 ataattacatatacgattttatcaacaagttctgatcttgtccaaaaacgaattcaacca 1638

Qy   1124 gatataaagtcgcagctgaagtgaaagggtgttataattgcgcttttgttttgatattta 1183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1639 gatataaagtcgcagctgaagtgaaagggtgttataattgcgcttttgttttgatattta 1698

Qy   1184 aggtatcgagatctttttttatgggcaggattcatcaactgcagaaaacctccataccatc 1243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1699 aggtatcgagatctttttttatgggcaggattcatcaactgcagaaaacctccataccatc 1758

Qy   1244 aaccttcctatgcctgtttgtattaattaactgataataatactgtatggtttggtactt 1303
```

```
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 aaccttcctatgcttgtttgtattaattaactgataataatactgtatggtttggtactt 1818

Qy   1304 gctaaataaa 1313
          ||||||||||
Db   1819 gctaaataaa 1828
```

RESULT 3
US-60-125-818-7041
; Sequence 7041, Application US/60125818
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15761)A
; CURRENT APPLICATION NUMBER: US/60/125,818
; CURRENT FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 11068
; SEQ ID NO 7041
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: jC-gmfl02220102f11a1
US-60-125-818-7041

Query Match 38.6%; Score 513.6; DB 79; Length 538;
Best Local Similarity 97.0%; Pred. No. 1.9e-144;
Matches 522; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy    156 aataaggcacagaacagttgaagtgaatggcataaaaatgcatgttgcagagaaaggaga 215
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 aataaagcacagaacagttgaagtgaatggcataaaaatgcatgttgcagagaaaggaga 60

Qy    216 gggtccagtggtgttgttcctccacggcttccctgagctctggtactcatggcgccatca 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gggtccagtggtgttgttcctccacggcttccctgagctctggtactcatggcgccatca 120

Qy    276 gattctctctctcagctccctcggctaccgcgccgtcgctcccgatctccgtggctacgg 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gattctctctctcagctccctcggctaccgcgccgtcgctcccgatctccgtggctacgg 180

Qy    336 tgacaccgaggcaccaccttcaatcagcagctacaactgcttccacatagtgggtgatct 395
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 tgacaccgaagcaccaccttcaatcagcagctacaactgcttccacatagtgggtgatct 240

Qy    396 cgttgcgcttattgactctctgggtgtccaacaagtgttccttgtggctcatgactgggg 455
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    241 cgttgcgcttattgactctctgggtgtccaacaagtgttccttgtggctcatgactgngg 300

Qy    456 agccatcataggttggtatctatgcatgtttcgccctgacaaagttaaggcctatgtctg 515
          |       ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 gagccatcatagttggtatctatgcatgtttcgccctgacaaagttaaggcctatgtctg 360

Qy    516 cctcagtgtccctctcctccgcagagacccaaacatcagaacggtggatggcatgcgtgc 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 cctcagtgtccctctcctccgcagagacccaaacatcagaacggtggatggcatgcgtgc 420

Qy    576 tttgtatggagacgactactatgtctgcagatttcagaaaccaggggaaatggaggctca 635
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    421 tttgtatggagacgactactatgtctgcagatttcagaaaccagnggaaatggaggctca 480

Qy    636 gatggctgaagttggcactgagtatgttctcaaaaacatccttacaactcgcaatcct 693
          |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db    481 gatggctgaagttggcactgagtatgttctcgaaaacattcttacaactcgcaatcct 538
```

RESULT 4

US-60-130-174-968
; Sequence 968, Application US/60130174
; GENERAL INFORMATION:
; APPLICANT: Buehler, Robert E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Coombs, Brian E.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15763)A
; CURRENT APPLICATION NUMBER: US/60/130,174
; CURRENT FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 2262
; SEQ ID NO 968
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: jC-gmro02800032b05a1
US-60-130-174-968

Query Match 38.5%; Score 513.2; DB 80; Length 564;
Best Local Similarity 95.8%; Pred. No. 2.6e-144;
Matches 527; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

```
Qy    145 gagatggagcaaataaggcacagaacagttgaagtgaatggcataaaaatgcatgttgca 204
          ||||||||    |||   |||||||||||||||||||| ||||||||||||||||||||
Db     15 gagatggaaggcatagaacacagaacagttgaagtgaacggcataaaaatgcatgttgca 74

Qy    205 gagaaaggagagggtccagtggtgttgttcctccacggcttccctgagctctggtactca 264
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     75 gagaaaggagagggtccagtggtgttgttcctccatggcttccctgagctctggtactca 134

Qy    265 tggcgccatcagattctctctctcagctccctcggctaccgcgccgtcgctcccgatctc 324
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    135 tggcgccaccagattctctctctcagctccctcggctaccgcgccgtcgctcccgatctc 194

Qy    325 cgtggctacggtgacaccgaggcaccaccttcaatcagcagctacaactgcttccacata 384
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    195 cgtggctacggtgacaccgaggcaccaccttcaatcagcagctacaactgctttcacata 254

Qy    385 gtgggtgatctcgttgcgcttattgactctctgggtgtccaacaagtgttccttgtggct 444
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    255 gtgggtgatctcgttgcgcttattgactctctgggtgtccaacaagttttccttgtggct 314

Qy    445 catgactggggagccatcataggttggtatctatgcatgtttcgccctgacaaagttaag 504
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    315 catgactggggagccatcataggttggtatctctgcatgtttcgccctgacaaagttaag 374

Qy    505 gcctatgtctgcctcagtgtccctctcctccgcagagacccaaacatcagaacggtggat 564
          |||||||||||||||||| ||| | ||||||||||||||||||||||||||||||| |||
Db    375 gcctatgtctgcctcagtgttccttttctccgcagagacccaaacatcagaacggtagat 434

Qy    565 ggcatgcgtgctttgtatggagacgactactatgtctgcagatttcagaaaccaggggaa 624
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    435 ggcatgcgtgctttgtatggagacgactactatgtctgcagatttcagaaaccaggcgaa 494

Qy    625 atggaggctcagatggctgaagttggcactgagtatgttctcaaaaacatccttacaact 684
          ||||| |||||||||||||||||||||||| ||||||||||||||||||||||||||| |
Db    495 atggaagctcagatggctgaagttggcactgggtatgttctcaaaaacatccttacaagt 554

Qy    685 cgcaatcctg 694
          |||||  |||
Db    555 cgcaaaactg 564
```

RESULT 5
US-60-130-174-1974
; Sequence 1974, Application US/60130174
; GENERAL INFORMATION:
; APPLICANT: Buehler, Robert E.
; APPLICANT: Byrum, Joseph R.

```
;  APPLICANT: Coombs, Brian E.
;  APPLICANT: Thompson, Michael D.
;  TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
;  TITLE OF INVENTION: Plants
;  FILE REFERENCE: 38-21(15763)A
;  CURRENT APPLICATION NUMBER: US/60/130,174
;  CURRENT FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 2262
; SEQ ID NO 1974
;   LENGTH: 562
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: jC-gmro02800040g06a1
US-60-130-174-1974


  Query Match             36.5%;  Score 486.6;  DB 80;  Length 562;
  Best Local Similarity   95.3%;  Pred. No. 3e-136;
  Matches  512;  Conservative    0;  Mismatches   24;  Indels    1;  Gaps    1;

Qy    145 gagatggagcaaataaggcacagaacagttgaagtgaatggcataaaaatgcatgttgca 204
          ||||||||    |||  ||||||||||||||||||| ||||||||||||||||||||
Db     26 gagatggaaggcatagaacacagaacagttgaagtgaacggcataaaaatgcatgttgca 85

Qy    205 gagaaaggagagggtccagtggtgttgttcctccacggcttccctgagctctggtactca 264
          |||||||||||||||||||||||||||||||| ||||  ||||||||||||||||||
Db     86 gagaaaggagagggtccagtggtgttgttcctccatggctatcctgagctctggtactca 145

Qy    265 tggcgccatcagattctctctctcagctccctcggctaccgcgccgtcgctcccgatctc 324
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    146 tggcgccaccagattctctctctcagctccctcggctaccgcgccgtcgctcccgatctc 205

Qy    325 cgtggctacggtgacaccgaggcaccaccttcaatcagcagctacaactgcttccacata 384
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    206 cgtggctacggtgacaccgaggcaccaccttcaatcagcagctacaactgctttcacata 265

Qy    385 gtgggtgatctcgttgcgcttattgactctctgggtgtccaacaagtgttccttgtggct 444
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    266 gtgggtgatctcgttgcgcttattgactctctgggtgtccaacaagttttccttgtggct 325

Qy    445 catgactggggagccatcataggttggtatctatgcatgtttcgccctgacaaagttaag 504
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    326 catgactggggagccatcataggttggtatctctgcatgtttcgccctgacaaagttaag 385

Qy    505 gcctatgtctgcctcagtgtcccctctcctccgcagagacccaaacatcagaacggtggat 564
          |||||||||||||||||||| ||| | || ||||||||||||||||||||||||||| |||
Db    386 gcctatgtctgcctcagtgttccttttctgcgcagagacccaaacatcagaacggtagat 445

Qy    565 ggcatgcgtgctttgtatggagacgactactatgtctgcagatttcagaaaccaggggaa 624
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    446 ggcatgcgtgctttgtatggagacgactactatgtctgcagatttcagaaaccaggcgaa 505

Qy    625 atggaggctcagatggctgaagttggcactgagtatg-ttctcaaaaacatccttac 680
          ||||| |||||||||||||||||||||||||| ||||| ||||||| ||||||||||
Db    506 atggaagctcagatggctgaagttggcactgggtatgtttctcaagaacatccttac 562


RESULT   6
US-60-125-818-7499/c
; Sequence 7499, Application US/60125818
; GENERAL INFORMATION:
;  APPLICANT: Byrum, Joseph R.
;  APPLICANT: Heck, Gregory R.
;  APPLICANT: La Rosa, Thomas J.
;  TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
;  TITLE OF INVENTION: Plants
;  FILE REFERENCE: 38-21(15761)A
;  CURRENT APPLICATION NUMBER: US/60/125,818
;  CURRENT FILING DATE: 1999-03-23
;  NUMBER OF SEQ ID NOS: 11068
; SEQ ID NO 7499
;   LENGTH: 489
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: jC-gmf102220106f01d1
US-60-125-818-7499


  Query Match             34.9%;  Score 465;  DB 79;  Length 489;
  Best Local Similarity   98.9%;  Pred. No. 9.3e-130;
  Matches  468;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    841 aatttcaacttaaattgggagttgacggcaccatggacaggagggccaatcaaggtgccc 900
          |||||||||||||||||| |||||||||||||||||||| ||||| ||||||||||||
Db    489 AATTTCAACTTAAATTGGAAGTTGACGGCACCATGGACAGAAGGGCAAATCAAGGTGCCC 430

Qy    901 gtaaaatacataacaggtgagttggacatggtatacaactcgctgaacttgaaggagtat 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429 GTAAAATACATAACAGGTGAGTTGGACATGGTATACAACTCGCTGAACTTGAAGGAGTAT 370

Qy    961 atccacggcggagggttcaagcaagatgtgccaaatttagaacaagtgattgtgcagaaa 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 ATCCACGGCGGAGGGTTCAAGCAAGATGTGCCAAATTTAGAACAAGTGATTGTGCAGAAA 310

Qy   1021 ggagtggctcacttcaataatcaagaagcagcagaggaaatcgataattacatatacgat 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 GGAGTGGCTCACTTCAATAATCAAGAAGCAGCAGAGGAAATCGATAATTACATATACGAT 250

Qy   1081 tttatcaaaaagttctgatcttgtccaaaaacgaattcaaccagatataaagtcgcagct 1140
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 TTTATCAACAAGTTCTGATCTTGTCCAAAAACGAATTCAACCAGATATAAAGTCGCAGCT 190

Qy   1141 gaagtgaaagggtgttataattgcgcttttgttttgatatttaaggtatcgagatctttt 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 GAAGTGAAAGGGTGTTATAATTGCGCTTTTGTTTTGATATTTAAGGTATCGAGATCTTTT 130

Qy   1201 ttatgggcaggattcatcaactgcagaaaacctccataccatcaaccttcctatgcctgt 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    129 TTATGGGCAGGATTCATCAACTGCAGAAAACCTCCATACCATCAACCTTCCTATGCTTGT 70

Qy   1261 ttgtattaattaactgataataatactgtatggtttggtacttgctaaataaa 1313
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 TTGTATTAATTAACTGATAATAATACTGTATGGTTTGGTACTTGCTAAATAAA 17


RESULT   7
US-60-125-818-9582
; Sequence 9582, Application US/60125818
; GENERAL INFORMATION:
;  APPLICANT: Byrum, Joseph R.
;  APPLICANT: Heck, Gregory R.
;  APPLICANT: La Rosa, Thomas J.
;  TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
;  TITLE OF INVENTION: Plants
;  FILE REFERENCE: 38-21(15761)A
;  CURRENT APPLICATION NUMBER: US/60/125,818
;  CURRENT FILING DATE: 1999-03-23
;  NUMBER OF SEQ ID NOS: 11068
; SEQ ID NO 9582
;   LENGTH: 549
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: jC-gmf102220136h02a1
US-60-125-818-9582


  Query Match             33.7%;  Score 449.4;  DB 79;  Length 549;
  Best Local Similarity   92.0%;  Pred. No. 5.3e-125;
  Matches  474;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy    207 gaaaggagagggtccagtggtgttgttcctccacggcttccctgagctctggtactcatg 266
          |||||||||||||||| |||||||||||| ||||||||||||||||||||||||||||
Db      1 gaaaggagagggtccagcggtgttgttcctcctcggcttccctgagctctggtactcatg 60
```

```
Qy    267 gcgccatcagattctctctctcagctccctcggctaccgcgccgtcgctcccgatctccg 326
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gcgccaccagattctctctctcagctccctcggctaccgcgccgtcgctcccgatctccg 120

Qy    327 tggctacggtgacaccgaggcaccaccttcaatcagcagctacaactgcttccacatagt 386
          ||||||||||||||||||||||||||||||||||    ||||||||  ||||| ||||||||
Db    121 tggctacggtgacaccgaggcaccaccttcaatagacagctacacttgctttcacatagt 180

Qy    387 gggtgatctcgttgcgcttattgactctctgggtgtccaacaagtgttccttgtggctca 446
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    181 gggtgatctcgttgcgcttatagactctctgggtgtccaacaagtgttccttgtggctca 240

Qy    447 tgactggggagccatcataggttggtatctatgcatgtttcgccctgacaaagttaaggc 506
          |||||||||||||| |||| |||||||||||| |||||||||||||||| || || |||||
Db    241 tgactggggagccctcatgggttggtatctgtgcatgtttcgccctgagaaggtgaaggc 300

Qy    507 ctatgtctgcctcagtgtcccctcctccgcagagacccaaacatcagaacggtggatgg 566
          ||| |||||||||||||||||| || ||| |||| |||| ||| |||||||| || |||||
Db    301 ctacgtctgcctcagtgtccctttcatccccagaaaccccaacgtcagaaccgtagatgg 360

Qy    567 catgcgtgctttgtatggagacgactactatgtctgcagatttcagaaaccaggggaaat 626
          | |||||||| |||||||||| |||| ||  ||| ||||||||||||||||||||||||
Db    361 cttgcgtgctatgtatggagaagactattacatctccagatttcagaaaccaggggaaat 420

Qy    627 ggaggctcagatggctgaagttggcactgagtatgttctcaaaaacatccttacaactcg 686
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    421 ggaggctcagatggctgaagttggcactgagtatgttctcaaaaacctccttacaactcg 480

Qy    687 caatcctggtcctccaattcttcccaagggaaggt 721
          |||  ||||||||||| |   |||||||||||  ||
Db    481 caaaactggtcctccgacctttcccaagggagagt 515


RESULT   8
US-60-125-818-3076
; Sequence 3076, Application US/60125818
; GENERAL INFORMATION:
;  APPLICANT: Byrum, Joseph R.
;  APPLICANT: Heck, Gregory R.
;  APPLICANT: La Rosa, Thomas J.
;  TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
;  TITLE OF INVENTION: Plants
;  FILE REFERENCE: 38-21(15761)A
;  CURRENT APPLICATION NUMBER: US/60/125,818
;  CURRENT FILING DATE: 1999-03-23
;  NUMBER OF SEQ ID NOS: 11068
; SEQ ID NO 3076
;   LENGTH: 418
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: jC-gmfl02220072e01a1
US-60-125-818-3076


  Query Match            28.6%;  Score 381.2;  DB 79;  Length 418;
  Best Local Similarity   94.5%;  Pred. No. 1.9e-104;
  Matches  395;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy    115 gtgagaacacagaggatagtggagttcaacgagatggagcaaataaggcacagaacagtt 174
          |||||||||||||||||||||| |||||||||||||||| ||| | ||||| |||||||
Db      1 gtgagaacacagaggatagtggtgttcaacgagatggagctaattatgcacaaaacagtt 60

Qy    175 gaagtgaatggcataaaaatgcatgttgcagagaaaggagagggtccagtggtgttgttc 234
          || |||||||||||||||||||||| |||| |||||||| |||||||||||| ||
Db     61 gatgtgaatggcataaaaatgcatgttgcatagaatggagagggcccagtggtgttgctc 120

Qy    235 ctccacggcttccctgagctctggtactcatggcgccatcagattctctctctcagctcc 294
          |||||||||| ||||| ||||||||||||||||||||||||||||||||||| | ||||
Db    121 ctccacggcttacctgatctctggtactcatggcgccatcagattctctctctgagctgc 180

Qy    295 ctcggctaccgcgccgtcgctcccgatctccgtggctacggtgacaccgaggcaccacct 354
          |||||| |||||||||||||| | |||||||||||||||||||||||||||| |||||||||
Db    181 ctcggataccgcgccgtcgttaccgatctccgtggctacggtgacaccgaagcaccacct 240

Qy    355 tcaatcagcagctacaactgcttccacatagtgggtgatctcgttgcgcttattgactct 414
          || |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    241 tctatcagcagctacaactgcttccacatagtgggtgatctcgatgcgcttattgactct 300

Qy    415 ctgggtgtccaacaagtgttccttgtggctcatgactggggagccatcataggttggtat 474
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    301 ctgggtgtccaacaagtgttccttgtgactcatgactggggagccatcataggttggtat 360

Qy    475 ctatgcatgtttcgccctgacaaagttaaggcctatgtctgcctcagtgtccctctcc 532
          |||||||||||||||||||| |||||||||||||||||||||||||||||| |||||||
Db    361 ctatgcatgtttcgccctgactaagttaaggcctatgtctgcctcagtgtacctctcc 418


RESULT   9
US-60-125-818-6049
; Sequence 6049, Application US/60125818
; GENERAL INFORMATION:
;  APPLICANT: Byrum, Joseph R.
;  APPLICANT: Heck, Gregory R.
;  APPLICANT: La Rosa, Thomas J.
;  TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
;  TITLE OF INVENTION: Plants
;  FILE REFERENCE: 38-21(15761)A
;  CURRENT APPLICATION NUMBER: US/60/125,818
;  CURRENT FILING DATE: 1999-03-23
;  NUMBER OF SEQ ID NOS: 11068
; SEQ ID NO 6049
;   LENGTH: 395
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: jC-gmfl02220093c09a1
US-60-125-818-6049


  Query Match            27.9%;  Score 371.6;  DB 79;  Length 395;
  Best Local Similarity   96.4%;  Pred. No. 1.5e-101;
  Matches  380;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    157 ataaggcacagaacagttgaagtgaatggcataaaaatgcatgttgcagagaaaggagag 216
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 ataaagcacagaacagttgaagtgaatggcataaaaatgcatgttgcagagaaaggagag 61

Qy    217 ggtccagtggtgttgttcctccacggcttccctgagctctggtactcatggcgccatcag 276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 ggtccagtggtgttgttcctccacggcttccctgagctctggtactcatggcgccatcag 121

Qy    277 attctctctctcagctccctcggctaccgcgccgtcgctcccgatctccgtggctacggt 336
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 attctctctctcagctccctcggctaccgcgccgtcgctcccgatctccgtggctacggt 181

Qy    337 gacaccgaggcaccaccttcaatcagcagctacaactgcttccacatagtgggtgatctc 396
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 gacaccgaagcaccaccttcaatcagcagctacaactgcttccacatagtgggtgatctt 241

Qy    397 gttgcgcttattgactctctgggtgtccaacaagtgttccttgtggctcatgactgggga 456
            |||| | || |||||| |||||||||| || ||||||||||||  | ||||||||||
Db    242 cgtgcgttaatggactctttgggtgtccaccaggtgttccttgtgcttaatgactgggga 301

Qy    457 gccatcataggttggtatctatgcatgtttcgccctgacaaagttaaggcctatgtctgc 516
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 gccatcataggttggtatctatgcatgtttcgccctgacaaagttaaggcctatgtctgc 361

Qy    517 ctcagtgtccctctcctccgcagagacccaaaca 550
          |||||||||||||||||||||||||||||||||
Db    362 ctcagtgtccctctcctccgcagagacccaaaca 395


RESULT  10
US-60-089-524-1471
```

```
; Sequence 1471, Application US/60089524
;  GENERAL INFORMATION:
;    APPLICANT:  Joseph R. Byrum
;    APPLICANT:  Michael D. Thompson
;    TITLE OF INVENTION:  Nucleic Acid Molecules and Other Molecules
;    TITLE OF INVENTION:  Associated With Plants.
;    NUMBER OF SEQUENCES:  4769
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lawrence M. Lavin, Jr.
;      STREET:  BB4F
;      STREET:  Monsanto Company
;      STREET:  700 Chesterfield Parkway North
;      CITY:  St. Louis
;      STATE:  MO
;      COUNTRY:  United States
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette (3.5in, 1.44 Mb)
;      COMPUTER:  IBM PC/XT/AT, IBM PS/2 or compatibles
;      OPERATING SYSTEM:  Windows 95/NT
;      SOFTWARE:  WinZip 6.3
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/089,524
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lavin Jr., Lawrence M.
;      REGISTRATION NUMBER:  30,768
;      REFERENCE/DOCKET NUMBER:  38-21(15401)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314) 737-6670
;      TELEFAX:  (314) 737-6047
;  INFORMATION FOR SEQ ID NO:  1471:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  380 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Glycine max
;      DEVELOPMENTAL STAGE:  partially to fully opened
;      TISSUE TYPE:  flower
;    IMMEDIATE SOURCE:
;      LIBRARY:  LIB3028
;      CLONE:  LIB3028-017-Q1-B1-G3
US-60-089-524-1471


  Query Match             27.3%;  Score 364;  DB 71;  Length 380;
  Best Local Similarity   97.9%;  Pred. No. 2.9e-99;
  Matches  367;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy    135 ggagttcaacgagatggagcaaataaggcacagaacagttgaagtgaatggcataaaaat 194
          ||||||||||||||||||||||||| |||||||| ||||||||||||||||||||||||
Db      3 GGAGTTCAACGAGATGGAGCAAATAAAGCACAGAATAGTTGAAGTGAATGGCATAAAAAT 62

Qy    195 gcatgttgcagagaaaggagagggtccagtggtgttgttcctccacggcttccctgagct 254
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 GCATGTTGCAGAGAAAGGAGAGGGTCCAGTGGTGTTGTTCCTCCACGGCTTCCCTGAGCT 122

Qy    255 ctggtactcatggcgccatcagattctctctctcagctccctcggctaccgcgccgtcgc 314
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    123 CTGGTACTCATGGCGCCACCAGATTCTCTCTCTCAGCTCCCTCGGCTACCGCGCCGTCGC 182

Qy    315 tcccgatctccgtggctacggtgacaccgaggcaccaccttcaatcagcagctacaactg 374
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 TCCCGATCTCCGTGGCTACGGTGACACCGAGGCACCACCTTCAATCAGCAGCTACAACTG 242

Qy    375 cttccacatagtgggtgatctcgttgcgcttattgactctctgggtgtccaacaagtgtt 434
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 CTTCCACATAGTGGGTGATCTCGTTGCGCTTATTGACTCTCTGGGTGTCCAACAAGTGTT 302

Qy    435 ccttgtggctcatgactggggagccatcataggttggtatctatgcatgtttcgccctga 494
          |||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||||
Db    303 CCTTGTGGCTCATGACTGGGGAGCCATCATANGTTGGTATCTCTGCATGTTTCGCCCTGA 362

Qy    495 caaagttaaggccta 509
          ||||||| | | |||
Db    363 CAAAGTTNANGGCTA 377


RESULT  11
US-09-391-630-9354
; Sequence 9354, Application US/09391630
; GENERAL INFORMATION:
;  APPLICANT: Byrum, Joseph R.
;  APPLICANT: Heck, Gregory R.
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT: Shukla, Hridayabhiramjam
;  APPLICANT: Thompson, Michael D.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
;  TITLE OF INVENTION: PLANTS
;  FILE REFERENCE: 38-21(15441)B
;  CURRENT APPLICATION NUMBER: US/09/391,630
;  CURRENT FILING DATE: 1999-09-08
;  NUMBER OF SEQ ID NOS: 18889
; SEQ ID NO 9354
;   LENGTH: 362
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: unsure at all n locations
;   OTHER INFORMATION: Clone ID: LIB3049-032-Q1-E1-F10
US-09-391-630-9354


  Query Match             26.5%;  Score 353.6;  DB 52;  Length 362;
  Best Local Similarity   98.6%;  Pred. No. 4e-96;
  Matches  356;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    138 gttcaacgagatggagcaaataaggcacagaacagttgaagtgaatggcataaaaatgca 197
          ||||||||||||||||||||||| |||||||| ||||||||||||||||||||||||||||
Db      2 gttcaacgagatggagcaaataaagcacagaatagttgaagtgaatggcataaaaatgca 61

Qy    198 tgttgcagagaaaggagagggtccagtggtgttgttcctccacggcttccctgagctctg 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 tgttgcagagaaaggagagggtccagtggtgttgttcctccacggcttccctgagctctg 121

Qy    258 gtactcatggcgccatcagattctctctctcagctccctcggctaccgcgccgtcgctcc 317
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    122 gtactcatggcgccaccagattctctctctcagctccctcggctaccgcgccgtcgctcc 181

Qy    318 cgatctccgtggctacggtgacaccgaggcaccaccttcaatcagcagctacaactgctt 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 cgatctccgtggctacggtgacaccgaggcaccaccttcaatcagcagctacaactgctt 241

Qy    378 ccacatagtgggtgatctcgttgcgcttattgactctctgggtgtccaacaagtgttcct 437
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    242 ccacatagtgggtgatctcgttgcgcttattgactctctgggtgtncaacaagtgttcct 301

Qy    438 tgtggctcatgactggggagccatcataggttggtatctatgcatgtttcgccctgacaa 497
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    302 tgtggctcatgactggggagccatcataggttggtatctctgcatgtttcgccctgacaa 361

Qy    498 a 498
          |
Db    362 a 362


RESULT  12
US-60-144-084-8742
; Sequence 8742, Application US/60144084
; GENERAL INFORMATION:
```

```
;  APPLICANT: Abad, Mark S.
;  APPLICANT: Buehler, Robert E.
;  APPLICANT: Byrum, Joseph R.
;  APPLICANT: Coombs, Brian E.
;  APPLICANT: Heck, Gregory R.
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT: Nelson, Donald E.
;  APPLICANT: Shukla, Hridayabhiramjam
;  APPLICANT: Thompson, Michael D.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
;  TITLE OF INVENTION: PLANTS
;  FILE REFERENCE: 38-21(15444)B
;  CURRENT APPLICATION NUMBER: US/60/144,084
;  CURRENT FILING DATE: 1999-07-16
;  NUMBER OF SEQ ID NOS: 47776
; SEQ ID NO 8742
;   LENGTH: 362
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: unsure at all n locations
;   OTHER INFORMATION: Clone ID: LIB3049-032-Q1-E1-F10
US-60-144-084-8742


  Query Match             26.5%;  Score 353.6;  DB 83;  Length 362;
  Best Local Similarity   98.6%;  Pred. No. 4e-96;
  Matches  356;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    138 gttcaacgagatggagcaaataaggcacagaacagttgaagtgaatggcataaaaatgca 197
          ||||||||||||||||||||| |||||||| ||||||||||||||||||||||||||||
Db      2 gttcaacgagatggagcaaataaagcacagaatagttgaagtgaatggcataaaaatgca 61

Qy    198 tgttgcagagaaaggagagggtccagtggtgttgttcctccacggcttccctgagctctg 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 tgttgcagagaaaggagagggtccagtggtgttgttcctccacggcttccctgagctctg 121

Qy    258 gtactcatggcgccatcagattctctctctcagctccctcggctaccgcgccgtcgctcc 317
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    122 gtactcatggcgccaccagattctctctctcagctccctcggctaccgcgccgtcgctcc 181

Qy    318 cgatctccgtggctacggtgacaccgaggcaccaccttcaatcagcagctacaactgctt 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 cgatctccgtggctacggtgacaccgaggcaccaccttcaatcagcagctacaactgctt 241

Qy    378 ccacatagtgggtgatctcgttgcgcttattgactctctgggtgtccaacaagtgttcct 437
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    242 ccacatagtgggtgatctcgttgcgcttattgactctctgggtgtncaacaagtgttcct 301

Qy    438 tgtggctcatgactggggagccatcataggttggtatctatgcatgtttcgccctgacaa 497
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    302 tgtggctcatgactggggagccatcataggttggtatctctgcatgtttcgccctgacaa 361

Qy    498 a 498
          |
Db    362 a 362


RESULT  13
US-08-054-920-3
; Sequence 3, Application US/08054920
;  GENERAL INFORMATION:
;    APPLICANT:  Stapleton, Andrew
;    APPLICANT:  Belknap, William R
;    APPLICANT:  Friedman, Mendell
;    APPLICANT:  Garbarino, Joan E
;    APPLICANT:  Rockhold, David R
;    APPLICANT:  Allen, Paul V
;    TITLE OF INVENTION:  DNA Sequences Encoding Solanidine
;    TITLE OF INVENTION:  UDP-Glucose Glucosyltransferase and Use To Reduce
;    TITLE OF INVENTION:  Glycoalkaloids in  Solanaceous Plants
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Margaret A. Connor
;      STREET:  800 Buchanan Street
;      CITY:  Albany
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94710
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/054,920
;      FILING DATE:  19930428
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connor, Margaret A
;      REGISTRATION NUMBER:  30043
;      REFERENCE/DOCKET NUMBER:  PC0129.93
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-559-6067
;      TELEFAX:  510-559-5777
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1205 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Solanum tuberosum
;      STRAIN:  Lemhi Russet
;    IMMEDIATE SOURCE:
;      LIBRARY:  Wounded Lemhi
;      CLONE:  SGT4.1 (NRRL B-21077)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  57..1022
;      OTHER INFORMATION:  /EC_number= 2.4.1
;      OTHER INFORMATION:  /product= "UDP-glucose: solanidine
;      OTHER INFORMATION:  glucosyltransferase"
;      OTHER INFORMATION:  /citation= ([1])
;    PUBLICATION INFORMATION:
;      AUTHORS:  Stapleton, Andrew
;      AUTHORS:  Allen, Paul V
;      AUTHORS:  Tao, H. Peggy
;      AUTHORS:  Belknap, William R
;      AUTHORS:  Friedman, Mendel
;      TITLE:  Partial Amino Acid Sequence of Potato
;      TITLE:  Solanidine UDP-glucose Glucosyltransferase
;      TITLE:  Purified by New Anion-Exchange and Size Exclusion
;      TITLE:  Media
;      JOURNAL:  Protein Expression and Purification
;      VOLUME:  3
;      PAGES:  85-92
;      DATE:  April-1992
US-08-054-920-3


  Query Match             26.0%;  Score 346.6;  DB 3;  Length 1205;
  Best Local Similarity   61.9%;  Pred. No. 1.1e-93;
  Matches  607;  Conservative    0;  Mismatches  359;  Indels   15;  Gaps    3;

Qy    141 caacgagatggagcaaataaggcacagaacagttgaagtgaatggcataaaaatgcatgt 200
          |||  | |||||| | |||  ||||| ||  || |  || |||||| |||| |||||| |
Db     50 CAAAAAAATGGAGAAGATAGAGCACAAAATGGTAGCTGTAAATGGCCTAAATATGCATAT 109

Qy    201 tgcagagaaaggagagggtccagtggtgttgttcctccacggcttccctgagctctggta 260
          |||||   |||  | || |||    |  | ||| |||| ||||||||||||||||||||
Db    110 AGCAGAATTAGGCCAAGGCCCAACAATCCTCTTCATCCATGGCTTCCCTGAGCTCTGGTA 169
```

```
Qy     261 ctcatggcgccatcagattctctctctcagctccctcggctaccgcgccgtcgctcccga 320
           |||||||||||| || ||  |||   |       |  || ||||| || || || || ||
Db     170 CTCATGGCGCCACCAAATGGTCTACTTAGCTGAACGTGGGTACCGTGCTGTGGCGCCTGA 229

Qy     321 tctccgtggctacggtgacaccgaggcaccaccttcaatcagcagctacaactgc----- 376
             |  | || || || || ||    |   ||||    |    |   |  || | |
Db     230 CTTAAGGGGTTATGGAGATACTACTGGTGCACCAATTAATGACCCTTCGAAGTTCAGTAT 289

Qy     376 -ttccacatagtgggtgatctcgttgcgcttattga------ctctctgggtgtccaaca 428
            || ||| | |||||||||| | || ||  |  ||||         |||    ||   |  |
Db     290 TTTTCACCTTGTGGGTGATGTTGTAGCATTGCTTGAAGCCATTGCTCCTAATGAAGACAA 349

Qy     429 agtgttccttgtggctcatgactggggagccatcataggttggtatctatgcatgtttcg 488
           |||||  |||| || ||||||||||| ||  | || | |||| || ||||| | ||| |
Db     350 GGTGTTTGTTGTTGCGCATGACTGGGGCGCGTTAATTGCTTGGCATTTATGCCTTTTTAG 409

Qy     489 ccctgacaaagttaaggcctatgtctgcctcagtgtccctctcctccgcagagacccaaa 548
           || || |||||||| ||||  ||     | |||||| |  || ||  ||  || ||||
Db     410 GCCAGATAAAGTTAAAGCCTTGGTGAATTTGAGTGTCCATTACCACCCAAGGAACTCAAA 469

Qy     549 catcagaacggtggatggcatgcgtgctttgtatggagacgactactatgtctgcagatt 608
           || |   |  | || ||  |    ||||| ||||| || || || ||| ||||||||||
Db     470 TATGAATCCTATTGAGGGGCTAAAGGCTTTATATGGGGAAGATTATTATATCTGCAGATT 529

Qy     609 tcagaaaccaggggaaatggaggctcagatggctgaagttggcactgagtatgttctcaa 668
           ||||  ||| || ||||| || ||| |  | |||  | ||||  || ||| ||||| ||
Db     530 TCAGGTACCGGGCGAAATTGAAGCTGAATTTGCTCCAATTGGTGCTAAGTCTGTTCTTAA 589

Qy     669 aaacatccttacaactcgcaatcctggtcctccaattcttcccaagggaa---ggtttca 725
           || ||  | |||   ||| ||||||  ||      | |||| || || |   |  || |
Db     590 GAAAATGTTGACATACCGCGATCCTGCACCCTTTTATTTTCCTAAAGGCAAAGGCCTTGA 649

Qy     726 attcaatccagaaatgcccaacaccttgccctcttggctcacagaagaagatctcgccta 785
           |   |   | ||    || |    | |  |  | |||||| | || |||||  | |  ||
Db     650 AGCTATCGCTGATGCTCCGATTGTCCTTTCAACATGGCTCTCTGAGGAAGAGTTGGATTA 709

Qy     786 ttatgtctccaaatttgagaaaaccggattcactggacccttgaactactacagaaattt 845
           |||| |  ||| |||||  | || || |||||||  |  | |||||  ||| ||  |||
Db     710 CTATGCCAACAAGTTTGAACAGACTGGTTTCACTGGTGCACTTAACTATTACCGAGCTTT 769

Qy     846 caacttaaattgggagttgacggcaccatggacaggagggccaatcaaggtgcccgtaaa 905
             | ||||||  ||  | || ||||||||||||||| |  | | | || || ||    ||
Db     770 ATCCATAAATTCAGAACTCACTGCACCATGGACAGGGGCACAAGTTAATGTTCCAACCAA 829

Qy     906 atacataacaggtgagttggacatggtatacaactcgctgaacttgaaggagtatatcca 965
           |  ||  || || || ||| |||  ||| |   ||          || ||||| || ||
Db     830 GTTTATTGTCGGGGAATTCGACTTGGCGTACCATATGCGAGGTGCTAAAGAGTACATACA 889

Qy     966 cggcggagggttcaagcaagatgtgccaaatttagaacaagtgattgtgcagaaaggagt 1025
           |   || || || ||| || |||| |||   || ||  ||||  | ||   | |||| |
Db     890 CAATGGCGGATTTAAGAAATATGTTCCATTGTTGGAGGAAGTTGTGGTTTTGGAAGGTGC 949

Qy    1026 ggctcacttcaataatcaagaagcagcagaggaaatcgataattacatatacgattttat 1085
           ||||||||    |||||||||    || | || ||    ||  |||| || || || ||
Db     950 AGCTCACTTTGTCAATCAAGAAAGGCCACATGAGATTAGCAAGCACATTTATGACTTCAT 1009

Qy    1086 caaaaagttctgatcttgtcc 1106
             |||||||| | ||| | |
Db    1010 TCAAAAGTTCTAAACTTCTTC 1030
```

```
RESULT  14
US-60-089-524-2117
; Sequence 2117, Application US/60089524
;  GENERAL INFORMATION:
;    APPLICANT:  Joseph R. Byrum
;    APPLICANT:  Michael D. Thompson
;    TITLE OF INVENTION:  Nucleic Acid Molecules and Other Molecules
;    TITLE OF INVENTION:  Associated With Plants.
;    NUMBER OF SEQUENCES:  4769
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lawrence M. Lavin, Jr.
;      STREET:  BB4F
;      STREET:  Monsanto Company
;      STREET:  700 Chesterfield Parkway North
;      CITY:  St. Louis
;      STATE:  MO
;      COUNTRY:  United States
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette (3.5in, 1.44 Mb)
;      COMPUTER:  IBM PC/XT/AT, IBM PS/2 or compatibles
;      OPERATING SYSTEM:  Windows 95/NT
;      SOFTWARE:  Winzip 6.3
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/089,524
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lavin Jr., Lawrence M.
;      REGISTRATION NUMBER:  30,768
;      REFERENCE/DOCKET NUMBER:  38-21(15401)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314) 737-6670
;      TELEFAX:  (314) 737-6047
;  INFORMATION FOR SEQ ID NO:  2117:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  371 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Glycine max
;      DEVELOPMENTAL STAGE:  partially to fully opened
;      TISSUE TYPE:  flower
;    IMMEDIATE SOURCE:
;      LIBRARY:  LIB3028
;      CLONE:  LIB3028-025-Q1-B1-D5
US-60-089-524-2117
```

```
  Query Match           26.0%;  Score 345.8;  DB 71;  Length 371;
  Best Local Similarity  97.5%;  Pred. No. 9.3e-94;
  Matches  350;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy     178 gtgaatggcataaaaatgcatgttgcagagaaaggagagggtccagtggtgttgttcctc 237
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GTGAATGGCATAAAAATGCATGTTGCAGAGAAAGGAGAGGGTCCAGTGGTGTTGTTCCTC 60

Qy     238 cacggcttccctgagctctggtactcatggcgccatcagattctctctctcagctccctc 297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CACGGCTTCCCTGAGCTCTGGTACTCATGGCGCCATCAGATTCTCTCTCTCAGCTCCCTC 120

Qy     298 ggctaccgcgccgtcgctcccgatctccgtggctacggtgacaccgaggcaccaccttca 357
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     121 GGCTACCGCGCCGTCGCTCCCGATCTCCGTGGCTACGGTGACACCGAAGCACCACCTTCA 180

Qy     358 atcagcagctacaactgcttccacatagtgggtgatctcgttgcgcttattgactctctg 417
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATCAGCAGCTACAACTGCTTCCACATAGTGGGTGATCTCGTTGCGCTTATTGACTCTCTG 240

Qy     418 ggtgtccaacaagtgttccttgtggctcatgactggggagccatcataggttggtatcta 477
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     241 GGTGTCCAACAAGTGTTCCTTGTGGCTCATGACTGGGGAGCCATCATANGTTGGTATCTA 300

Qy     478 tgcatgtttcgccctgacaaagttaaggcctatgtctgcctcagtgtccctctcctccg 536
           |||||||||||||||||||||||||| | ||| ||||||   | ||||||||||||||
Db     301 TGCATGTTTCGCCCTGACAAAGTTAANGGCTAAGTCTGCTCAATTGTCCCTCTCCTCCG 359
```

```
RESULT  15
US-60-130-174-1975/c
; Sequence 1975, Application US/60130174
```

```
; GENERAL INFORMATION:
;  APPLICANT: Buehler, Robert E.
;  APPLICANT: Byrum, Joseph R.
;  APPLICANT: Coombs, Brian E.
;  APPLICANT: Thompson, Michael D.
;  TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
;  TITLE OF INVENTION: Plants
;  FILE REFERENCE: 38-21(15763)A
;  CURRENT APPLICATION NUMBER: US/60/130,174
;  CURRENT FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 2262
; SEQ ID NO 1975
;   LENGTH: 593
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: jC-gmro02800040g06d1
US-60-130-174-1975


  Query Match             25.9%;  Score 344.4;  DB 80;  Length 593;
  Best Local Similarity   85.9%;  Pred. No. 3.3e-93;
  Matches  419;  Conservative    0;  Mismatches   61;  Indels    8;  Gaps    3;

Qy     644 aagttggcactgagtatgttctcaaaaacatccttacaactcgcaatcctggtcctccaa 703
           |||||| ||||| ||||| ||||||||||||||| ||||| ||||||  ||||||||||
Db     592 AAGTTGCCACTGGGTATG-TCTCAAAAACATCC-TACAAGTCGCAAAACTGGTCCTCCAT 535

Qy     704 ttcttcccaagggaaggtttca------attcaatccagaaatgcccaacaccttgccct 757
           | |||||  | |||  ||||        |||||||||| | |||    |  |||| ||||
Db     534 TCCTTCCGCATGGAGAGTTTGGAACTGGATTCAATCCAAATATGTTTGATTCCTTACCCT 475

Qy     758 cttggctcacagaagaagatctcgcctattatgtctccaaatttgagaaaaccggattca 817
           |||||||||||||||| ||||| || |||||||||||||||| || ||||| || ||||
Db     474 CTTGGCTCACAGAAGATGATCTTGCTTATTATGTCTCCAAATTCGAAAAAACTGGCTTCA 415

Qy     818 ctggacccttgaactactacagaaatttcaacttaaattgggagttgacggcaccatgga 877
           |||||  |||||||||||||||||||||||||||| |||||||| |||| || |||||||
Db     414 CTGGAGGCTTGAACTACTACAGAAATTTCAACTTAGATTGGGAGCTGACAGCTCCATGGA 355

Qy     878 caggagggccaatcaaggtgcccgtaaaatacataacaggtgagttggacatggtataca 937
           |||||| || |||||||||||||||||||| ||| ||||||||||||||  |||||| |
Db     354 CAGGAGTGCAAATCAAGGTGCCCGTAAAATTCATTACAGGTGAGTTGGACTCGGTATATA 295

Qy     938 actcgctgaacttgaaggagtatatccacggcggagggttcaagcaagatgtgccaaatt 997
            |||||| |||||||||||||||||| ||| |||||||||||||||||||||||||| |
Db     294 CCTCGCTAAACTTGAAGGAGTATATCCTCGGTGGAGGGTTCAAGCAAGATGTGCCAAACT 235

Qy     998 tagaacaagtgattgtgcagaaaggagtggctcacttcaataatcaagaagcagcagagg 1057
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| || ||||
Db     234 TAGAACAAGTGATTGTGCAGAAAGGAGTGGCTCACTTCAATAATCAAGAAGCCGCCGAGG 175

Qy    1058 aaatcgataattacatatacgattttatcaaaaagttctgatcttgtccaaaaacgaatt 1117
           ||||| ||| | |||| |||||||||||||| ||||| | ||||  ||||||||||||||
Db     174 AAATCAATACTCACATTTACGATTTTATCAAGAAGTTTTAATCTCATCCAAAAACGAATT 115

Qy    1118 caaccaga 1125
           || || ||
Db     114 CATCCTGA 107


Search completed: March 10, 2000, 11:07:24
Job time: 1032 sec
```

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2000, 09:51:37 ; Search time 439.26 Seconds
(without alignments)
56.822 Million cell updates/sec

Title: US-09-030-832-2
Perfect score: 1312
Sequence: 1 MVMTIFFNVSRRFGYVAFQN.....VFPVTFFFFNVLYWLVCLNL 242

Scoring table: BLOSUM62

Searched: 659037 seqs, 103139215 residues

Database : Pending_Patents_AA:*

Word size : 0

Number of hits that pass the threshold : 659037
1: /cgn2_6/ptodata/2/paa/PCTUS9_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US084A_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US084B_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep:*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep:*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep:*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep:*
19: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*
20: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
21: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
22: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
23: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
24: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1312	100.0	242	12	US-08-888-012-2	Sequence 2, Appli
2	1312	100.0	242	14	US-09-030-832-2	Sequence 2, Appli
3	1312	100.0	506	14	US-09-030-832-42	Sequence 42, Appl
4	458.5	34.9	467	11	US-08-716-396-8	Sequence 8, Appli
5	363.5	27.7	554	12	US-08-809-802-8	Sequence 8, Appli
6	361	27.5	453	2	US-07-971-767-18	Sequence 18, Appl
7	361	27.5	453	6	US-08-341-610-4	Sequence 4, Appli
8	341.5	26.0	462	2	US-07-971-767-16	Sequence 16, Appl
9	341.5	26.0	462	6	US-08-341-610-2	Sequence 2, Appli
10	335	25.5	474	2	US-07-971-767-20	Sequence 20, Appl
11	335	25.5	474	6	US-08-341-610-6	Sequence 6, Appli
12	333.5	25.4	919	19	US-60-164-769-15096	Sequence 15096, A
13	333.5	25.4	496	19	US-60-167-216-505	Sequence 505, App
14	333.5	25.4	496	19	US-60-173-383-27057	Sequence 27057, A
15	333.5	25.4	496	19	US-60-173-464-21214	Sequence 21214, A
16	329	25.1	451	2	US-07-971-767-12	Sequence 12, Appl
17	329	25.1	451	6	US-08-341-610-8	Sequence 8, Appli
18	327.5	25.0	492	2	US-07-971-767-14	Sequence 14, Appl
19	327.5	25.0	492	6	US-08-341-610-10	Sequence 10, Appl
20	304.5	23.2	496	1	PCT-US98-08563-2	Sequence 2, Appli
21	304.5	23.2	467	1	PCT-US98-08563-3	Sequence 3, Appli
22	304.5	23.2	496	14	US-09-002-361-2	Sequence 2, Appli
23	304.5	23.2	467	14	US-09-002-361-3	Sequence 3, Appli
24	294.5	22.4	481	1	PCT-US98-08563-5	Sequence 5, Appli
25	294.5	22.4	459	1	PCT-US98-08563-6	Sequence 6, Appli
26	294.5	22.4	481	14	US-09-002-361-5	Sequence 5, Appli
27	294.5	22.4	459	14	US-09-002-361-6	Sequence 6, Appli
28	291.5	22.2	452	12	US-08-809-802-12	Sequence 12, Appl
29	288.5	22.0	1431	19	US-60-161-932-1074	Sequence 1074, Ap
30	288.5	22.0	1431	19	US-60-164-769-7494	Sequence 7494, Ap
31	286.5	21.8	485	19	US-60-167-216-423	Sequence 423, App
32	286.5	21.8	485	19	US-60-173-383-17300	Sequence 17300, A
33	286.5	21.8	485	19	US-60-173-464-13598	Sequence 13598, A
34	284	21.6	165	16	US-09-270-767-33201	Sequence 33201, A
35	284	21.6	165	16	US-09-270-767-48418	Sequence 48418, A
36	279	21.3	637	2	US-07-770-881D-1	Sequence 1, Appli
37	279	21.3	606	6	US-08-333-956A-1	Sequence 1, Appli
38	279	21.3	504	19	US-60-167-216-225	Sequence 225, App
39	279	21.3	504	19	US-60-173-383-9379	Sequence 9379, Ap
40	279	21.3	504	19	US-60-173-464-7237	Sequence 7237, Ap
41	271.5	20.7	437	19	US-60-164-769-2660	Sequence 2660, Ap
42	271.5	20.7	387	19	US-60-173-383-35869	Sequence 35869, A
43	271.5	20.7	387	19	US-60-173-464-27455	Sequence 27455, A
44	268.5	20.5	438	19	US-60-164-769-414	Sequence 414, App
45	268.5	20.5	683	19	US-60-173-464-13676	Sequence 13676, A

ALIGNMENTS

```
RESULT 1
US-08-888-012-2
; Sequence 2, Application US/08888012
; GENERAL INFORMATION:
;   APPLICANT: Hanna, Michael C.
;   APPLICANT: Kirkness, Ewen F.
;   TITLE OF INVENTION: ET2: An Alternative Transcript of the GABA-A
;   TITLE OF INVENTION: Receptor n Subunit
;   NUMBER OF SEQUENCES: 40
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;     STREET: 1100 New York Avenue, NW, Suite 600
;     CITY: Washington
;     STATE: DC
;     COUNTRY: USA
;     ZIP: 20005-3934
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/888,012
;     FILING DATE: Herewith
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Steffe, Eric K.
;     REGISTRATION NUMBER: 36,688
;     REFERENCE/DOCKET NUMBER: 1488.0950000/EKS/SGW
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202) 371-2600
;     TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 242 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
```

US-08-888-012-2

Query Match 100.0%; Score 1312; DB 12; Length 242;
Best Local Similarity 100.0%; Pred. No. 6.9e-126;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120

Qy     121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 180

Qy     181 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 240

Qy     241 NL 242
           ||
Db     241 NL 242
```

RESULT 2
US-09-030-832-2
; Sequence 2, Application US/09030832
; GENERAL INFORMATION:
; APPLICANT: Hanna, Michael C.
; APPLICANT: Kirkness, Ewen F.
; TITLE OF INVENTION: GABAA Receptor Epsilon Subunit
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,832
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/888,012
; FILING DATE: 03-JUL-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0950001/EKS/SGW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-030-832-2

Query Match 100.0%; Score 1312; DB 14; Length 242;
Best Local Similarity 100.0%; Pred. No. 6.9e-126;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120

Qy     121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 180

Qy     181 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 240

Qy     241 NL 242
           ||
Db     241 NL 242
```

RESULT 3
US-09-030-832-42
; Sequence 42, Application US/09030832
; GENERAL INFORMATION:
; APPLICANT: Hanna, Michael C.
; APPLICANT: Kirkness, Ewen F.
; TITLE OF INVENTION: GABAA Receptor Epsilon Subunit
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,832
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/888,012
; FILING DATE: 03-JUL-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0950001/EKS/SGW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 506 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-030-832-42

Query Match 100.0%; Score 1312; DB 14; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.6e-125;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    265 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 324

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 384

Qy    121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 444

Qy    181 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 504

Qy    241 NL 242
          ||
Db    505 NL 506
```

RESULT 4
US-08-716-396-8
; Sequence 8, Application US/08716396
; GENERAL INFORMATION:
; APPLICANT: Whiting, Paul J.
; TITLE OF INVENTION: HUMAN GAMMA 3 GABA-A- RECEPTOR SUBUNIT
; TITLE OF INVENTION: AND STABLY CO-TRANSFECTED CELL LINES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. Mark Hand - Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue - P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,396
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: T1271
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-716-396-8

Query Match 34.9%; Score 458.5; DB 11; Length 467;
Best Local Similarity 37.3%; Pred. No. 2e-38;
Matches 97; Conservative 44; Mismatches 68; Indels 51; Gaps 6;

```
Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          :||||:| :||| ||   | |:|  :| :||||||||| :: ||||:||||:|||||||
Db    241 VVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFWIKKDATPARTALGITTVLTMTTLS 300

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPK----LRHP 116
          | :||: |||||:||:| :: :||:| | ||:|:|  ||:  |:  :   : |    | ||
Db    301 TIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEYATLNY--YSSCRKPTTTKKTTSLLHP 358

Qy    117 --------RINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPG 168
                  ||: :| :                                    |    :|| |
Db    359 DSSRWIPERISLQAPSNY----------------------------SLLDMRPPPPA 387

Qy    169 SPEGPRSLC---SKLACCEWC---KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 222
                |:     :  |   |   |  : :||   :|:  :|::||: | :  ||:||||
Db    388 MITLNNSVYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSWRKGRIHIDILELDSYSRV 447

Qy    223 VFPVTFFFFNVLYWLVCLNL 242
            || :|  ||::||:  | |
Db    448 FFPTSFLLFNLVYWVGYLYL 467
```

RESULT 5
US-08-809-802-8
; Sequence 8, Application US/08809802
; GENERAL INFORMATION:
; APPLICANT: Le Bourdelles, Beatrice
; APPLICANT: Whiting, Paul John
; TITLE OF INVENTION: HUMAN ALPHA 4 RECEPTOR SUBUNIT
; TITLE OF INVENTION: OF THE GABA-A RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,802
; FILING DATE: 19-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02323
; FILING DATE: 29-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Yablonsky, Michael D
; REGISTRATION NUMBER: 40,407
; REFERENCE/DOCKET NUMBER: T1292
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-4678
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 554 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-802-8

Query Match 27.7%; Score 363.5; DB 12; Length 554;
Best Local Similarity 31.7%; Pred. No. 1.2e-28;
Matches 100; Conservative 43; Mismatches 83; Indels 89; Gaps 11;

```
Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          :|||::|:: |: ||   | |:|  :| :|| ||||| || |||| |||:|||||||
Db    244 IVMTVYFHLRRKMGYFMIQTYIPCIMTVILSQVSFWINKESVPARTVFGITTVLTMTTLS 303

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ-----------TKAH 108
          :| : |:||| ||:|::||:|| | | ||:||| :|:    |             :
Db    304 ISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNIQMEKAKRKTSKPPQEVP 363

Qy    109 ASP--KLRHPRI---NSRAHARTRARSRACARQHQEAFV-----------CQIVTTEGS 151
          |:|  : :||     |: |:   | |: |    | |: |             |  | |
Db    364 AAPVQREKHPEAPLQNTNANLNMRKRTNALV--HSESDVGNRTEVGNHSSKSSTVVQESS 421
```

```
Qy    152 DGEER-------------------------PSCS--------AQQPPSPGSPEGPRSLCS 178
          |  |                          || |          :  | ||        |
Db    422 KGTPRSYLASSPNPFSRANAAETISAARALPSASPTSIRTGYMPRKASVGSASTRHVFGS 481

Qy    179 KLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCI-----------HVYRLDNYSRVVFPV 226
          :|      :| |      :    |:|   |:|                  ::| |:|::|||
Db    482 RL------QRIKTTVNTI----GAT---GKLSATPPPSAPPPSGSGTSKIDKYARILFPV 528

Qy    227 TFFFFNVLYWLVCLN 241
          ||  ||::||:| |:
Db    529 TFGAFNMVYWVVYLS 543


RESULT   6
US-07-971-767-18
; Sequence 18, Application US/07971767
;  GENERAL INFORMATION:
;    APPLICANT:  Hadingham, Karen L.
;    APPLICANT:  Le Bourdelles, Beatrice
;    APPLICANT:  Whiting, Paul J.
;    APPLICANT:  Wingrove, Peter B.
;    TITLE OF INVENTION:  GABA-A RECEPTOR SUBUNITS (ALPHA-2,
;    TITLE OF INVENTION:  ALPHA-3, ALPHA-5, ALPHA-6, BETA-2) AND TRANSFECTED CELLS
;    TITLE OF INVENTION:  EXPRESSING THEM
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robert J. North
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,767
;      FILING DATE:  19930202
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  North, Robert J.
;      REGISTRATION NUMBER:  27,366
;      REFERENCE/DOCKET NUMBER:  T-1109
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908 594-7262
;      TELEFAX:  908 594-4720
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  453 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-971-767-18


  Query Match           27.5%;  Score 361;  DB 2;  Length 453;
  Best Local Similarity  33.6%;  Pred. No. 1.8e-28;
  Matches   88;  Conservative   39;  Mismatches   67;  Indels   68;  Gaps    7;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          ::||::|:: |: ||   | | |  :| :|| |||||  || |||| ||||:|||||||
Db    228 VIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPARTVLGITTVLTMTTLS 287

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTK------AHASPK-- 113
            :| : |:||| ||:|::||:|| | | ||:||| :|:    ||:        |:|
Db    288 ISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQTQKAKRKAQFAAPPTV 347

Qy    113 -------------LRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSC 159
                        : ||  :|: | : |  | : |  ||::      |
Db    348 TISKATEPLEAEIVLHP--DSKYHLKKRITSLS----------LPIVSS-----SEANKV 390

Qy    160 SAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNY 219
            : |    :|  | |                  |   | |          ::| |
Db    391 LTRAPILQSTPVTPPPL------------------PPAFGGT----------SKIDQY 420

Qy    220 SRVVFPVTFFFFNVLYWLVCLN 241
          ||::||| |  ||::||:| |:
Db    421 SRILFPVAFAGFNLVYWVVYLS 442


RESULT   7
US-08-341-610-4
; Sequence 4, Application US/08341610
;  GENERAL INFORMATION:
;    APPLICANT:  Karen Hadingham
;    APPLICANT:  Paul John Whiting
;    TITLE OF INVENTION:  Stably transfected cell lines expressing GABA-A receptors
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jack L. Tribble
;      STREET:  126 E. Lincoln Avenue, P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/341,610
;      FILING DATE:  17-NOV-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tribble, Jack L.
;      REGISTRATION NUMBER:  32,633
;      REFERENCE/DOCKET NUMBER:  T-1220Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)594-5321
;      TELEFAX:  (908)594-4720
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  453 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-341-610-4


  Query Match           27.5%;  Score 361;  DB 6;  Length 453;
  Best Local Similarity  33.6%;  Pred. No. 1.8e-28;
  Matches   88;  Conservative   39;  Mismatches   67;  Indels   68;  Gaps    7;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          ::||::|:: |: ||   | | |  :| :|| |||||  || |||| ||||:|||||||
Db    228 VIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPARTVLGITTVLTMTTLS 287

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTK------AHASPK-- 113
            :| : |:||| ||:|::||:|| | | ||:||| :|:    ||:        |:|
Db    288 ISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQTQKAKRKAQFAAPPTV 347

Qy    113 -------------LRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSC 159
                        : ||  :|: | : |  | : |  ||::      |
Db    348 TISKATEPLEAEIVLHP--DSKYHLKKRITSLS----------LPIVSS-----SEANKV 390

Qy    160 SAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNY 219
            : |    :|  | |                  |   | |          ::| |
Db    391 LTRAPILQSTPVTPPPL------------------PPAFGGT----------SKIDQY 420
```

```
Qy    220 SRVVFPVTFFFFNVLYWLVCLN 241
          ||::||| |  ||::||:| |:
Db    421 SRILFPVAFAGFNLVYWVVYLS 442


RESULT   8
US-07-971-767-16
; Sequence 16, Application US/07971767
;  GENERAL INFORMATION:
;    APPLICANT:  Hadingham, Karen L.
;    APPLICANT:  Le Bourdelles, Beatrice
;    APPLICANT:  Whiting, Paul J.
;    APPLICANT:  Wingrove, Peter B.
;    TITLE OF INVENTION:  GABA-A RECEPTOR SUBUNITS (ALPHA-2,
;    TITLE OF INVENTION:  ALPHA-3, ALPHA-5, ALPHA-6, BETA-2) AND TRANSFECTED CELLS
;    TITLE OF INVENTION:  EXPRESSING THEM
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robert J. North
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,767
;      FILING DATE:  19930202
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  North, Robert J.
;      REGISTRATION NUMBER:  27,366
;      REFERENCE/DOCKET NUMBER:  T-1109
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908 594-7262
;      TELEFAX:  908 594-4720
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  462 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-971-767-16


  Query Match             26.0%;  Score 341.5;  DB 2;  Length 462;
  Best Local Similarity   31.5%;  Pred. No. 1.8e-26;
  Matches   78;  Conservative   42;  Mismatches   77;  Indels   51;  Gaps    5;

Qy      2 VMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGT 61
          :||  |:: |: ||   | |:|  :| :|| ||||:  || ||||  |:|:|||||||
Db    246 IMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSI 305

Qy     62 FSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL-----IYNQTKAHASPKLRHP 116
           :| : |:|:| ||:|:::||:|: | | ||:||| :|:       ::  ||  : |::
Db    306 SARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGWAWDGKKALEAAKIKKK 365

Qy    117 R---INSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGP 173
          |   :|   :| |  :                            |:   :|     :| |
Db    366 REVILNKSTNAFTTGKM----------------------SHPPNIPKEQ-----TPAGT 397

Qy    174 RSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNV 233
           :  |                  |   |  | :  :    : ::|  ||:|||| |  ||:
Db    398 SNTTS--------------VSVKPSEEKTSESKKTYNSISKIDKMSRIVFPVLFGTFNL 442

Qy    234 LYWLVCLN 241
          :||   ||
Db    443 VYWATYLN 450


RESULT   9
US-08-341-610-2
; Sequence 2, Application US/08341610
;  GENERAL INFORMATION:
;    APPLICANT:  Karen Hadingham
;    APPLICANT:  Paul John Whiting
;    TITLE OF INVENTION:  Stably transfected cell lines expressing GABA-A receptors
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jack L. Tribble
;      STREET:  126 E. Lincoln Avenue, P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/341,610
;      FILING DATE:  17-NOV-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tribble, Jack L.
;      REGISTRATION NUMBER:  32,633
;      REFERENCE/DOCKET NUMBER:  T-1220Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)594-5321
;      TELEFAX:  (908)594-4720
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  462 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-341-610-2


  Query Match             26.0%;  Score 341.5;  DB 6;  Length 462;
  Best Local Similarity   31.5%;  Pred. No. 1.8e-26;
  Matches   78;  Conservative   42;  Mismatches   77;  Indels   51;  Gaps    5;

Qy      2 VMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGT 61
          :||  |:: |: ||   | |:|  :| :|| ||||:  || ||||  |:|:|||||||
Db    246 IMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSI 305

Qy     62 FSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL-----IYNQTKAHASPKLRHP 116
           :| : |:|:| ||:|:::||:|: | | ||:||| :|:       ::  ||  : |::
Db    306 SARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGWAWDGKKALEAAKIKKK 365

Qy    117 R---INSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGP 173
          |   :|   :| |  :                            |:   :|     :| |
Db    366 REVILNKSTNAFTTGKM----------------------SHPPNIPKEQ-----TPAGT 397

Qy    174 RSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNV 233
           :  |                  |   |  | :  :    : ::|  ||:|||| |  ||:
Db    398 SNTTS--------------VSVKPSEEKTSESKKTYNSISKIDKMSRIVFPVLFGTFNL 442

Qy    234 LYWLVCLN 241
          :||   ||
Db    443 VYWATYLN 450


RESULT  10
US-07-971-767-20
; Sequence 20, Application US/07971767
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  Hadingham, Karen L.
;    APPLICANT:  Le Bourdelles, Beatrice
;    APPLICANT:  Whiting, Paul J.
;    APPLICANT:  Wingrove, Peter B.
;    TITLE OF INVENTION:  GABA-A RECEPTOR SUBUNITS (ALPHA-2,
;    TITLE OF INVENTION:  ALPHA-3, ALPHA-5, ALPHA-6, BETA-2) AND TRANSFECTED CELLS
;    TITLE OF INVENTION:  EXPRESSING THEM
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robert J. North
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,767
;      FILING DATE:  19930202
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  North, Robert J.
;      REGISTRATION NUMBER:  27,366
;      REFERENCE/DOCKET NUMBER:  T-1109
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908 594-7262
;      TELEFAX:  908 594-4720
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  474 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-971-767-20


  Query Match             25.5%;  Score 335;  DB 2;  Length 474;
  Best Local Similarity   30.1%;  Pred. No. 8.3e-26;
  Matches   80;  Conservative   47;  Mismatches   89;  Indels   50;  Gaps    7;

Qy       3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
           ::: | : |  ||   | |:|| : |:||||||||  ::: || :|||||||||: |
Db     232 LSLSFKLKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALGITTVLTMTTINTH 291

Qy      63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRA 122
            |:  |:: |: |:| |:  |||| | ||||:|::|:: :           | |:   :|
Db     292 LRETLPKIPYVKAIDMYLMGCFVFVFMALLEYALVNYIFFG----------RGPQRQKKA 341

Qy     123 HARTRARSRACAR-------QHQEAFVC------QIVTTEGSDGEERP-------SCSAQ 162
             :  : :    |        |:   :       :: |:|   |   |          |:
Db     342 AEKAASANNEKMRLDVNKMDPHENILLSTLEIKNEMATSEAVMGLGDPRSTMLAYDASSI 401

Qy     163 QPPSPGSPEG-------PRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYR 215
           |    | |           | :  | :     :|  :    :||                |
Db     402 QYRKAGLPRHSFGRNALERHVAQKKSRLR--RRASELKITIPD----------LTDVNA 448

Qy     216 LDNYSRVVFPVTFFFFNVLYWLVCLN 241
           :| :||: ||| | |||::|||  :|
Db     449 IDRWSRIFFPVVFSFFNIVYWLYYVN 474


RESULT  11
US-08-341-610-6
; Sequence 6, Application US/08341610
;  GENERAL INFORMATION:
;    APPLICANT:  Karen Hadingham
;    APPLICANT:  Paul John Whiting
;    TITLE OF INVENTION:  Stably transfected cell lines expressing GABA-A receptors
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jack L. Tribble
;      STREET:  126 E. Lincoln Avenue, P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/341,610
;      FILING DATE:  17-NOV-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tribble, Jack L.
;      REGISTRATION NUMBER:  32,633
;      REFERENCE/DOCKET NUMBER:  T-1220Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)594-5321
;      TELEFAX:  (908)594-4720
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  474 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-341-610-6


  Query Match             25.5%;  Score 335;  DB 6;  Length 474;
  Best Local Similarity   30.1%;  Pred. No. 8.3e-26;
  Matches   80;  Conservative   47;  Mismatches   89;  Indels   50;  Gaps    7;

Qy       3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
           ::: | : |  ||   | |:|| : |:||||||||  ::: || :|||||||||: |
Db     232 LSLSFKLKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALGITTVLTMTTINTH 291

Qy      63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRA 122
            |:  |:: |: |:| |:  |||| | ||||:|::|:: :           | |:   :|
Db     292 LRETLPKIPYVKAIDMYLMGCFVFVFMALLEYALVNYIFFG----------RGPQRQKKA 341

Qy     123 HARTRARSRACAR-------QHQEAFVC------QIVTTEGSDGEERP-------SCSAQ 162
             :  : :    |        |:   :       :: |:|   |   |          |:
Db     342 AEKAASANNEKMRLDVNKMDPHENILLSTLEIKNEMATSEAVMGLGDPRSTMLAYDASSI 401

Qy     163 QPPSPGSPEG-------PRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYR 215
           |    | |           | :  | :     :|  :    :||                |
Db     402 QYRKAGLPRHSFGRNALERHVAQKKSRLR--RRASQLKITIPD----------LTDVNA 448

Qy     216 LDNYSRVVFPVTFFFFNVLYWLVCLN 241
           :| :||: ||| | |||::|||  :|
Db     449 IDRWSRIFFPVVFSFFNIVYWLYYVN 474


RESULT  12
US-60-164-769-15096
; Sequence 15096, Application US/60164769
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
;  TITLE OF INVENTION: Acid Sequences, Systems Containin the Nucleic Acid Sequences
;  TITLE OF INVENTION: and Uses Thereof
;  FILE REFERENCE: CL000144
;  CURRENT APPLICATION NUMBER: US/60/164,769
;  CURRENT FILING DATE: 1999-11-12
;  NUMBER OF SEQ ID NOS: 27328
;  SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 15096
;   LENGTH: 919
;   TYPE: PRT
;   ORGANISM: Drosophila
US-60-164-769-15096


  Query Match             25.4%;  Score 333.5;  DB 19;  Length 919;
  Best Local Similarity   31.2%;  Pred. No. 2.5e-25;
  Matches   82;  Conservative   40;  Mismatches   96;  Indels   45;  Gaps    5;

Qy      3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
          ::: | : |  ||  || |:|| :  |||||||||  |:  || :||||:||||||: |
Db    669 LSLSFKLQRNIGYFVFQTYLPSILIVMLSWVSFWINHEATSARVALGITTVLTMTTISTG 728

Qy     63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRA 122
           | : ||:||: |:| |: :|||| | ||||:| :|:  : :    |  |::  :
Db    729 VRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWGK---RAKKKIKKVKECCPG 785

Qy    123 HARTRARSRACA-------------------RQHQEAFVCQIVTTEGSDGEERPSCSAQ 162
                ||  |:                    |    | :  | |   : |:  ||
Db    786 KIGKSERSETCSTTEDIIELQDVRMSPIPSLRRGTYNATLDSIGTETMNLGKFPPSFRIT 845

Qy    163 QPPSPGSPE----GPRSLCSKLACCEWCKR----FKKYFCMVPDCEGSTWQQGRLCIHVY 214
          :    | :      | : ::       ||     |     : |                |
Db    846 RNYGTGHSQLRRRAQRGISTRPRMLHALKRGASAIKATIPKIKD-------------VN 891

Qy    215 RLDNYSRVVFPVTFFFFNVLYWL 237
            :| |||::||::|  ||: |||
Db    892 IIDKYSRMIFPISFLAFNLGYWL 914


RESULT  13
US-60-167-216-505
; Sequence 505, Application US/60167216
; GENERAL INFORMATION:
;  APPLICANT: Li, Peter W.D.
;  TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL000150
;  CURRENT APPLICATION NUMBER: US/60/167,216
;  CURRENT FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 593
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 505
;   LENGTH: 496
;   TYPE: PRT
;   ORGANISM: Drosophila
US-60-167-216-505


  Query Match             25.4%;  Score 333.5;  DB 19;  Length 496;
  Best Local Similarity   31.2%;  Pred. No. 1.2e-25;
  Matches   82;  Conservative   40;  Mismatches   96;  Indels   45;  Gaps    5;

Qy      3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
          ::: | : |  ||  || |:|| :  |||||||||  |:  || :||||:||||||: |
Db    246 LSLSFKLQRNIGYFVFQTYLPSILIVMLSWVSFWINHEATSARVALGITTVLTMTTISTG 305

Qy     63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRA 122
           | : ||:||: |:| |: :|||| | ||||:| :|:  : :    |  |::  :
Db    306 VRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWGK---RAKKKIKKVKECCPG 362

Qy    123 HARTRARSRACA-------------------RQHQEAFVCQIVTTEGSDGEERPSCSAQ 162
                ||  |:                    |    | :  | |   : |:  ||
Db    363 KIGKSERSETCSTTEDIIELQDVRMSPIPSLRRGTYNATLDSIGTETMNLGKFPPSFRIT 422

Qy    163 QPPSPGSPE----GPRSLCSKLACCEWCKR----FKKYFCMVPDCEGSTWQQGRLCIHVY 214
          :    | :      | : ::       ||     |     : |                |
Db    423 RNYGTGHSQLRRRAQRGISTRPRMLHALKRGASAIKATIPKIKD-------------VN 468

Qy    215 RLDNYSRVVFPVTFFFFNVLYWL 237
            :| |||::||::|  ||: |||
Db    469 IIDKYSRMIFPISFLAFNLGYWL 491


RESULT  14
US-60-173-383-27057
; Sequence 27057, Application US/60173383
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. CRAIG
;  TITLE OF INVENTION: The Drosophila Genome: Primary Nucleic
;  TITLE OF INVENTION: Acid Sequences of Genes and Transcripts Provided As
;  TITLE OF INVENTION: Detection Reagents, Nucleic Acid Arrays and Kits
;  FILE REFERENCE: CL000175
;  CURRENT APPLICATION NUMBER: US/60/173,383
;  CURRENT FILING DATE: 1999-12-28
;  NUMBER OF SEQ ID NOS: 42698
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27057
;   LENGTH: 496
;   TYPE: PRT
;   ORGANISM: Drosophila
US-60-173-383-27057


  Query Match             25.4%;  Score 333.5;  DB 19;  Length 496;
  Best Local Similarity   31.2%;  Pred. No. 1.2e-25;
  Matches   82;  Conservative   40;  Mismatches   96;  Indels   45;  Gaps    5;

Qy      3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
          ::: | : |  ||  || |:|| :  |||||||||  |:  || :||||:||||||: |
Db    246 LSLSFKLQRNIGYFVFQTYLPSILIVMLSWVSFWINHEATSARVALGITTVLTMTTISTG 305

Qy     63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRA 122
           | : ||:||: |:| |: :|||| | ||||:| :|:  : :    |  |::  :
Db    306 VRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWGK---RAKKKIKKVKECCPG 362

Qy    123 HARTRARSRACA-------------------RQHQEAFVCQIVTTEGSDGEERPSCSAQ 162
                ||  |:                    |    | :  | |   : |:  ||
Db    363 KIGKSERSETCSTTEDIIELQDVRMSPIPSLRRGTYNATLDSIGTETMNLGKFPPSFRIT 422

Qy    163 QPPSPGSPE----GPRSLCSKLACCEWCKR----FKKYFCMVPDCEGSTWQQGRLCIHVY 214
          :    | :      | : ::       ||     |     : |                |
Db    423 RNYGTGHSQLRRRAQRGISTRPRMLHALKRGASAIKATIPKIKD-------------VN 468

Qy    215 RLDNYSRVVFPVTFFFFNVLYWL 237
            :| |||::||::|  ||: |||
Db    469 IIDKYSRMIFPISFLAFNLGYWL 491


RESULT  15
US-60-173-464-21214
; Sequence 21214, Application US/60173464
; GENERAL INFORMATION:
;  APPLICANT: Li, Peter W.D.
;  TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL000173
;  CURRENT APPLICATION NUMBER: US/60/173,464
;  CURRENT FILING DATE: 1999-12-29
;  NUMBER OF SEQ ID NOS: 30269
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21214
;   LENGTH: 496
;   TYPE: PRT
;   ORGANISM: Drosophila
US-60-173-464-21214


  Query Match             25.4%;  Score 333.5;  DB 19;  Length 496;
  Best Local Similarity   31.2%;  Pred. No. 1.2e-25;
  Matches   82;  Conservative   40;  Mismatches   96;  Indels   45;  Gaps    5;
```

```
Qy       3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
Db     246 LSLSFKLQRNIGYFVFQTYLPSILIVMLSWVSFWINHEATSARVALGITTVLTMTTISTG 305

Qy      63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRA 122
Db     306 VRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWGK---RAKKKIKKVKECCPG 362

Qy     123 HARTRARSRACA------------------RQHQEAFVCQIVTTEGSDGEERPSCSAQ 162
Db     363 KIGKSERSETCSTTEDIIELQDVRMSPIPSLRRGTYNATLDSIGTETMNLGKFPPSFRIT 422

Qy     163 QPPSPGSPE----GPRSLCSKLACCEWCKR----FKKYFCMVPDCEGSTWQQGRLCIHVY 214
Db     423 RNYGTGHSQLRRRAQRGISTRPRMLHALKRGASAIKATIPKIKD-------------VN 468

Qy     215 RLDNYSRVVFPVTFFFFNVLYWL 237
Db     469 IIDKYSRMIFPISFLAFNLGYWL 491
```

Search completed: March 10, 2000, 10:50:02
Job time: 3505 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2000, 07:23:47 ; Search time 47.6 Seconds
(without alignments)
120.421 Million cell updates/sec

Title: US-09-030-832-2
Perfect score: 1312
Sequence: 1 MVMTIFFNVSRRFGYVAFQN.....VFPVTFFFFNVLYWLVCLNL 242

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database : A_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 188963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1312	100.0	506	1	W59048	GABA-A receptor ep
2	1312	100.0	474	1	W59049	Variant of GABA-A
3	1312	100.0	506	1	W61045	Human GABA recepto
4	452.5	34.5	467	1	R83968	GABA-A receptor ga
5	363.5	27.7	554	1	R97298	Human GABA-A recep
6	361	27.5	453	1	R31187	GABA-A receptor al
7	361	27.5	453	1	R59865	Human GABA recepto
8	341.5	26.0	462	1	R31186	GABA-A receptor al
9	341.5	26.0	462	1	R59864	Human GABA recepto
10	335	25.5	474	1	R31188	GABA-A receptor be
11	335	25.5	474	1	R59866	Human GABA recepto
12	333.5	25.4	496	1	R89336	GABA receptor subu
13	333.5	25.4	496	1	W86161	Insect GABA recept
14	329	25.1	451	1	R31184	GABA-A receptor al
15	329	25.1	451	1	R59862	Human GABA recepto
16	327.5	25.0	492	1	R31185	GABA-A receptor al
17	327.5	25.0	492	1	R59863	Human GABA recepto
18	304.5	23.2	496	1	W81633	GABA-gated chlorid
19	304.5	23.2	467	1	W81634	GABA-gated chlorid
20	294.5	22.4	481	1	W81635	GABA-gated chlorid
21	294.5	22.4	459	1	W81636	GABA-gated chlorid
22	292.5	22.3	488	1	W69285	GABA gated chlorid
23	291.5	22.2	452	1	R97299	Human GABA-A recep
24	289.5	22.1	488	1	W69286	GABA gated chlorid
25	279	21.3	637	1	R34035	Sequence of a GABA
26	278.5	21.2	440	1	R93118	Human GABA-A recep
27	278.5	21.2	440	1	W26464	Human GABA-A recep
28	277	21.1	456	1	W05246	Drosophila glutama
29	274.5	20.9	561	1	W97413	Lucilia cuprina GA
30	268.5	20.5	686	1	W86162	Insect GABA recept
31	268	20.4	510	1	R88360	Caenorhabditis ele
32	262.5	20.0	487	1	R88361	Caenorhabditis ele
33	261.5	19.9	455	1	W97860	Cat flea glutamate
34	259.5	19.8	627	1	W85597	Human GABA-A recep
35	256.5	19.6	627	1	W85596	Human GABA-A recep
36	235	17.9	222	1	W81637	GABA-gated chlorid
37	150	11.4	57	1	R89337	GABA receptor subu
38	118	9.0	50	1	W05247	Glutamate-gated ch
39	90	6.9	459	1	P96202	Human muscarinic a
40	88	6.7	479	1	R60695	Fragment of the mu
41	83.5	6.4	342	1	R48688	G-protein coupled
42	83.5	6.4	342	1	W02660	G-protein coupled
43	83	6.3	404	1	W31344	Human G-protein co
44	83	6.3	404	1	W34984	Human G-protein co
45	83	6.3	404	1	W59035	Human G-protein co

ALIGNMENTS

RESULT 1
W59048
ID W59048 standard; Protein; 506 AA.
AC W59048;
DT 25-SEP-1998 (first entry)
DE GABA-A receptor epsilon sub-unit related protein.
KW GABA-A receptor; diagnosis; therapy; drug screening.
OS Mammalia.
PN DE19644501-A1.
PD 30-APR-1998.
PF 25-OCT-1996; 044501.
PR 25-OCT-1996; DE-044501.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR WPI; 98-252096/23.
DR N-PSDB; V11776.
PT Protein related to GABA-A receptor sub-unit epsilon - useful for
PT diagnosis, therapy or drug screening
PS Example 1; Fig 1; 12pp; German.
CC The GABA-A receptor sub-unit epsilon related protein is used for the
CC diagnosis and/or therapy of related disorders. It can also be used to
CC screen for substances that modulate the activity of the protein.
SQ Sequence 506 AA;

Query Match 100.0%; Score 1312; DB 1; Length 506;
Best Local Similarity 100.0%; Pred. No. 2.1e-120;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     265 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 324

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     325 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 384

Qy     121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 444

Qy     181 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     445 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 504

Qy     241 NL 242
          ||
Db     505 NL 506
```

RESULT 2
W59049
ID W59049 standard; Protein; 474 AA.
AC W59049;
DT 25-SEP-1998 (first entry)
DE Variant of GABA-A receptor epsilon sub-unit related protein.
KW GABA-A receptor; diagnosis; therapy; drug screening.
OS Mammalia.
PN DE19644501-A1.
PD 30-APR-1998.
PF 25-OCT-1996; 044501.
PR 25-OCT-1996; DE-044501.

```
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI   Bilke K, Gaul R; Kioschis P, Poustka A, Wilke K;
DR   WPI; 98-252096/23.
DR   N-PSDB; V11777.
PT   Protein related to GABA-A receptor sub-unit epsilon - useful for
PT   diagnosis, therapy or drug screening
PS   Disclosure; Fig 2; 12pp; German.
CC   The GABA-A receptor sub-unit epsilon related protein is used for the
CC   diagnosis and/or therapy of related disorders.  It can also be used to
CC   screen for substances that modulate the activity of the protein.
SQ   Sequence   474 AA;

  Query Match           100.0%;  Score 1312;  DB 1;  Length 474;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-120;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 292

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 352

Qy    121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    353 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 412

Qy    181 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    413 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 472

Qy    241 NL 242
          ||
Db    473 NL 474


RESULT   3
W61045
ID   W61045 standard; Protein; 506 AA.
AC   W61045;
DT   12-OCT-1998  (first entry)
DE   Human GABA receptor epsilon subunit.
KW   GABA receptor; gamma-amino butyric acid receptor; human;
KW   appetite; cognition.
OS   Homo sapiens.
PN   WO9823742-A1.
PD   04-JUN-1998.
PF   18-NOV-1997; G03159.
PR   03-OCT-1997; GB-020995.
PR   25-NOV-1996; GB-024442.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Whiting PJ;
DR   WPI; 98-322722/28.
DR   N-PSDB; V36319.
PT   New isolated GABA receptor subunit, epsilon - used to develop
PT   products for the screening and design of drugs, e.g. for modulating
PT   appetite behaviours, hormonal interactions and cognition
PS   Claim 15; Fig 1; 37pp; English.
CC   This polypeptide comprises a novel class of subunit, classified as
CC   as epsilon, within the human GABA receptor gene family.  Its amino
CC   acid sequence was deduced from a cDNA clone (see V36319) isolated
CC   from a human brain cDNA library.  A stably co-transfected eukaryotic
CC   cell line capable of expressing the GABA epsilon receptor subunit,
CC   at least one alpha receptor subunit and at least one beta receptor
CC   subunit is claimed.  A recombinant expression vector, and protein
CC   and membrane preparations of the GABA receptor obtained from the
CC   co-transfected cells are also claimed.  The new GABA-A receptor
CC   epsilon subunit and products can be used in the screening and
CC   design of drugs which act upon the GABA receptor.  The ligands or
CC   drug candidates identified may be used as therapeutic agents, e.g.
CC   for the modulation of appetite behaviours, hormonal interactions
CC   and cognition.  They can also be used for the study of structure,
CC   pharmacology and function of the various GABA receptor subtypes.
SQ   Sequence   506 AA;

  Query Match           100.0%;  Score 1312;  DB 1;  Length 506;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-120;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    265 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 324

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 384

Qy    121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 444

Qy    181 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 504

Qy    241 NL 242
          ||
Db    505 NL 506


RESULT   4
R83968
ID   R83968 standard; Protein; 467 AA.
AC   R83968;
DT   02-FEB-1996  (first entry)
DE   GABA-A receptor gamma-3 subunit.
KW   GABA-A receptor; gamma-aminobutyric acid receptor; gamma-3 subunit.
OS   Homo sapiens.
PN   WO9529234-A1.
PD   02-NOV-1995.
PF   12-APR-1995; G00834.
PR   22-APR-1994; GB-008064.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Whiting PJ;
DR   WPI; 95-382983/49.
DR   N-PSDB; T02334.
PT   New cell line expressing human GABA-A receptor sub-units - useful in
PT   drug screening and design
PS   Disclosure; Page 21-23; 30pp; English.
CC   A cDNA clone isolated from a human foetal brain cDNA library
CC   encoded the GABA-A receptor gamma-3 subunit (R83968).
CC   The cDNA can be expressed in eukaryotic (pref. rodent fibroblast)
CC   cell lines to produce recombinant gamma-3 subunit or hybrid
CC   GABA-A receptors having novel subunit compositions.
SQ   Sequence   467 AA;

  Query Match           34.5%;  Score 452.5;  DB 1;  Length 467;
  Best Local Similarity  36.9%;  Pred. No. 1.8e-36;
  Matches   96;  Conservative   44;  Mismatches   69;  Indels   51;  Gaps    6;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          :|||||:| :| | ||   | |:|  :| :|||||||| :: |||||||||||||||
Db    241 VVMTIYFELSTRMGYFTIQTYIPCILTVVLSWVSFWIKKDATPARTALGITTVLTMTTLS 300

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPK----LRHP 116
          | :||: |||||:||:| :: :||:| | ||:|:| ||:  |:  :   : |    | ||
Db    301 TIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEYATLNY--YSSCRKPTTTKKTTSLLHP 358

Qy    117 --------RINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPG 168
                  ||: :| :                          |    :|| |
Db    359 DSSRWIPERISLQAPSNY----------------------------SLLDMRPPPPA 387
```

```
Qy    169 SPEGPRSLC---SKLACCEWC---KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 222
Db    388 MITLNNSVYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSWRKGRIHIDILELDSYSRV 447

Qy    223 VFPVTFFFFNVLYWLVCLNL 242
Db    448 FFPTSFLLFNLVYWVGYLYL 467


RESULT  5
R97298
ID   R97298 standard; Protein; 554 AA.
AC   R97298;
DT   06-JAN-1997  (first entry)
DE   Human GABA-A receptor alpha 4 subunit.
KW   GABA-A receptor; gamma-aminobutyric acid; alpha-4 subunit.
OS   Homo sapiens.
PN   WO9610637-A1.
PD   11-APR-1996.
PF   29-SEP-1995; G02323.
PR   01-OCT-1994; GB-020010.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Le Bourdelles B,  Whiting PJ;
DR   WPI; 96-209359/21.
DR   N-PSDB; T28988.
PT   DNA encoding alpha-4 and delta subunit(s) of the human GABAa
PT   receptor  - also stably co-transfected eukaryotic cells expressing
PT   receptors contg. these subunit(s), used for screening and designing
PT   drugs
PS   Example 1; Fig 2; 45pp; English.
CC   The amino acid sequence (R97298) of the alpha-4 subunit of the
CC   human GABA-A receptor was deduced from a cDNA clone (T28988)
CC   isolated from a human brain thalamus cDNA library.  The alpha-4
CC   subunit can be produced in transfected host cells, partic. rodent
CC   fibroblasts.  Co-transfected host cells capable of expressing the
CC   alpha-4, delta (see also R97299) and beta subunits can be used to
CC   screen or design drugs that act on GABA-A receptors, e.g.
CC   benzodiazepines, barbiturates, beta-carbolines and neurosteroids.
CC   Construction of recombinant receptors contg. the alpha-4 and
CC   delta subunits becomes possible for the first time.
SQ   Sequence   554 AA;


  Query Match             27.7%;  Score 363.5;  DB 1;  Length 554;
  Best Local Similarity   31.7%;  Pred. No. 1.1e-27;
  Matches  100;  Conservative   43;  Mismatches   83;  Indels   89;  Gaps   11;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
Db    244 IVMTVYFHLRRKMGYFMIQTYIPCIMTVILSQVSFWINKESVPARTVFGITTVLTMTTLS 303

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ-----------TKAH 108
Db    304 ISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNIQMEKAKRKTSKPPQEVP 363

Qy    109 ASP--KLRHPRI---NSRAHARTRARSRACARQHQEAFV-----------CQIVTTEGS 151
Db    364 AAPVQREKHPEAPLQNTNANLNMRKRTNALV--HSESDVGNRTEVGNHSSKSSTVVQESS 421

Qy    152 DGEER-----------------------PSCS--------AQQPPSPGSPEGPRSLCS 178
Db    422 KGTPRSYLASSPNPFSRANAAETISAARALPSASPTSIRTGYMPRKASVGSASTRHVFGS 481

Qy    179 KLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCI-----------HVYRLDNYSRVVFPV 226
Db    482 RL------QRIKTTVNTI----GAT---GKLSATPPPSAPPPSGSGTSKIDKYARILFPV 528

Qy    227 TFFFFNVLYWLVCLN 241
Db    529 TFGAFNMVYWVVYLS 543


RESULT   6
R31187
ID   R31187 standard; Protein; 453 AA.
AC   R31187;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-6 subunit.
KW   Primer; human; alpha-6; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta.
OS   Homo sapiens.
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   N-PSDB; Q33130.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Disclosure; Fig 5; 43pp; English.
CC   This sequence represents the human alpha-6 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Rat alpha-6 cDNA was used as a probe
CC   and a human alpha-6 cDNA clone was isolated from a cerebellum cDNA
CC   library.  No full length cDNA's were isolated. To obtain a full length
CC   cDNA 3 clones were joined together using convenient restriction sites.
CC   GABA-A receptor comprises a multimeric protein of molecular size
CC   230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   453 AA;


  Query Match             27.5%;  Score 361;  DB 1;  Length 453;
  Best Local Similarity   33.6%;  Pred. No. 1.5e-27;
  Matches   88;  Conservative   39;  Mismatches   67;  Indels   68;  Gaps    7;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
Db    228 VIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPARTVLGITTVLTMTTLS 287

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTK------AHASPK-- 113
Db    288 ISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQTQKAKRKAQFAAPPTV 347

Qy    113 -------------LRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSC 159
Db    348 TISKATEPLEAEIVLHP--DSKYHLKKRITSLS----------LPIVSS-----SEANKV 390

Qy    160 SAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNY 219
Db    391 LTRAPILQSTPVTPPPL--------------------PPAFGGT----------SKIDQY 420

Qy    220 SRVVFPVTFFFFNVLYWLVCLN 241
Db    421 SRILFPVAFAGFNLVYWVVYLS 442


RESULT   7
R59865
ID   R59865 standard; Protein; 453 AA.
AC   R59865;
DT   20-MAR-1995  (first entry)
```

```
DE   Human GABA receptor alpha6 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   N-PSDB; Q69142.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.5; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   453 AA;

  Query Match             27.5%;  Score 361;  DB 1;  Length 453;
  Best Local Similarity   33.6%;  Pred. No. 1.5e-27;
  Matches   88;  Conservative   39;  Mismatches   67;  Indels   68;  Gaps    7;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           ::||::|:: |: ||   | | |  :| :|| ||||| || |||| ||||:|||||||
Db     228 VIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPARTVLGITTVLTMTTLS 287

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTK------AHASPK-- 113
             :| : |:||| ||:|::||:|| | | ||:||| :|:    ||:        |:|
Db     288 ISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQTQKAKRKAQFAAPPTV 347

Qy     113 ------------LRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSC 159
                       : ||  :|: | : |  | :           ||::      |
Db     348 TISKATEPLEAEIVLHP--DSKYHLKKRITSLS----------LPIVSS-----SEANKV 390

Qy     160 SAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNY 219
             : |    :|  |  |                    |   | |           ::| |
Db     391 LTRAPILQSTPVTPPPL------------------PPAFGGT----------SKIDQY 420

Qy     220 SRVVFPVTFFFFNVLYWLVCLN 241
           ||::||| |  ||::||:| |:
Db     421 SRILFPVAFAGFNLVYWVVYLS 442


RESULT   8
R31186
ID   R31186 standard; Protein; 462 AA.
AC   R31186;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-5 subunit.
KW   Primer; human; alpha-5; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta.
OS   Homo sapiens.
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   N-PSDB; Q33129.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Disclosure; Fig 4; 43pp; English.
CC   This sequence represents the human alpha-5 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Rat alpha-5 cDNA was used as a probe
CC   and a human alpha-5 cDNA clone was isolated from a hippocampal cDNA
CC   library.  GABA-A receptor comprises a multimeric protein of molecular
CC   size 230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   462 AA;

  Query Match             26.0%;  Score 341.5;  DB 1;  Length 462;
  Best Local Similarity   31.5%;  Pred. No. 1.2e-25;
  Matches   78;  Conservative   42;  Mismatches   77;  Indels   51;  Gaps    5;

Qy       2 VMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGT 61
           :||  |:: |: ||   | |:|  :| :|| ||||:  || ||||  |:|:|||||||
Db     246 IMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSI 305

Qy      62 FSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL-----IYNQTKAHASPKLRHP 116
             :| : |:|:| ||:|::||:|: | | ||:||| :|:       ::  ||  : |::
Db     306 SARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGWAWDGKKALEAAKIKKK 365

Qy     117 R---INSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGP 173
           |   :|   :| |  :                          |:   :|     :| |
Db     366 REVILNKSTNAFTTGKM----------------------SHPPNIPKEQ-----TPAGT 397

Qy     174 RSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNV 233
           :  |                  |   |  | : :    : ::|  ||:|||| |  ||:
Db     398 SNTTS--------------VSVKPSEEKTSESKKTYNSISKIDKMSRIVFPVLFGTFNL 442

Qy     234 LYWLVCLN 241
           :||   ||
Db     443 VYWATYLN 450


RESULT   9
R59864
ID   R59864 standard; Protein; 462 AA.
AC   R59864;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha5 subunit.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   N-PSDB; Q69141.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.4; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   462 AA;

  Query Match             26.0%;  Score 341.5;  DB 1;  Length 462;
```

```
  Best Local Similarity   31.5%;  Pred. No. 1.2e-25;
  Matches   78;  Conservative   42;  Mismatches   77;  Indels   51;  Gaps    5;

Qy       2 VMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGT 61
           :||  |:: |: ||   | |:|  :| :|| |||:  || ||||  |:|:|||||||
Db     246 IMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSI 305

Qy      62 FSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL-----IYNQTKAHASPKLRHP 116
           :| : |:|:| ||:|:::||:|: | | ||:||| :|:       ::  ||  : |::
Db     306 SARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGWAWDGKKALEAAKIKKK 365

Qy     117 R---INSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGP 173
           |   :|   :| |  :                            |:   :|     :| |
Db     366 REVILNKSTNAFTTGKM----------------------SHPPNIPKEQ-----TPAGT 397

Qy     174 RSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNV 233
           :  |                  |   |  | :  :    : ::|  ||:|||| |  ||:
Db     398 SNTTS--------------VSVKPSEEKTSESKKTYNSISKIDKMSRIVFPVLFGTFNL 442

Qy     234 LYWLVCLN 241
           :||   ||
Db     443 VYWATYLN 450


RESULT  10
R31188
ID   R31188 standard; Protein; 474 AA.
AC   R31188;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor beta-2 subunit.
KW   Primer; human; beta-2; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta.
OS   Homo sapiens.
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   N-PSDB; Q33131.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Disclosure; Fig 6; 43pp; English.
CC   This sequence represents the human beta-2 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Short human beta-2 cDNA was used as
CC   a probe and a human beta-2 cDNA clone was isolated from a hippocampal
CC   cDNA library.  The largest cDNA clone isolated lacked the 5' 500 bp of
CC   the beta-2 coding sequence.  This missing fragment was isolated by PCR.
CC   The two fragments were ligated together to give a full length beta-2
CC   cDNA.  GABA-A receptor comprises a multimeric protein of molecular size
CC   230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   474 AA;


  Query Match           25.5%;  Score 335;  DB 1;  Length 474;
  Best Local Similarity   30.1%;  Pred. No. 5.4e-25;
  Matches   80;  Conservative   47;  Mismatches   89;  Indels   50;  Gaps    7;

Qy       3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
           ::: | : |  ||   | |:|| : |:||||||||  ::: || :||||:||||||: |
Db     232 LSLSFKLKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALGITTVLTMTTINTH 291

Qy      63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRA 122
            |:  |:: |: |:| |:  |||| | ||||:|::|:: :           | |:   :|
Db     292 LRETLPKIPYVKAIDMYLMGCFVFVFMALLEYALVNYIFFG----------RGPQRQKKA 341

Qy     123 HARTRARSRACAR-------QHQEAFVC------QIVTTEGSDGEERP-------SCSAQ 162
           :  : :    |         |:   :       :: |:|   |   |          |:
Db     342 AEKAASANNEKMRLDVNKMDPHENILLSTLEIKNEMATSEAVMGLGDPRSTMLAYDASSI 401

Qy     163 QPPSPGSPEG-------PRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYR 215
           |   | |           | :  | :      :|  :    :||            |
Db     402 QYRKAGLPRHSFGRNALERHVAQKKSRLR--RRASQLKITIPD-----------LTDVNA 448

Qy     216 LDNYSRVVFPVTFFFFNVLYWLVCLN 241
           :| :||: ||| | |||::|||  :|
Db     449 IDRWSRIFFPVVFSFFNIVYWLYYVN 474


RESULT  11
R59866
ID   R59866 standard; Protein; 474 AA.
AC   R59866;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor beta2 subunit.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   Q-PSDB; Q69143.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.6; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   474 AA;


  Query Match           25.5%;  Score 335;  DB 1;  Length 474;
  Best Local Similarity   30.1%;  Pred. No. 5.4e-25;
  Matches   80;  Conservative   47;  Mismatches   89;  Indels   50;  Gaps    7;

Qy       3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
           ::: | : |  ||   | |:|| : |:|||||||||  ::: || :||||:||||||: |
Db     232 LSLSFKLKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALGITTVLTMTTINTH 291

Qy      63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRA 122
            |:  |:: |: |:| |:  |||| | ||||:|::|:: :           | |:   :|
Db     292 LRETLPKIPYVKAIDMYLMGCFVFVFMALLEYALVNYIFFG----------RGPQRQKKA 341

Qy     123 HARTRARSRACAR-------QHQEAFVC------QIVTTEGSDGEERP-------SCSAQ 162
           :  : :    |         |:   :       :: |:|   |   |          |:
Db     342 AEKAASANNEKMRLDVNKMDPHENILLSTLEIKNEMATSEAVMGLGDPRSTMLAYDASSI 401

Qy     163 QPPSPGSPEG-------PRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYR 215
           |   | |           | :  | :      :|  :    :||            |
Db     402 QYRKAGLPRHSFGRNALERHVAQKKSRLR--RRASQLKITIPD-----------LTDVNA 448

Qy     216 LDNYSRVVFPVTFFFFNVLYWLVCLN 241
           :| :||: ||| | |||::|||  :|
Db     449 IDRWSRIFFPVVFSFFNIVYWLYYVN 474
```

```
RESULT  12
R89336
ID   R89336 standard; Protein; 496 AA.
AC   R89336;
DT   13-APR-1996  (first entry)
DE   GABA receptor subunit.
KW   Gamma-aminobutyric acid receptor; GABA receptor; subunit; LCCH3;
KW   ligand-gated chloride channel; polymerase chain reaction; PCR;
KW   probe; hybridisation; primer; cloning; pupa; signature motif;
KW   transmembrane domain; extracellular domain; intracellular domain;
KW   disulphide bond; loop; vector; insecticide; pesticide; screening.
OS   Drosophila melanogaster.
FH   Key             Location/Qualifiers
FT   peptide         1. .20
FT                   /note= "Signal peptide"
FT   domain          21. .258
FT                   /note= "Extracellular domain"
FT   modified_site   39
FT                   /note= "N-glycosylation site"
FT   disulfide_bond  176. .190
FT                   /note= "Forms loop in extracellular domain"
FT   modified_site   189
FT                   /note= "N-glycosylation site"
FT   domain          259. .280
FT                   /note= "Transmembrane domain M1"
FT   domain          285. .306
FT                   /note= "Transmembrane domain M2"
FT   peptide         294. .301
FT                   /note= "Signature motif (R89338)"
FT   domain          318. .342
FT                   /note= "Transmembrane domain M3"
FT   peptide         326. .331
FT                   /note= "Conserved motif (R89339)"
FT   domain          343. .472
FT                   /note= "Intracellular domain"
FT   modified_site   388
FT                   /note= "Phosphorylation site"
FT   modified_site   454
FT                   /note= "Phosphorylation site"
FT   domain          473. .494
FT                   /note= "Transmembrane domain M4"
PN   US5487976-A.
PD   30-JAN-1996.
PF   15-OCT-1993; 137614.
PR   15-OCT-1993; US-137614.
PA   (CORR ) CORNELL RES FOUND INC.
PI   Henderson JE,  Knipple DC,  Soderlund DM;
DR   WPI; 96-105226/11.
DR   N-PSDB; Q99330.
PT   DNA molecule encoding gamma-aminobutyric acid receptor subunit  -
PT   used to screen for insect, e.g. Drosophila melanogaster, control
PT   pesticides
PS   Claim 1; Column 23-26; 37pp; English.
CC   The sequence represents a Drosophila melanogaster GABA receptor
CC   subunit with homology to the ligand-gated chloride channel family,
CC   designated LCCH3.  A cDNA encoding the receptor has been isolated by
CC   polymerase chain reaction (PCR)-based homology probing, along with
CC   a gene encoding LCCH2 (R89337), using primers Q99333-35 (based on
CC   conserved signature motif R89338) and probe Q99336 (based on
CC   conserved motif R89339), followed by screening of a pupa cDNA
CC   library.  The protein (mol.wt. 54,442) has several typical features
CC   of ligand-gated chloride channel subunits, including 4 hydrophobic
CC   domains capable of forming transmembrane helices, a large
CC   intracellular domain, and cysteine residues forming a
CC   disulphide-bridged loop structure in the extracellular domain.  DNA
CC   encoding the protein may be expressed in heterologous cells using a
CC   vector, for screening of insecticides by evaluating their
CC   specificity for the GABA receptor.
SQ   Sequence   496 AA;
```

```
  Query Match           25.4%;  Score 333.5;  DB 1;  Length 496;
  Best Local Similarity  31.2%;  Pred. No. 8e-25;
  Matches   82;  Conservative   40;  Mismatches   96;  Indels   45;  Gaps    5;

Qy       3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
           ::: | : |  ||  || |:|| :  |||||||||  |:  || :||||:||||||: |
Db     246 LSLSFKLQRNIGYFVFQTYLPSILIVMLSWVSFWINHEATSARVALGITTVLTMTTISTG 305

Qy      63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRA 122
            | : |':||: |:| |: :|||| | ||||:| :|:  : :    |  |::  :
Db     306 VRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWGK---RAKKKIKKVKECCPG 362

Qy     123 HARTRARSRACA------------------RQHQEAFVCQIVTTEGSDGEERPSCSAQ 162
                ||  |:                    |   | :  | |   : |:  ||
Db     363 KIGKSERSETCSTTEDIIELQDVRMSPIPSLRRGTYNATLDSIGTETMNLGKFPPSFRIT 422

Qy     163 QPPSPGSPE----GPRSLCSKLACCEWCKR----FKKYFCMVPDCEGSTWQQGRLCIHVY 214
           :   |  :     | : ::       ||     |     : |              |
Db     423 RNYGTGHSQLRRRAQRGISTRPRMLHALKRGASAIKATIPKIKD-------------VN 468

Qy     215 RLDNYSRVVFPVTFFFFNVLYWL 237
            :| |||::||::|  ||: |||
Db     469 IIDKYSRMIFPISFLAFNLGYWL 491


RESULT  13
W86161
ID   W86161 standard; Protein; 496 AA.
AC   W86161;
DT   04-MAR-1999  (first entry)
DE   Insect GABA receptor subunit LCCH3.
KW   GABA; gamma-aminobutyric acid receptor; LCCH3; GABA recognition site;
KW   Grd; insecticide; insect; pharmacological; screening.
OS   Drosophila sp.
PN   US5854002-A.
PD   29-DEC-1998.
PF   17-DEC-1996; 768301.
PR   17-DEC-1996; US-768301.
PA   (RHON ) RHONE-POULENC INC.
PI   Gant DB, Tomalski MD;
DR   WPI; 99-094901/08.
DR   N-PSDB; V84685.
PT   Host cells that express LCCH3 and Grd subunits of insect
PT   gamma-aminobutyric acid receptor - comprises separate vectors or a
PT   single vector, used for screening compounds for insecticidal
PT   activity
PS   Claim 1; Columns 17-20; 27pp; English.
CC   This represents an insect gamma-aminobutyric acid (GABA) receptor subunit
CC   LCCH3. The invention provides host cells comprising (i) two expression
CC   vectors, one containing a sequence encoding the GABA receptor subunit
CC   LCCH3 and the other containing a sequence encoding the GABA receptor Grd
CC   subunit, with the sequences under control of separate promoters; or (ii)
CC   a single expression vector containing both GABA receptor subunits LCCH3
CC   and Grd linked to one or more regulatory elements. Membrane preparation
CC   from these cells are used to screen compounds for their ability to bind
CC   to the GABA recognition site of an insect GABA receptor, specifically to
CC   identify new insecticides. Co-expression of LCCH3 and Grd generates a
CC   GABA recognition site in the host cell membrane that has pharmacological
CC   properties very similar to those of the native receptor. The cells and
CC   membrane preparations are suitable for high throughput screening.
SQ   Sequence   496 AA;


  Query Match           25.4%;  Score 333.5;  DB 1;  Length 496;
  Best Local Similarity  31.2%;  Pred. No. 8e-25;
  Matches   82;  Conservative   40;  Mismatches   96;  Indels   45;  Gaps    5;

Qy       3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
           ::: | : |  ||  || |:|| :  |||||||||  |:  || :||||:||||||: |
Db     246 LSLSFKLQRNIGYFVFQTYLPSILIVMLSWVSFWINHEATSARVALGITTVLTMTTISTG 305

Qy      63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRA 122
            | : ||:||: |:| |: :|||| | ||||:| :|:  : :    |  |::  :
```

```
Db    306 VRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWGK---RAKKKIKKVKECCPG 362

Qy    123 HARTRARSRACA-------------------RQHQEAFVCQIVTTEGSDGEERPSCSAQ 162
Db    363 KIGKSERSETCSTTEDIIELQDVRMSPIPSLRRGTYNATLDSIGTETMNLGKFPPSFRIT 422

Qy    163 QPPSPGSPE----GPRSLCSKLACCEWCKR----FKKYFCMVPDCEGSTWQQGRLCIHVY 214
Db    423 RNYGTGHSQLRRRAQRGISTRPRMLHALKRGASAIKATIPKIKD--------------VN 468

Qy    215 RLDNYSRVVFPVTFFFFNVLYWL 237
Db    469 IIDKYSRMIFPISFLAFNLGYWL 491


RESULT  14
R31184
ID   R31184 standard; Protein; 451 AA.
AC   R31184;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-2 subunit.
KW   Primer; human; alpha-3; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta.
OS   Homo sapiens.
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   N-PSDB; Q33127.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Disclosure; Fig 2; 43pp; English.
CC   This sequence represents the human alpha-2 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Bovine alpha-2 cDNA was used as a
CC   probe and an alpha-2 cDNA clone was isolated from a human foetal
CC   brain cDNA library. GABA-A receptor comprises a multimeric protein
CC   of molecular size 230-270 kD with specific binding sites for various
CC   drugs including benzodiazepines, barbiturates, and beta-carbolines,
CC   in addition to the agonist ligand GABA.  The receptor is composed of
CC   several distinct types of subunit, which are divided into four classes
CC   (alpha, beta, gamma and delta) based on sequence homology.  To date
CC   six types of alpha, three types of beta, two types of gamma and one
CC   type of delta subunit have been identified.  It has been found that
CC   in addition to an alpha and a beta subunit, either gamma-1 or gamma-2
CC   is also required to confer benzodiazipine sensitivity.  The benzo-
CC   diazepine pharmacology of the receptor is largely dependent on the
CC   identity of the alpha and gamma subunits present.  Receptors
CC   containing a delta subunit do not appear to bind benzodiazepines.
SQ   Sequence   451 AA;


  Query Match             25.1%;  Score 329;  DB 1;  Length 451;
  Best Local Similarity   32.4%;  Pred. No. 2e-24;
  Matches   79;  Conservative   38;  Mismatches   83;  Indels   44;  Gaps    5;

Qy      2 VMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGT 61
Db    239 VMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSI 298

Qy     62 FSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSR 121
Db    299 SARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYF----TK-------RGWTWDGK 347

Qy    122 AHARTRARSRACARQHQEAFVCQIVTTEGSDGEE----RPSCSAQQPPSPGSPEGPRSLC 177
Db    348 SVVNDKKKEKASVMIQNNAYAVAVANYAPNLSKDPVLSTISKSATTPEPNKKPENKPA-- 406

Qy    178 SKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWL 237
Db    406 ------EAKKTFNS--------------------VSKIDRMSRIVFPVLFGTFNLVYWA 438

Qy    238 VCLN 241
Db    439 TYLN 442


RESULT  15
R59862
ID   R59862 standard; Protein; 451 AA.
AC   R59862;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha2 subunit.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   N-PSDB; Q69139.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.2; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   451 AA;


  Query Match             25.1%;  Score 329;  DB 1;  Length 451;
  Best Local Similarity   32.4%;  Pred. No. 2e-24;
  Matches   79;  Conservative   38;  Mismatches   83;  Indels   44;  Gaps    5;

Qy      2 VMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGT 61
Db    239 VMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSI 298

Qy     62 FSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSR 121
Db    299 SARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYF----TK-------RGWTWDGK 347

Qy    122 AHARTRARSRACARQHQEAFVCQIVTTEGSDGEE----RPSCSAQQPPSPGSPEGPRSLC 177
Db    348 SVVNDKKKEKASVMIQNNAYAVAVANYAPNLSKDPVLSTISKSATTPEPNKKPENKPA-- 406

Qy    178 SKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWL 237
Db    406 ------EAKKTFNS--------------------VSKIDRMSRIVFPVLFGTFNLVYWA 438

Qy    238 VCLN 241
Db    439 TYLN 442


Search completed: March 10, 2000, 08:51:51
Job time: 5284 sec
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 05:42:51 ; Search time 34.6 Seconds
(without alignments)
93.006 Million cell updates/sec

Title: US-09-030-832-2
Perfect score: 1312
Sequence: 1 MVMTIFFNVSRRFGYVAFQN.....VFPVTFFFFNVLYWLVCLNL 242

Scoring table: BLOSUM62

Searched: 133990 seqs, 13297546 residues

Database : Issued_Patents_AA:*

Word size : 0

Number of hits that pass the threshold : 133990
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/PCTUS9_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	447	34.1	467	1	US-08-459-100A-3	Sequence 3, Appli
2	361	27.5	453	1	US-08-417-330A-18	Sequence 18, Appl
3	341.5	26.0	462	1	US-08-417-330A-16	Sequence 16, Appl
4	335	25.5	474	1	US-08-417-330A-20	Sequence 20, Appl
5	333.5	25.4	496	1	US-08-137-614A-2	Sequence 2, Appli
6	333.5	25.4	496	2	US-08-768-301-2	Sequence 2, Appli
7	329.5	25.1	474	1	US-08-459-100A-4	Sequence 4, Appli
8	329	25.1	451	1	US-08-417-330A-12	Sequence 12, Appl
9	327.5	25.0	492	1	US-08-417-330A-14	Sequence 14, Appl
10	297	22.6	617	1	US-08-137-614A-24	Sequence 24, Appl
11	292.5	22.3	488	1	US-08-554-659-2	Sequence 2, Appli
12	289.5	22.1	488	1	US-08-554-659-4	Sequence 4, Appli
13	282	21.5	637	3	US-08-072-064-4	Sequence 4, Appli
14	282	21.5	637	3	US-08-072-064-6	Sequence 6, Appli
15	281.5	21.5	617	1	US-08-137-614A-25	Sequence 25, Appl
16	279	21.3	617	1	US-08-137-614A-26	Sequence 26, Appl
17	279	21.3	637	3	US-08-072-064-1	Sequence 1, Appli
18	279	21.3	637	4	PCT-US92-08558-1	Sequence 1, Appli
19	278.5	21.2	440	1	US-08-459-100A-2	Sequence 2, Appli
20	278.5	21.2	440	4	PCT-US94-09589-2	Sequence 2, Appli
21	278	21.2	637	3	US-08-072-064-8	Sequence 8, Appli
22	277	21.1	456	1	US-08-435-933-6	Sequence 6, Appli
23	277	21.1	456	4	PCT-US96-06035-6	Sequence 6, Appli
24	268.5	20.5	686	2	US-08-768-301-4	Sequence 4, Appli
25	268	20.4	510	1	US-08-249-112-3	Sequence 3, Appli
26	268	20.4	510	4	PCT-US95-06556-3	Sequence 3, Appli
27	262.5	20.0	487	1	US-08-249-112-4	Sequence 4, Appli
28	262.5	20.0	487	4	PCT-US95-06556-4	Sequence 4, Appli
29	198	15.1	57	1	US-08-137-614A-21	Sequence 21, Appl
30	174	13.3	57	1	US-08-137-614A-19	Sequence 19, Appl
31	171	13.0	57	1	US-08-137-614A-17	Sequence 17, Appl
32	167	12.7	57	1	US-08-137-614A-23	Sequence 23, Appl
33	166	12.7	57	1	US-08-137-614A-18	Sequence 18, Appl
34	161	12.3	57	1	US-08-137-614A-22	Sequence 22, Appl
35	158	12.0	57	1	US-08-137-614A-20	Sequence 20, Appl
36	150	11.4	57	1	US-08-137-614A-16	Sequence 16, Appl
37	137	10.4	52	1	US-08-137-614A-15	Sequence 15, Appl
38	118	9.0	50	1	US-08-435-933-3	Sequence 3, Appli
39	118	9.0	50	4	PCT-US96-06035-3	Sequence 3, Appli
40	94	7.2	53	4	PCT-US92-08558-12	Sequence 12, Appl
41	88	6.7	479	1	US-08-313-553-7	Sequence 7, Appli
42	88	6.7	479	3	US-08-767-993-7	Sequence 7, Appli
43	83.5	6.4	342	1	US-08-118-270-9	Sequence 9, Appli
44	83.5	6.4	342	4	PCT-US93-08528-9	Sequence 9, Appli
45	83	6.3	404	1	US-08-696-770-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT   1
US-08-459-100A-3
; Sequence 3, Application US/08459100A
; Patent No. 5654172
;  GENERAL INFORMATION:
;    APPLICANT:  Li, ET AL.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,100A
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09589
;      FILING DATE:  26 AUG 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-325
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-459-100A-3


  Query Match             34.1%;  Score 447;  DB 1;  Length 467;
  Best Local Similarity   34.3%;  Pred. No. 6.2e-36;
  Matches   85;  Conservative   52;  Mismatches   65;  Indels   46;  Gaps    5;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
             :||:::|::||| ||    | |:| ::  :||||||||  :: |||||||||:|||||||
Db     260 VVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLS 319

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRH---PR 117
           | :||: |:||||:||:| ::::|||:| | ||:|:  |:: : |:  :    | :    |
Db     320 TIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPAPT 379
```

```
Qy     118 INSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPR 174
           |: |  : |   : |      |  :  : |        ||::   |::
Db     380 IDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD---CAS------------ 417

Qy     175 SLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVL 234
                       :||   ||    |: ||: | : ::|:|:|: ||  |  ||::
Db     417 ----------------FFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLV 459

Qy     235 YWLVCLNL 242
           ||:  | |
Db     460 YWVSYLYL 467


RESULT   2
US-08-417-330A-18
; Sequence 18, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  453 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-18


  Query Match           27.5%;  Score 361;  DB 1;  Length 453;
  Best Local Similarity   33.6%;  Pred. No. 1.4e-27;
  Matches   88;  Conservative   39;  Mismatches   67;  Indels   68;  Gaps    7;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
             ::||::|:: |: ||   | | |  :| :|| |||||  || |||| ||||:|||||||
Db     228 VIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPARTVLGITTVLTMTTLS 287

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTK------AHASPK-- 113
                                                                        :| : |:||| ||:|::||:|| | | ||:||| :|:    ||:        |:|
Db     288 ISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQTQKAKRKAQFAAPPTV 347

Qy     113 ------------LRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSC 159
                       : ||  :|: | : |  | :            ||::      |
Db     348 TISKATEPLEAEIVLHP--DSKYHLKKRITSLS----------LPIVSS-----SEANKV 390

Qy     160 SAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNY 219
             : |    :|  |  |                  |   | |          ::| |
Db     391 LTRAPILQSTPVTPPPL------------------PPAFGGT----------SKIDQY 420

Qy     220 SRVVFPVTFFFFNVLYWLVCLN 241
           ||::||| |  ||::||:| |:
Db     421 SRILFPVAFAGFNLVYWVVYLS 442


RESULT   3
US-08-417-330A-16
; Sequence 16, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  462 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-16


  Query Match           26.0%;  Score 341.5;  DB 1;  Length 462;
  Best Local Similarity   31.5%;  Pred. No. 1.2e-25;
  Matches   78;  Conservative   42;  Mismatches   77;  Indels   51;  Gaps    5;

Qy       2 VMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGT 61
             :||  |:: |: ||   | |:|  :| :|| ||||:  || ||||  |:|:|||||||
```

```
Db    246 IMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSI 305

Qy     62 FSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL-----IYNQTKAHASPKLRHP 116
          :| : |:|:| ||:|::||:|: | | ||:||| :|:       ::  ||  : |::
Db    306 SARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGWAWDGKKALEAAKIKKK 365

Qy    117 R---INSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGP 173
          |   :|   :| |  :                          |:   :|     :| |
Db    366 REVILNKSTNAFTTGKM----------------------SHPPNIPKEQ-----TPAGT 397

Qy    174 RSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNV 233
          :  |                |   |  | :  :    : ::|  ||:|||| |  ||:
Db    398 SNTTS--------------VSVKPSEEKTSESKKTYNSISKIDKMSRIVFPVLFGTFNL 442

Qy    234 LYWLVCLN 241
          :||   ||
Db    443 VYWATYLN 450


RESULT   4
US-08-417-330A-20
; Sequence 20, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  474 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-20


  Query Match             25.5%;  Score 335;  DB 1;  Length 474;
  Best Local Similarity   30.1%;  Pred. No. 5.1e-25;
  Matches   80;  Conservative   47;  Mismatches   89;  Indels   50;  Gaps    7;

Qy      3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
          ::: | : |  ||   | |:|| : |:||||||||  ::: || :||||:||||||: |
Db    232 LSLSFKLKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALGITTVLTMTTINTH 291

Qy     63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRA 122
           |:  |:: |: |:| |:  |||| | ||||:|::|:: :           | |:   :|
Db    292 LRETLPKIPYVKAIDMYLMGCFVFVFMALLEYALVNYIFFG----------RGPQRQKKA 341

Qy    123 HARTRARSRACAR-------QHQEAFVC------QIVTTEGSDGEERP-------SCSAQ 162
          :  : :   |          |:  :      :: |:|   |   |           |:
Db    342 AEKAASANNEKMRLDVNKMDPHENILLSTLEIKNEMATSEAVMGLGDPRSTMLAYDASSI 401

Qy    163 QPPSPGSPEG-------PRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYR 215
          |    | |          | :  | :     :|  :    :||             |
Db    402 QYRKAGLPRHSFGRNALERHVAQKKSRLR--RRASQLKITIPD----------LTDVNA 448

Qy    216 LDNYSRVVFPVTFFFFNVLYWLVCLN 241
          :| :||: ||| | |||::|||  :|
Db    449 IDRWSRIFFPVVFSFFNIVYWLYYVN 474


RESULT   5
US-08-137-614A-2
; Sequence 2, Application US/08137614A
; Patent No. 5487976
;  GENERAL INFORMATION:
;    APPLICANT:  Soderlund, David M.
;    APPLICANT:  Knipple, Douglas C.
;    APPLICANT:  Henderson, Joseph E.
;    TITLE OF INVENTION:  Gene Encoding An Insect
;    TITLE OF INVENTION:  Gamma-Aminobutyric Acid (GABA) Receptor Subunit
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,614A
;      FILING DATE:  15-OCT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716)263-1636
;      TELEFAX:  (716)263-1600
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  496 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-137-614A-2


  Query Match             25.4%;  Score 333.5;  DB 1;  Length 496;
  Best Local Similarity   31.2%;  Pred. No. 7.6e-25;
  Matches   82;  Conservative   40;  Mismatches   96;  Indels   45;  Gaps    5;

Qy      3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
          ::: | : |  ||  || |:|| : |||||||||  |:  || :||||:||||||: |
Db    246 LSLSFKLQRNIGYFVFQTYLPSILIVMLSWVSFWINHEATSARVALGITTVLTMTTISTG 305
```

```
Qy      63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRA 122
           | : ||:||: |:| |: :|||| | ||||:| :|:  : :    |  |::  :
Db     306 VRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWGK---RAKKKIKKVKECCPG 362

Qy     123 HARTRARSRACA-------------------RQHQEAFVCQIVTTEGSDGEERPSCSAQ 162
                 ||  |:                    |    | :  | |   : |:  ||
Db     363 KIGKSERSETCSTTEDIIELQDVRMSPIPSLRRGTYNATLDSIGTETMNLGKFPPSFRIT 422

Qy     163 QPPSPGSPE----GPRSLCSKLACCEWCKR----FKKYFCMVPDCEGSTWQQGRLCIHVY 214
           :    |  :      | : ::       ||     |     : |                |
Db     423 RNYGTGHSQLRRRAQRGISTRPRMLHALKRGASAIKATIPKIKD-------------VN 468

Qy     215 RLDNYSRVVFPVTFFFFNVLYWL 237
           :| |||::||::|  ||: |||
Db     469 IIDKYSRMIFPISFLAFNLGYWL 491


RESULT   6
US-08-768-301-2
; Sequence 2, Application US/08768301
; Patent No. 5854002
;  GENERAL INFORMATION:
;    APPLICANT:  Tomalski, Michael D.
;    APPLICANT:  Gant, Daniel B.
;    TITLE OF INVENTION:  METHOD OF IDENTIFYING COMPOUNDS THAT BIND
;    TITLE OF INVENTION:  TO THE INSECT GABA RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brumbaugh, Graves, Donohue & Raymond
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  10112-0228
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/768,301
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacLeod, Janet M
;      REGISTRATION NUMBER:  35,263
;      REFERENCE/DOCKET NUMBER:  A30693
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-408-2500
;      TELEFAX:  212-765-2519
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  496 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
US-08-768-301-2


  Query Match           25.4%;  Score 333.5;  DB 2;  Length 496;
  Best Local Similarity   31.2%;  Pred. No. 7.6e-25;
  Matches   82;  Conservative   40;  Mismatches   96;  Indels   45;  Gaps    5;

Qy       3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
```

```
           ::: | : |  ||  || |:|| :  |||||||||  |:  || :||||:||||||: |
Db     246 LSLSFKLQRNIGYFVFQTYLPSILIVMLSWVSFWINHEATSARVALGITTVLTMTTISTG 305

Qy      63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRA 122
           | : ||:||: |:| |: :|||| | ||||:| :|:  : :    |  |::  :
Db     306 VRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWGK---RAKKKIKKVKECCPG 362

Qy     123 HARTRARSRACA-------------------RQHQEAFVCQIVTTEGSDGEERPSCSAQ 162
                 ||  |:                    |    | :  | |   : |:  ||
Db     363 KIGKSERSETCSTTEDIIELQDVRMSPIPSLRRGTYNATLDSIGTETMNLGKFPPSFRIT 422

Qy     163 QPPSPGSPE----GPRSLCSKLACCEWCKR----FKKYFCMVPDCEGSTWQQGRLCIHVY 214
           :    |  :      | : ::       ||     |     : |                |
Db     423 RNYGTGHSQLRRRAQRGISTRPRMLHALKRGASAIKATIPKIKD-------------VN 468

Qy     215 RLDNYSRVVFPVTFFFFNVLYWL 237
           :| |||::||::|  ||: |||
Db     469 IIDKYSRMIFPISFLAFNLGYWL 491


RESULT   7
US-08-459-100A-4
; Sequence 4, Application US/08459100A
; Patent No. 5654172
;  GENERAL INFORMATION:
;    APPLICANT:  Li, ET AL.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,100A
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09589
;      FILING DATE:  26 AUG 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-325
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  474 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-459-100A-4


  Query Match           25.1%;  Score 329.5;  DB 1;  Length 474;
  Best Local Similarity   30.5%;  Pred. No. 1.8e-24;
  Matches   79;  Conservative   43;  Mismatches   92;  Indels   45;  Gaps    5;

Qy       3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
           ::: | : |  ||    | |:||:: |:||||||||  ::: || :||||:||||||: |
Db     233 LSLSFRLKRNIGYFILQTYMPSTLITILSWVSFWINYDASAARVALGITTVLTMTTISTH 292
```

```
Qy      63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ----------TKAHASP 111
Db     293 LRETLPKIPYVKAIDIYLMGCFVFVFLALLEYAFVNYIFFGKGPQKKGASKQDQSANEKN 352

Qy     112 KLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ--QPPSP-- 168
Db     353 KLEMNKVQVDAHGNILLSTLEIRNETSGSEVLTSVSDPKATMYSYDSASIQYRKPLSSRE 412

Qy     168 ---------GSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDN 218
Db     413 AYGRALDRHGVPSKGRIR----------RRASQLKVKIPD----------LTDVNSIDK 451

Qy     219 YSRVVFPVTFFFFNVLYWL 237
Db     452 WSRMFFPITFSLFNVVYWL 470


RESULT   8
US-08-417-330A-12
; Sequence 12, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  451 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-12


  Query Match           25.1%;  Score 329;  DB 1;  Length 451;
  Best Local Similarity  32.4%;  Pred. No. 1.8e-24;
  Matches   79;  Conservative   38;  Mismatches   83;  Indels   44;  Gaps    5;

Qy       2 VMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGT 61
Db     239 VMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSI 298

Qy      62 FSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSR 121
Db     299 SARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYF----TK-------RGWTWDGK 347

Qy     122 AHARTRARSRACARQHQEAFVCQIVTTEGSDGEE----RPSCSAQQPPSPGSPEGPRSLC 177
Db     348 SVVNDKKKEKASVMIQNNAYAVAVANYAPNLSKDPVLSTISKSATTPEPNKKPENKPA-- 406

Qy     178 SKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWL 237
Db     406 ------EAKKTFNS--------------------VSKIDRMSRIVFPVLFGTFNLVYWA 438

Qy     238 VCLN 241
Db     439 TYLN 442


RESULT   9
US-08-417-330A-14
; Sequence 14, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  492 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-14


  Query Match           25.0%;  Score 327.5;  DB 1;  Length 492;
  Best Local Similarity  29.5%;  Pred. No. 2.9e-24;
```

```
  Matches   79;  Conservative   39;  Mismatches   73;  Indels   77;  Gaps    5;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           :|||  |:: |: ||   | |:|  :| :|| ||||:  || ||||  |:|:|||||||
Db     263 VVMTTHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLS 322

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
             :| : |:|:| ||:|::||:|: | | ||:||| :|:     ||
Db     323 ISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYF----TK-------------- 365

Qy     121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 180
                 || |                 :|:: |     :  :| :|    |    :
Db     365 --------RSWAW-----------------EGKKVPEALEMKKKTPAAPAKKTSTTFNI 398

Qy     181 ACCEWCKRFKKYFCMVPDCEGSTWQQG-------------------------RLCIHV 213
             :     |      | | ||  :|                            :    |
Db     399 VGTTYPINLAK------DTEFSTISKGAAPSASSTPTIIASPKATYVQDSPTETKTYNSV 452

Qy     214 YRLDNYSRVVFPVTFFFFNVLYWLVCLN 241
           ::|  ||::||| |  ||::||   :|
Db     453 SKVDKISRIIFPVLFAIFNLVYWATYVN 480


RESULT  10
US-08-137-614A-24
; Sequence 24, Application US/08137614A
; Patent No. 5487976
;  GENERAL INFORMATION:
;    APPLICANT:  Soderlund, David M.
;    APPLICANT:  Knipple, Douglas C.
;    APPLICANT:  Henderson, Joseph E.
;    TITLE OF INVENTION:  Gene Encoding An Insect
;    TITLE OF INVENTION:  Gamma-Aminobutyric Acid (GABA) Receptor Subunit
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,614A
;      FILING DATE:  15-OCT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716)263-1636
;      TELEFAX:  (716)263-1600
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  617 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-137-614A-24


  Query Match           22.6%;  Score 297;  DB 1;  Length 617;
  Best Local Similarity   45.0%;  Pred. No. 3.5e-21;
  Matches   58;  Conservative   22;  Mismatches   41;  Indels    8;  Gaps    2;

Qy       3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
           ::: | : |  ||  || |:|| :  |||||||||  |:  || :||||:|||||:
Db     267 LSLIFQLQRNIGYFIFQTYLPSILIVMLSWVSFWINHEATSARVALGITTVLTMTTISNG 326

Qy      63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRA 122
             | : ||:||: |:| |: :|||| | ||||:| :|:  :      |  | :  |:  ||
Db     327 VRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWG-----ARAKRKAKRLRERA 381

Qy     123 HARTRARSR 131
               | | |
Db     382 ---TSVRKR 387


RESULT  11
US-08-554-659-2
; Sequence 2, Application US/08554659
; Patent No. 5767261
;  GENERAL INFORMATION:
;    APPLICANT:  Wingate, Vincent
;    APPLICANT:  Wolff, Mark
;    TITLE OF INVENTION:  LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
;    TITLE OF INVENTION:  AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/554,659
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9732
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  488 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-554-659-2


  Query Match           22.3%;  Score 292.5;  DB 1;  Length 488;
  Best Local Similarity   28.8%;  Pred. No. 7.3e-21;
  Matches   74;  Conservative   42;  Mismatches   78;  Indels   63;  Gaps    7;

Qy      14 GYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYI 73
             ||   | |:|| :  ::|||||||:   : ||| |||:|:|||||||| : :    |::||:
Db     252 GYYLIQIYIPSGLIVIISWVSFWLNRNATPARVSLGVTTVLTMTTLMSSTNAALPKISYV 311

Qy      74 TALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRAC 133
             ::| |:  |||  | :|||:| : ::                ||  |       : |
Db     312 KSIDVYLGTCFVMVFTSLLEYATVGYMA-------------KRIQMR-------KQRFT 350

Qy     134 ARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEW----CKRF 189
           | | :             ||   |  ||:  | | :    |   |:|:   :     | :
Db     351 AVQKMQI-----------DG---PPGSAEPIPPPRTSTLSRPPPSRLSEVRFKVHDPKAY 396

Qy     190 KKYFCMVPDCEGSTWQQGRL-----------CIHVYR-----------LDNYSRVVFP 225
           |   :     |:  | |               :| ::           :| |||:|||
Db     397 SKGGTLENTINGARGQPGPAPPADEEAGPPPHLVHAFQGINKLLGTTPSDIDKYSRIVFP 456
```

```
Qy    226 VTFFFFNVLYWLVCLNL 242
          |    ||::||:: |::
Db    457 VCCVCFNLMYWIIYLHV 473


RESULT  12
US-08-554-659-4
; Sequence 4, Application US/08554659
; Patent No. 5767261
;  GENERAL INFORMATION:
;    APPLICANT:  Wingate, Vincent
;    APPLICANT:  Wolff, Mark
;    TITLE OF INVENTION:  LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
;    TITLE OF INVENTION:  AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/554,659
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9732
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  488 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-554-659-4


  Query Match             22.1%;  Score 289.5;  DB 1;  Length 488;
  Best Local Similarity   28.4%;  Pred. No. 1.4e-20;
  Matches   73;  Conservative   43;  Mismatches   78;  Indels   63;  Gaps    7;

Qy     14 GYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYI 73
          ||   | |:|| :  ::|||||:   : ||| :||:|:|||||| : :    |::||:
Db    252 GYYLIQIYIPSGLIVIISWVSFWLNRNATPARVALGVTTVLTMTTLMSSTNAALPKISYV 311

Qy     74 TALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRAC 133
          ::| |:  |||  | :|||:| : ::              || |       : |
Db    312 KSIDVYLGTCFVMVFTSLLEYATVGYMA-------------KRIQMR-------KQRFT 350

Qy    134 ARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEW----CKRF 189
          | | :          ||   |  ||:  | | :   |   |:|:   :     | :
Db    351 AVQKMQI----------DG---PPGSAEPIPPPRTSTLSRPPPSRLSEVRFKVHDPKAY 396

Qy    190 KKYFCMVPDCEGSTWQQGRL-----------CIHVYR-----------LDNYSRVVFP 225
          |   :     |:  | |               :| ::           :| |||:|||
Db    397 SKGGTLENTINGARGQPGPAPPADEEAGPPPHLVHAFQGINKLLGTTPSDIDKYSRIVFP 456

Qy    226 VTFFFFNVLYWLVCLNL 242
          |    ||::||:: |::
Db    457 VCCVCFNLMYWIIYLHV 473


RESULT  13
US-08-072-064-4
; Sequence 4, Application US/08072064
; Patent No. 6008046
;  GENERAL INFORMATION:
;    APPLICANT:  FFRENCH-CONSTANT, RICHARD H.
;    APPLICANT:  JACKSON, MEYER B.
;    TITLE OF INVENTION:  DRUG AND PESTICIDE SCREENING
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER G. CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/072,064
;      FILING DATE:  19930602
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 770,881
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  OPHD-00574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  637 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-072-064-4


  Query Match             21.5%;  Score 282;  DB 3;  Length 637;
  Best Local Similarity   22.3%;  Pred. No. 1.1e-19;
  Matches   78;  Conservative   42;  Mismatches   91;  Indels  138;  Gaps    9;

Qy     11 RRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV 70
          |  ||    | |:|| :  ::|||||:   : ||| |||:|:|||||| : :    |::
Db    296 RSMGYYLIQIYIPSGLIVVISWVSFWLNRNATPARVSLGVTTVLTMTTLMSSTNAALPKI 355

Qy     71 SYITALDFYIAICFVFCFCALLEFAVLNFLI-------------------------YNQ 104
          ||: ::| |:  |||  | :|||:| : ::                          ||
Db    356 SYVKSIDVYLGTCFVMVFASLLEYATVGYMAKRIQMRKQRFMAIQKIAEQKKQQLDGANQ 415

Qy    105 TKAHASPKL-------------------------------------RHPRINSRAHA- 125
          :|: :|                                        |   :   ||
Db    416 QQANPNPNANVGGPGGVGVGPGGPGGPGGGVNVGVGMGMGPEHGHGHGHHAHSHGHPHAP 475

Qy    125 --------------RTRARSRACA---------------RQHQEAFVCQIVTTEGSDGE 154
                         :   :| |:                : | :    :     | |
Db    476 KQTVSNRPIGFSNIQQNVGTRGCSIVGPLFQEVRFKVHDPKAHSKGGTLENTVNGGRGGP 535

Qy    155 ERPSCSAQQPPSP-----------GSPEG--------PRSLC--SKLACCEWCKRFKKYF 193
          :       |   |           | |||        |  |    |:      |   |
Db    536 QSHGPGPGQGGGPPGGGGGGGGGGPPEGGGDPEAAVPAHLLHPGKVK-----KDINKLL 590

Qy    194 CMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 242
          : |              :| |||:|||| |  ||::||:: |::
Db    591 GITPS---------------DIDKYSRIVFPVCFVCFNLMYWIIYLHV 623
```

```
RESULT  14
US-08-072-064-6
; Sequence 6, Application US/08072064
; Patent No. 6008046
;  GENERAL INFORMATION:
;    APPLICANT:  FFRENCH-CONSTANT, RICHARD H.
;    APPLICANT:  JACKSON, MEYER B.
;    TITLE OF INVENTION:  DRUG AND PESTICIDE SCREENING
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER G. CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/072,064
;      FILING DATE:  19930602
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 770,881
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  OPHD-00574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  637 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-072-064-6

  Query Match           21.5%;  Score 282;  DB 3;  Length 637;
  Best Local Similarity  22.3%;  Pred. No. 1.1e-19;
  Matches   78;  Conservative   42;  Mismatches   91;  Indels  138;  Gaps    9;

Qy      11 RRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV 70
           |  ||    | |:|| :  ::|||||:   : ||| |||:|:|||||| : :    |::
Db     296 RSMGYYLIQIYIPSGLIVVISWVSFWLNRNATPARVSLGVTTVLTMTTLMSSTNAALPKI 355

Qy      71 SYITALDFYIAICFVFCFCALLEFAVLNFLI----------------------------YNQ 104
           ||: ::| |:  ||| | :|||:| : ::                              ||
Db     356 SYVKSIDVYLGTCFVMVFASLLEYATVGYMAKRIQIRKQRFMAIQKIAEQKKQQLDGANQ 415

Qy     105 TKAHASPKL-----------------------------------RHPRINSRAHA- 125
           :|: :|                                     |   :   ||
Db     416 QQANPNPNANVGGPGGVGVGPGGPGGPGGGVNVGVGMGMGPEHGHGHGHHAHSHGHPHAP 475

Qy     125 --------------RTRARSRACA---------------RQHQEAFVCQIVTTEGSDGE 154
                        :   :| |:                : | :    :     |  |
Db     476 KQTVSNRPIGFSNIQQNVGTRGCSIVGPLFQEVRFKVHDPKAHSKGGTLENTVNGGRGGP 535

Qy     155 ERPSCSAQQPPSP-----------GSPEG--------PRSLC--SKLACCEWCKRFKKYF 193
           :      |   |              | |||        |  |    |:       |  |
Db     536 QSHGPGPGQGGGPPGGGGGGGGGGGPPEGGGDPEAAVPAHLLHPGKVK-----KDINKLL 590

Qy     194 CMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 242
           : |                  :| |||:|||| |  ||::||:: |::
Db     591 GITPS---------------DIDKYSRIVFPVCFVCFNLMYWIIYLHV 623
```

```
RESULT  15
US-08-137-614A-25
; Sequence 25, Application US/08137614A
; Patent No. 5487976
;  GENERAL INFORMATION:
;    APPLICANT:  Soderlund, David M.
;    APPLICANT:  Knipple, Douglas C.
;    APPLICANT:  Henderson, Joseph E.
;    TITLE OF INVENTION:  Gene Encoding An Insect
;    TITLE OF INVENTION:  Gamma-Aminobutyric Acid (GABA) Receptor Subunit
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,614A
;      FILING DATE:  15-OCT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716)263-1636
;      TELEFAX:  (716)263-1600
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  617 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-137-614A-25

  Query Match           21.5%;  Score 281.5;  DB 1;  Length 617;
  Best Local Similarity  39.4%;  Pred. No. 1.1e-19;
  Matches   52;  Conservative   29;  Mismatches   40;  Indels   11;  Gaps    1;

Qy       3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
           ::: | : |  ||   | |:||:: |:|||||||  ::: || :||||:||||||: |
Db     267 LSLSFRLKRNIGYFILQTYMPSTLITILSWVSFWINYDASAARVALGITTVLTMTTISTH 326

Qy      63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ----------TKAHASP 111
             |:  |:: |: |:| |:  |||| | ||||:| :|:: : :            |:
Db     327 LRETLPKIPYVKAIDIYLMGCFVFVFLALLEYAFVNYIFFGKGPQKKGASKQDQSANEKN 386

Qy     112 KLRHPRINSRAH 123
           ||   ::   ||
Db     387 KLEMNKVQVDAH 398


Search completed: March 11, 2000, 06:01:22
Job time: 1111 sec
```

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:04:22 ; Search time 52.39 Seconds
(without alignments)
217.885 Million cell updates/sec

Title: US-09-030-832-2
Perfect score: 1312
Sequence: 1 MVMTIFFNVSRRFGYVAFQN.....VFPVTFFFFNVLYWLVCLNL 242

Scoring table: BLOSUM62

Searched: 142080 seqs, 47169319 residues

Database : PIR_62:*

Word size : 0

Number of hits that pass the threshold : 142080
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	532.5	40.6	457	2	S38296	gamma-aminobutyric
2	456.5	34.8	464	2	JH0824	gamma-aminobutyric
3	453	34.5	474	2	S13086	gamma-aminobutyric
4	452.5	34.5	467	2	S16915	gamma-aminobutyric
5	451.5	34.4	467	2	S19317	gamma-aminobutyric
6	448	34.1	474	2	JH0317	gamma-aminobutyric
7	447	34.1	467	2	S03905	gamma-aminobutyric
8	447	34.1	466	2	JQ0077	gamma-aminobutyric
9	447	34.1	466	2	JH0316	gamma-aminobutyric
10	446	34.0	465	2	S12056	gamma-aminobutyric
11	444	33.8	475	2	B39272	gamma-aminobutyric
12	374.5	28.5	552	2	S17551	gamma-aminobutyric
13	369	28.1	453	2	S11087	gamma-aminobutyric
14	364.5	27.8	554	2	G01928	gamma-aminobutyric
15	362.5	27.6	556	2	S06838	gamma-aminobutyric
16	362	27.6	443	2	S11396	gamma-aminobutyric
17	349	26.6	488	2	JH0359	gamma-aminobutyric
18	348	26.5	473	2	A55275	gamma-aminobutyric
19	345	26.3	451	2	C49970	glycine receptor a
20	345	26.3	449	2	S12382	glycine receptor a
21	345	26.3	473	2	S04466	gamma-aminobutyric
22	345	26.3	473	2	S53532	gamma-aminobutyric
23	344	26.2	457	2	S20662	glycine receptor a
24	341.5	26.0	464	2	B34130	gamma-aminobutyric
25	341.5	26.0	462	2	A48933	gamma-aminobutyric
26	340.5	26.0	452	2	S12381	glycine receptor a
27	334.5	25.5	455	1	CHCHA1	gamma-aminobutyric
28	334.5	25.5	452	2	S14816	glycine receptor a
29	334.5	25.5	452	2	S18836	glycine receptor a
30	333.5	25.4	451	2	B49970	glycine receptor a
31	333.5	25.4	496	2	JN0603	gamma-aminobutyric
32	333	25.4	456	2	A60652	gamma-aminobutyric
33	333	25.4	455	2	JQ0158	gamma-aminobutyric
34	333	25.4	456	2	A27142	gamma-aminobutyric
35	333	25.4	455	2	A39062	gamma-aminobutyric
36	332.5	25.3	499	2	S17785	gamma-aminobutyric
37	332	25.3	474	2	S04465	gamma-aminobutyric
38	332	25.3	474	2	S53531	gamma-aminobutyric
39	331.5	25.3	474	2	B27142	gamma-aminobutyric
40	330.5	25.2	476	2	S11440	gamma-aminobutyric
41	330	25.2	474	2	JH0829	gamma-aminobutyric
42	329.5	25.1	474	2	B60039	gamma-aminobutyric
43	329.5	25.1	474	2	A40336	gamma-aminobutyric
44	329	25.1	451	1	ACBOG2	gamma-aminobutyric
45	329	25.1	451	2	I57947	gamma-aminobutyric

ALIGNMENTS

RESULT 1
S38296
gamma-aminobutyric acid receptor A gamma-4 chain precursor - chicken
N;Alternate names: GABA(A) receptor gamma-4 chain
C;Species: Gallus gallus (chicken)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S38296
R;Harvey, R.J.; Kim, H.C.; Darlison, M.G.
FEBS Lett. 331, 211-216, 1993
A;Title: Molecular cloning reveals the existence of a fourth gamma subunit of the ver
A;Reference number: S38296; MUID:93387470
A;Accession: S38296
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-457 <HAR>
A;Cross-references: EMBL:X73533; NID:g414021; PIDN:CAA51939.1; PID:g414022
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein

Query Match 40.6%; Score 532.5; DB 2; Length 457;
Best Local Similarity 41.5%; Pred. No. 1.6e-40;
Matches 107; Conservative 36; Mismatches 56; Indels 59; Gaps 5;

```
Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           ||||: |::||| || | | |:|  :| :|||||||| :| |||||||||:|||||||
Db     243 MVMTVSFDLSRRMGYFAIQTYIPCILTVVLSWVSFWIKRDSTPARTSLGITTVLTMTTLS 302

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTK-AHASPKLRHP--- 117
           | |||: |||||||||:| ::::||:| | ||:|:| ||:|: |:    |:| | | |
Db     303 TISRKHLPRVSYITAMDLFVSVCFIFVFAALMEYATLNYLVGNKKPLEHSSRKARLPPAG 362

Qy     117 ------------RINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQP 164
                       ||:  |                                |     :
Db     363 AQVMPSFTAININNNIMH-----------------------------WPPEIEEDED 391

Qy     165 PSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVF 224
             ||||           | |  |  :::|| : ||:   |::||: ||: |||:|||| |
Db     392 DDPGSP----------CLEG-KECERFFCCIEDCQTGMWREGRVRIHISRLDSYSRVFF 439

Qy     225 PVTFFFFNVLYWLVCLNL 242
           |  |  ||::||:  | |
Db     440 PTAFLLFNIVYWIAYLYL 457
```

RESULT 2
JH0824
gamma-aminobutyric acid A receptor gamma 1 chain precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
C;Accession: JH0824
R;Glencorse, T.A.; Darlison, M.G.; Barnard, E.A.; Bateson, A.N.
J. Neurochem. 61, 2294-2302, 1993
A;Title: Sequence and novel distribution of the chicken homologue of the mammalian ga
A;Reference number: JH0824; MUID:94065817
A;Accession: JH0824
A;Molecule type: mRNA
A;Residues: 1-464 <GLE>

```
C;Comment: This protein mediates gamma-aminobutyric acid-induced synaptic inhibition in
C;Superfamily: acetylcholine receptor
C;Keywords: ion channel; neurotransmitter receptor; transmembrane protein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-464/Product: gamma-aminobutyric acid A receptor gamma 1 chain #status predicted <MA
F;269-290/Domain: transmembrane #status predicted <TM1>
F;295-316/Domain: transmembrane #status predicted <TM2>
F;328-349/Domain: transmembrane #status predicted <TM3>
F;441-464/Domain: transmembrane #status predicted <TM4>


  Query Match             34.8%;  Score 456.5;  DB 2;  Length 464;
  Best Local Similarity   35.2%;  Pred. No. 1.1e-33;
  Matches   90;  Conservative   45;  Mismatches   62;  Indels   59;  Gaps    4;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           ::|||||::||| ||   | |:|  :| :|||||||  :: |||||||||:|||||||
Db     254 IIMTIFFDLSRRMGYFTIQTYIPCILTVVLSWVSFWINKDAVPARTSLGITTVLTMTTLS 313

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
           | :||: |:|||:||:| ::::||:| | ||:|:  |::   |:
Db     314 TIARKSLPKVSYVTAMDLFVSVCFIFVFAALMEYGTLHYFTSNR---------------- 358

Qy     121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPS-----PGSPEGPRS 175
                                       :|  |::: :     ||     |||   | :
Db     358 ----------------------------KGDKGKDKKAKPKPSKPSAIAVRPGSTLIPIN 389

Qy     176 LCSKL---------ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPV 226
             : |          | |  |    :||   ||   :|:::||: | : ::|:|||: ||
Db     390 NINNLPERDDDYGYECLEG-KDCASFFCCFEDCRTGSWREGRIHIRIAKIDSYSRIFFPT 448

Qy     227 TFFFFNVLYWLVCLNL 242
           |  ||::||:  | |
Db     449 AFALFNLVYWIGYLYL 464


RESULT   3
S13086
gamma-aminobutyric acid/benzodiazepine receptor A gamma-2 chain precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S13086
R;Glencorse, T.A.; Bateson, A.N.; Darlison, M.G.
Nucleic Acids Res. 18, 7157, 1990
A;Title: Sequence of the chicken GABA(A) receptor gamma-2-subunit cDNA.
A;Reference number: S13086; MUID:91088318
A;Accession: S13086
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <GLE>
A;Cross-references: EMBL:X54944; NID:g62896; PIDN:CAA38704.1; PID:g62897
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; phosphoprotein; transmembrane protein


  Query Match             34.5%;  Score 453;  DB 2;  Length 474;
  Best Local Similarity   34.8%;  Pred. No. 2.3e-33;
  Matches   89;  Conservative   50;  Mismatches   63;  Indels   54;  Gaps    6;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           :||:::||:||| ||   | |:| ::  :|||||||  :: |||||||||:|||||||
Db     259 VVMSVYFNLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLS 318

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYN------QTKAHASPKLR 114
           | :||: |:|||:||:| ::::||:| | ||:|:  |:: : |      : |   :| ||
Db     319 TIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPLLR 378

Qy     115 -----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPS 166
                | |: |  : |   : |     |  :  : |        ||::   |::
Db     379 MFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD---CAS----- 424

Qy     167 PGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPV 226
                                 :||   ||    |: ||: | : ::|:|:|: ||
Db     424 ----------------------FFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPT 458

Qy     227 TFFFFNVLYWLVCLNL 242
             |  ||::||:  | |
Db     459 AFCLFNLVYWVSYLYL 474


RESULT   4
S16915
gamma-aminobutyric acid/benzodiazepine receptor gamma-3 chain precursor - mouse
N;Alternate names: GABA(A) receptor gamma-3 chain
C;Species: Mus musculus (house mouse)
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 20-Aug-1999
C;Accession: S16915; S15469
R;Wilson-Shaw, D.; Robinson, M.; Gambarana, C.; Siegel, R.E.; Sikela, J.M.
FEBS Lett. 284, 211-215, 1991
A;Title: A novel gamma subunit of the GABA(A) receptor identified using the polymeras
A;Reference number: S16915; MUID:91285135
A;Accession: S16915
A;Molecule type: mRNA
A;Residues: 1-467 <WIL>
A;Cross-references: EMBL:X59300; NID:g51121; PIDN:CAA41988.1; PID:g51122
C;Superfamily: acetylcholine receptor
C;Keywords: disulfide bond; glycoprotein; ion channel; neurotransmitter receptor; tra
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-467/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-3 chain #stat
F;255-277/Domain: transmembrane #status predicted <TM1>
F;281-303/Domain: transmembrane #status predicted <TM2>
F;315-337/Domain: transmembrane #status predicted <TM3>
F;444-467/Domain: transmembrane #status predicted <TM4>
F;110,228/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;171-185/Disulfide bonds: #status predicted


  Query Match             34.5%;  Score 452.5;  DB 2;  Length 467;
  Best Local Similarity   38.7%;  Pred. No. 2.5e-33;
  Matches   96;  Conservative   44;  Mismatches   81;  Indels   27;  Gaps    5;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           :||||:| :||| ||   | |:|  :| :||||||||| :: ||||:||||:|||||||
Db     241 VVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFWIKKDATPARTTLGITTVLTMTTLS 300

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
           | :||: |||||:||:| :: :||:| | ||:|:| ||:  |:  :    | :|  : :
Db     301 TIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEYATLNY--YSSCR---KPTIRKKKTSL 355

Qy     121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLC--- 178
                ||      : |    :                |    :|| |       |:
Db     356 LHPDSTRWIPDRISLQAPSNY---------------SLLDMRPPPPVMITLNNSMYWQE 399

Qy     178 SKLACCEWC---KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVL 234
           :  |   |   |  : :||   :|:  :|::||: | |  ||:|||| || :|  ||::
Db     400 FEDTCVYECLDGKDCQSFFCCYEECKSGSWRRGRIHIDVSELDSYSRVFFPTSFLLFNLV 459

Qy     235 YWLVCLNL 242
           ||:  | |
Db     460 YWVGYLYL 467


RESULT   5
S19317
gamma-aminobutyric acid/benzodiazepine receptor gamma-3 chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: S19317; A40221
R;Knoflach, F.; Rhyner, T.; Villa, M.; Kellenberger, S.; Drescher, U.; Malherbe, P.;
FEBS Lett. 293, 191-194, 1991
A;Title: The gamma3-subunit of the GABA(A)-receptor confers sensitivity to benzodiaze
A;Reference number: S19317; MUID:92070559
A;Accession: S19317
A;Molecule type: mRNA
A;Residues: 1-467 <KNO>
A;Cross-references: EMBL:X63324; NID:g56181; PIDN:CAA44930.1; PID:g56182
```

```
R;Herb, A.; Wisden, W.; Luddens, H.; Puia, G.; Vicini, S.; Seeburg, P.H.
Proc. Natl. Acad. Sci. U.S.A. 89, 1433-1437, 1992
A;Title: The third gamma subunit of the gamma-aminobutyric acid type A receptor family.
A;Reference number: A40221; MUID:92159063
A;Accession: A40221
A;Molecule type: mRNA
A;Residues: 1-467 <HER>
A;Note: sequence extracted from NCBI backbone (NCBIP:82491)
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein


  Query Match             34.4%;  Score 451.5;  DB 2;  Length 467;
  Best Local Similarity   38.7%;  Pred. No. 3.1e-33;
  Matches   96;  Conservative   44;  Mismatches   81;  Indels   27;  Gaps    5;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          :|||||:| :||| ||   | |:|  :| :|||||||||| :: ||||:||||:|||||||
Db    241 VVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFWIKKDATPARTTLGITTVLTMTTLS 300

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
          | :||: |||||:||:| :: :||:|  | ||:|:| ||:  |:  :    | :|  : :
Db    301 TIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEYATLNY--YSSCR---KPTIRKKKTSL 355

Qy    121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLC--- 178
               ||      : |    :                  |    :|| |       |:
Db    356 LHPDSTRWIPDRISLQAPSNY---------------SLLDMRPPPPVMITLNNSMYWQE 399

Qy    178 SKLACCEWC---KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVL 234
           :  |   |   |  : :||   :|:  :|::||: | |  ||:|||| || :|  ||::
Db    400 FEDTCVYECLDGKDCQTFFCCYEECKSGSWRRGRIHIDVSELDSYSRVFFPTSFLLFNLV 459

Qy    235 YWLVCLNL 242
          ||:  | |
Db    460 YWVGYLYL 467


RESULT   6
JH0317
gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 13-Sep-1996
C;Accession: JH0317
R;Kofuji, P.; Wang, J.B.; Moss, S.J.; Huganir, R.L.; Burt, D.R.
J. Neurochem. 56, 713-715, 1991
A;Title: Generation of two forms of the gamma-aminobutyric acid A receptor gamma2-subuni
A;Reference number: JH0316; MUID:91108470
A;Accession: JH0317
A;Molecule type: mRNA
A;Residues: 1-474 <KOF>
A;Cross-references: GB:M57522
A;Experimental source: brain
C;Superfamily: acetylcholine receptor
C;Keywords: alternative splicing; glycoprotein; ion channel; neurotransmitter receptor;
F;1-38/Domain: signal sequence #status predicted <SIG>
F;29-375,384-474/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain,
F;39-474/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain, long fo
F;39-272/Domain: extracellular #status predicted <EXT>
F;273-295/Domain: transmembrane #status predicted <TM1>
F;299-321/Domain: transmembrane #status predicted <TM2>
F;333-355/Domain: transmembrane #status predicted <TM3>
F;356-450/Domain: intracellular #status predicted <INT>
F;451-473/Domain: transmembrane #status predicted <TM4>
F;51,128,246/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;381/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted


  Query Match             34.1%;  Score 448;  DB 2;  Length 474;
  Best Local Similarity   34.4%;  Pred. No. 6.5e-33;
  Matches   88;  Conservative   51;  Mismatches   63;  Indels   54;  Gaps    6;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          :||:::|::||| ||   | |:|  ::  :|||||||  :: |||||||||:|||||||
Db    259 VVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLS 318

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYN------QTKAHASPKLR 114
          | :||: |:|||:||:| ::::||:| | ||:|:  |:: : |      : |   :| ||
Db    319 TIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPLLR 378

Qy    115 -----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPS 166
                | |: |  : |   : |     |  :  : |          ||::   |::
Db    379 MFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD---CAS----- 424

Qy    167 PGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPV 226
                                      :||   ||    |: ||: | : ::|:|:|: ||
Db    424 ------------------------FFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPT 458

Qy    227 TFFFFNVLYWLVCLNL 242
           |  ||::||:  | |
Db    459 AFCLFNLVYWVSYLYL 474


RESULT   7
S03905
gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Aug-1999
C;Accession: S03905
R;Pritchett, D.B.; Sontheimer, H.; Shivers, B.D.; Ymer, S.; Kettenmann, H.; Schofield
Nature 338, 582-585, 1989
A;Title: Importance of a novel GABA(A) receptor subunit for benzodiazepine pharmacolo
A;Reference number: S03905; MUID:89181956
A;Accession: S03905
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-467 <PRI>
A;Cross-references: GB:X15376; NID:g31636; PIDN:CAA33437.1; PID:g31637
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein
F;1-39/Domain: signal sequence #status predicted <SIG>
F;40-467/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain #stat


  Query Match             34.1%;  Score 447;  DB 2;  Length 467;
  Best Local Similarity   34.3%;  Pred. No. 7.8e-33;
  Matches   85;  Conservative   52;  Mismatches   65;  Indels   46;  Gaps    5;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          :||:::|::||| ||   | |:|  ::  :|||||||  :: |||||||||:|||||||
Db    260 VVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLS 319

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRH---PR 117
          | :||: |:|||:||:| ::::||:| | ||:|:  |:: : |:  :    | :    |
Db    320 TIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPAPT 379

Qy    118 INSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPR 174
          |: |  : |   : |     |  :  : |        ||::   |::
Db    380 IDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD---CAS------------- 417

Qy    175 SLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVL 234
                          :||   ||    |: ||: | : ::|:|:|: ||  |  ||::
Db    417 ----------------FFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLV 459

Qy    235 YWLVCLNL 242
          ||:  | |
Db    460 YWVSYLYL 467


RESULT   8
JQ0077
gamma-aminobutyric acid receptor A gamma-2 chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Aug-1999
C;Accession: JQ0077; A37164
R;Shivers, B.D.; Killisch, I.; Sprengel, R.; Sontheimer, H.; Koehler, M.; Schofield,
Neuron 3, 327-337, 1989
```

```
A;Title: Two novel GABA-A receptor subunits exist in distinct neuronal subpopulations.
A;Reference number: JQ0076; MUID:90380375
A;Accession: JQ0077
A;Molecule type: mRNA
A;Residues: 1-466 <SHI>
A;Cross-references: GB:L08497; NID:g204217; PIDN:AAC42036.1; PID:g204218
A;Experimental source: brain
R;Malherbe, P.; Sigel, E.; Baur, R.; Persohn, E.; Richards, J.G.; Mohler, H.
J. Neurosci. 10, 2330-2337, 1990
A;Title: Functional characteristics and sites of gene expression of the alpha-1,beta-1,g
A;Reference number: A37164; MUID:90331051
A;Accession: A37164
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-21,'I',23-466 <MAL>
C;Comment: Neurotransmission effected by gamma-aminobutyric acid (GABA) is mediated main
C;Comment: The GABA-A receptor consists of subunits that are structurally related to lig
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F;1-38/Domain: signal sequence #status predicted <SIG>
F;39-466/Product: gamma-aminobutyric acid A receptor gamma-2 chain #status predicted <MA
F;273-295/Domain: transmembrane #status predicted <TM1>
F;299-321/Domain: transmembrane #status predicted <TM2>
F;333-355/Domain: transmembrane #status predicted <TM3>
F;443-465/Domain: transmembrane #status predicted <TM4>
F;51,128,246/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;189-203/Disulfide bonds: #status predicted


  Query Match             34.1%;  Score 447;  DB 2;  Length 466;
  Best Local Similarity   34.3%;  Pred. No. 7.8e-33;
  Matches   85;  Conservative   52;  Mismatches   65;  Indels   46;  Gaps    5;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           :||:::|::||| ||   | |:| ::  :||||||||  :: ||||||||||:|||||||
Db     259 VVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLS 318

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRH---PR 117
           | :||: |:|||:||:| ::::||:| | ||:|:  |:: : |:  :    | :    |
Db     319 TIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPAPT 378

Qy     118 INSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPR 174
           |: |  : |   : |    | :  : |        ||::   |::
Db     379 IDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD---CAS------------ 416

Qy     175 SLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVL 234
                       :||   ||    |: ||: | : ::|:|:|: ||  |  ||::
Db     416 ----------------FFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLV 458

Qy     235 YWLVCLNL 242
           ||:  | |
Db     459 YWVSYLYL 466


RESULT   9
JH0316
gamma-aminobutyric acid A receptor gamma 2 chain alternatively spliced precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 04-Sep-1998
C;Accession: JH0316
R;Kofuji, P.; Wang, J.B.; Moss, S.J.; Huganir, R.L.; Burt, D.R.
J. Neurochem. 56, 713-715, 1991
A;Title: Generation of two forms of the gamma-aminobutyric acid A receptor gamma2-subuni
A;Reference number: JH0316; MUID:91108470
A;Accession: JH0316
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-466 <KOF>
A;Cross-references: GB:M57522
C;Superfamily: acetylcholine receptor


  Query Match             34.1%;  Score 447;  DB 2;  Length 466;
  Best Local Similarity   34.3%;  Pred. No. 7.8e-33;
  Matches   85;  Conservative   52;  Mismatches   65;  Indels   46;  Gaps    5;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           :||:::|::||| ||   | |:| ::  :||||||||  :: ||||||||||:|||||||
Db     259 VVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLS 318

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRH---PR 117
           | :||: |:|||:||:| ::::||:| | ||:|:  |:: : |:  :    | :    |
Db     319 TIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPAPT 378

Qy     118 INSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPR 174
           |: |  : |   : |    | :  : |        ||::   |::
Db     379 IDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD---CAS------------ 416

Qy     175 SLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVL 234
                       :||   ||    |: ||: | : ::|:|:|: ||  |  ||::
Db     416 ----------------FFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLV 458

Qy     235 YWLVCLNL 242
           ||:  | |
Db     459 YWVSYLYL 466


RESULT  10
S12056
gamma-aminobutyric acid/benzodiazepine receptor gamma-1 chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S12056
R;Ymer, S.; Draguhn, A.; Wisden, W.; Werner, P.; Keinaenen, K.; Schofield, P.R.; Spre
EMBO J. 9, 3261-3267, 1990
A;Title: Structural and functional characterization of the gamma(1) subunit of GABA(A
A;Reference number: S12056; MUID:91006020
A;Accession: S12056
A;Molecule type: mRNA
A;Residues: 1-465 <YME>
A;Cross-references: GB:X57514; NID:g56175; PIDN:CAA40739.1; PID:g56176
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein


  Query Match             34.0%;  Score 446;  DB 2;  Length 465;
  Best Local Similarity   35.2%;  Pred. No. 9.6e-33;
  Matches   89;  Conservative   46;  Mismatches   62;  Indels   56;  Gaps    5;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           ::||||||::||| ||   | |:|  :| :||||||||  :: ||||||||||:|||||||
Db     258 IIMTIFFDLSRRMGYFTIQTYIPCILTVVLSWVSFWINKDAVPARTSLGITTVLTMTTLS 317

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYN----------QTKAHA 109
           | :||: |:|||:||:| ::::||:| | ||:|:  |::   |           ::|
Db     318 TIARKSLPKVSYVTAMDLFVSVCFIFVFAALMEYGTLHYFTSNNKGKTTRDRKLKSKTSV 377

Qy     110 SPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGS 169
           || |         | :      :     | :: :  | :  || |      |:
Db     378 SPGL------HAGSTLIPMNNISMPQGEDDYGYQCL--EGKD------CAT-------- 415

Qy     170 PEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFF 229
                              :||   ||   :|::||: | : ::|:|||: ||  |
Db     415 ----------------------FFCCFEDCRTGSWREGRIHIRIAKIDSYSRIFFPTAFA 452

Qy     230 FFNVLYWLVCLNL 242
           ||::||:  | |
Db     453 LFNLVYWVGYLYL 465


RESULT  11
B39272
gamma-aminobutyric acid receptor A gamma-2L chain - bovine
N;Contains: gamma-aminobutyric acid receptor A gamma-2S chain
C;Species: Bos primigenius taurus (cattle)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 30-May-1997
```

```
C;Accession: B39272; A39272
R;Whiting, P.; McKernan, R.M.; Iversen, L.L.
Proc. Natl. Acad. Sci. U.S.A. 87, 9966-9970, 1990
A;Title: Another mechanism for creating diversity in gamma-aminobutyrate type A receptor
sphorylation site.
A;Reference number: A39272; MUID:91088632
A;Accession: B39272
A;Molecule type: mRNA
A;Residues: 1-475 <WHI>
A;Cross-references: GB:M55563
A;Accession: A39272
A;Molecule type: mRNA
A;Residues: 1-376,385-475 <WH2>
A;Cross-references: GB:M55563
C;Superfamily: acetylcholine receptor
C;Keywords: alternative splicing; neurotransmitter receptor; phosphoprotein; transmembra
F;1-475/Product: gamma-aminobutyric acid receptor A gamma-2L chain #status predicted <MA
F;1-376,385-475/Product: gamma-aminobutyric acid receptor A gamma-2S chain #status predi
F;382/Binding site: phosphate (Ser) (covalent) #status predicted


  Query Match             33.8%;  Score 444;  DB 2;  Length 475;
  Best Local Similarity   34.4%;  Pred. No. 1.5e-32;
  Matches   88;  Conservative   50;  Mismatches   64;  Indels   54;  Gaps    6;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          :|||:: ::||| ||   | |:| ::  :|||||||  :: |||||||||:|||||||
Db    260 VVMTVYSDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLS 319

Qy     61 TFSRKNFPRVSYIITALDFYIAICFVFCFCALLEFAVLNFLIYN------QTKAHASPKLR 114
          | :||: |:|||:||:| ::::||:| | ||:|:  |:: : |      : |   :| ||
Db    320 TIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPLLR 379

Qy    115 -----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPS 166
               | |: |  : |   : |     |  :  : |        ||::   |::
Db    380 MFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD---CAS----- 425

Qy    167 PGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPV 226
                            :||   ||    |: ||: | : ::|:|:|: ||
Db    425 ------------------------FFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPT 459

Qy    227 TFFFFNVLYWLVCLNL 242
          |  ||::||:  | |
Db    460 AFCLFNLVYWVSYLYL 475


RESULT  12
S17551
gamma-aminobutyric acid/benzodiazepine receptor alpha-4 chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S17551
R;Wisden, W.; Herb, A.; Wieland, H.; Keinaenen, K.; Lueddens, H.; Seeburg, P.H.
FEBS Lett. 289, 227-230, 1991
A;Title: Cloning, pharmacological characteristics and expression pattern of the rat GABA
A;Reference number: S17551; MUID:92008629
A;Accession: S17551
A;Molecule type: mRNA
A;Residues: 1-552 <WIS>
A;Cross-references: GB:S55933; NID:g236011; PIDN:AAB19902.1; PID:g236012
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein


  Query Match             28.5%;  Score 374.5;  DB 2;  Length 552;
  Best Local Similarity   31.1%;  Pred. No. 3e-26;
  Matches   96;  Conservative   39;  Mismatches   95;  Indels   79;  Gaps    7;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          :|||::|:: |: ||   | |:|  :| :|| |||||  || ||||  |||:|||||||
Db    244 IVMTVYFHLRRKMGYFMIQTYIPCIMTVILSQVSFWINKESVPARTVFGITTVLTMTTLS 303

Qy     61 TFSRKNFPRVSYIITALDFYIAICFVFCFCALLEFAVLNFLIYNQ-----------TKAH 108
          :| : |:||| ||:|::||:|| | | ||:||| :|:    |              :
Db    304 ISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNIQMQKAKKKISKPPPEVP 363

Qy    109 ASPKLRHPRINS---RAHARTRARSRACARQHQEAFV---------CQIVTTEGSDGEER 156
          |:| |:      :     ||    | |  |  | |: |          |       |
Db    364 AAPVLKEKHTETSLQNTHANLNMRKRTNALVHSESDVNSRTEVGNHSSKTTAAQESSETT 423

Qy    157 PSCSAQQPPSP----------------------GSPEG---PRSLCSKLACCEWCKRFKK 191
          |       |:|                      || |   |  | | |   :  |  :
Db    424 PKAHLASSPNPFSRANAAETISAAARGLSSAASPSPHGTLQPAPLRSASARPAFGARLGR 483

Qy    192 YFCMV------------------PDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFN 232
              |                  |   |::           ::| |:|::|||||  ||
Db    484 IKTTVNTTGVPGNVSATPPPSAPPPSGSGTS----------KIDKYARILFPVTFGAFN 532

Qy    233 VLYWLVCLN 241
          ::||:| |:
Db    533 MVYWVVYLS 541


RESULT  13
S11087
gamma-aminobutyric acid receptor A, cerebellar - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Feb-1997
C;Accession: S11087
R;Lueddens, H.; Pritchett, D.B.; Koehler, M.; Killisch, I.; Keinaenen, K.; Monyer, H.
Nature 346, 648-651, 1990
A;Title: Cerebellar GABA(A) receptor selective for a behavioural alcohol antagonist.
A;Reference number: S11087; MUID:90348963
A;Accession: S11087
A;Molecule type: mRNA
A;Residues: 1-453 <LUE>
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein


  Query Match             28.1%;  Score 369;  DB 2;  Length 453;
  Best Local Similarity   32.3%;  Pred. No. 7.7e-26;
  Matches   83;  Conservative   42;  Mismatches   74;  Indels   58;  Gaps    4;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          ::||::|:: |: ||   | | |  :| :|| |||||  || ||||  |||:|||||||
Db    228 VIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPARTVFGITTVLTMTTLS 287

Qy     61 TFSRKNFPRVSYIITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
            :| : |:||| ||:|::||:|| | | ||:||| :|:    |::              :
Db    288 ISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQSQ------------KA 335

Qy    121 RAHARTRARSRACARQHQEAFVCQIVTTEGS---------------DGEERPSCSAQQP 164
            |:| |:      :  |:   :||    |                     |     :: |
Db    336 ERQAQTAAKPPVAKSKTTESLEAEIVVHSDSKYHLKKRISSLTLPIVPSSEASKVLSRTP 395

Qy    165 PSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVF 224
            | :|  |  |                  :|   |::           ::| |||::|
Db    396 ILPSTPVTPPLL------------------LPAIGGTS-----------KIDQYSRILF 425

Qy    225 PVTFFFFNVLYWLVCLN 241
          || |  ||::||:| |:
Db    426 PVAFAGFNLVYWIVYLS 442


RESULT  14
G01928
gamma-aminobutyric acid receptor A alpha-4 - human
N;Alternate names: GABA(A) receptor alpha-4 chain
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C;Accession: G01928; I38936
R;Yang, W.
submitted to the EMBL Data Library, June 1995
A;Reference number: G08852
A;Accession: G01928
```

A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-554 <YAN>
A;Cross-references: EMBL:U30461; NID:g905392; PIDN:AAB52519.1; PID:g905393
R;McLean, P.J.; Farb, D.H.; Russek, S.J.
Genomics 26, 580-586, 1995
A;Title: Mapping of the alpha 4 subunit gene (GABRA4) to human chromosome 4 defines an a
ed from an ancestral cluster.
A;Reference number: I38936; MUID:95331795
A;Accession: I38936
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-57 <MCL>
A;Cross-references: EMBL:U20166; NID:g924604; PIDN:AAA74743.1; PID:g924605
C;Genetics:
A;Gene: GDB:GABRA4
A;Cross-references: GDB:370881; OMIM:137141
A;Map position: 4p14-4q12
A;Introns: 29/2
A;Note: the list of introns is incomplete
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; neurotransmitter receptor
F;144,157,402,408/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.8%; Score 364.5; DB 2; Length 554;
Best Local Similarity 29.5%; Pred. No. 2.4e-25;
Matches 93; Conservative 46; Mismatches 87; Indels 89; Gaps 8;

```
Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          :|||::|:: |: ||   | |:|  :| :|| ||||| || |||| |||:|||||||
Db    244 IVMTVYFHLRRKMGYFMIQTYIPCIMTVILSQVSFWINKESVPARTVFGITTVLTMTTLS 303

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ-----------TKAH 108
           :| : |:|||:||:|::||:|| | | ||:||| :|:    |           :
Db    304 ISARHSLPKVSYLTAMDWFIAVCFAFVFSALIEFAAVNYFTNIQMEKAKRKTSKPPQEVP 363

Qy    109 ASP--KLRHPRINSR-AHARTRARSRACARQHQEAFV-----------CQIVTTEGSDG 153
          |:|  : :||    :  :|    | |  |  | |: |                |  | | |
Db    364 AAPVQREKHPEAPLQDTNANLNMRKRTNALVHSESDVGNRTEVGNHSSKSSTVVQESSKG 423

Qy    154 EERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRL---- 210
            |   ::   |:| |       |                :|    :: : | :
Db    424 TPRSYLASS--PNPFSRANAAETISAARA----------LPSASPTSIRTGHMPRKA 468

Qy    210 ------CIHVY-----------------------------------RLDNYSRVVFPV 226
                |||:                                    ::| |:|::|||
Db    469 SVGSASTRHVFGSRLQRIKTTVNTIGATGKLSATPPPSAPPPSGSGTSKIDKYARILFPV 528

Qy    227 TFFFFNVLYWLVCLN 241
          ||  ||::||:| |:
Db    529 TFGAFNMVYWVVYLS 543
```

RESULT 15
S06838
gamma-aminobutyric acid/benzodiazepine receptor alpha-4 chain precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
C;Accession: S06838
R;Ymer, S.; Draguhn, A.; Koehler, M.; Schofield, P.R.; Seeburg, P.H.
FEBS Lett. 258, 119-122, 1989
A;Title: Sequence and expression of a novel GABA(A) receptor alpha subunit.
A;Reference number: S06838; MUID:90076471
A;Accession: S06838
A;Molecule type: mRNA
A;Residues: 1-556 <YME>
A;Cross-references: EMBL:X61456; NID:g360; PIDN:CAA43696.1; PID:g361
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-556/Product: gamma-aminobutyric acid/benzodiazepine receptor alpha-4 chain #status

Query Match 27.6%; Score 362.5; DB 2; Length 556;
Best Local Similarity 32.1%; Pred. No. 3.6e-25;
Matches 101; Conservative 39; Mismatches 88; Indels 87; Gaps 10;

```
Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          :|||::|:: |: ||   | |:|  :| :|| ||||| || |||| |||:|||||||
Db    244 IVMTVYFHLRRKMGYFMIQTYIPCIMTVILSQVSFWINKESVPARTVFGITTVLTMTTLS 303

Qy     61 TFSRK-NFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ--------TKA---- 108
            :|  : |:||| ||:|::||:|| | | ||:||| :|:    |         :||
Db    304 ISARPISLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNVQMEKAKRKTSKAPQEI 363

Qy    108 HASPKLR--HPRIN-SRAHARTRARSRACARQHQEAFV----------CQIVTTEGSDGE 154
          |:| ||  ||       :|    | || |  | |: |          :  |      |
Db    364 SAAPVLREKHPETPLQNTNANLSMRKRANALVHSESDVGSRTDVGNHSSKSSTVVQGSSE 423

Qy    155 ERPSCSAQQPPSPGSPEG----------PRSLCSKLACCEWCKRFKKYFCMVPDCEGST 203
            |       |:| |               | :| |  :   :  |       ||    ||
Db    424 ATPQSYLASSPNPFSRANAAETISAARAIPSALPSTPSRTGYVPR------QVPVGSAST 477

Qy    204 WQQGRLCIHVY-----------------------------------RLDNYSRVVFPV 226
                ||:                                    ::| |:|::|||
Db    478 Q-------HVFGSRLQRIKTTVNSIGTSGKLSATTTPSAPPPSGSGTSKIDKYARILFPV 530

Qy    227 TFFFFNVLYWLVCLN 241
          ||  ||::||:| |:
Db    531 TFGAFNMVYWVVYLS 545
```

Search completed: March 11, 2000, 06:06:25
Job time: 123 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:17:32 ; Search time 41.51 Seconds
(without alignments)
404.212 Million cell updates/sec

Title: US-09-030-832-2
Perfect score: 1312
Sequence: 1 MVMTIFFNVSRRFGYVAFQN.....VFPVTFFFFNVLYWLVCLNL 242

Scoring table: BLOSUM62

Searched: 225878 seqs, 69334122 residues

Database : SPTREMBL_12:*

Word size : 0

Number of hits that pass the threshold : 225878
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1312	100.0	506	4	O15346	O15346 homo sapien
2	1312	100.0	505	4	Q99520	Q99520 homo sapien
3	846.5	64.5	384	11	O55209	O55209 rattus norv
4	360	27.4	438	13	Q90288	Q90288 carassius a
5	353	26.9	453	13	O57430	O57430 fugu rubrip
6	335.5	25.6	444	13	O93430	O93430 brachydanio
7	332	25.3	479	13	Q9YGQ5	Q9ygq5 morone amer
8	325.5	24.8	449	4	O75816	O75816 homo sapien
9	322.5	24.6	499	5	O17555	O17555 caenorhabdi
10	317	24.2	512	4	Q16323	Q16323 homo sapien
11	309	23.6	472	5	Q25035	Q25035 haemonchus
12	305.5	23.3	494	5	Q9XZW0	Q9xzw0 heliothis v
13	304.5	23.2	496	5	O18468	O18468 heliothis v
14	304	23.2	473	13	O42157	O42157 morone amer
15	302.5	23.1	256	5	Q26409	Q26409 blattella g
16	302.5	23.1	276	5	Q26412	Q26412 blattella g
17	299.5	22.8	254	5	Q26410	Q26410 blattella g
18	299.5	22.8	274	5	Q26411	Q26411 blattella g
19	297.5	22.7	533	5	Q16896	Q16896 aedes aegyp
20	297	22.6	476	13	Q9YGQ4	Q9ygq4 morone amer
21	295.5	22.5	442	5	Q19358	Q19358 caenorhabdi
22	294.5	22.4	481	5	O18471	O18471 heliothis v
23	292	22.3	365	5	O77249	O77249 apis mellif
24	290.5	22.1	416	5	Q17367	Q17367 caenorhabdi
25	290	22.1	487	5	Q9Y0I6	Q9y0i6 caenorhabdi
26	287	21.9	437	5	Q08861	Q08861 lymnaea sta
27	286.5	21.8	475	5	Q9Y0I4	Q9y0i4 caenorhabdi
28	285	21.7	466	13	Q9YGQ3	Q9ygq3 morone amer
29	280.5	21.4	487	5	Q9Y0I5	Q9y0i5 caenorhabdi
30	279	21.3	550	5	O17145	O17145 lucilia cup
31	279	21.3	601	5	P92138	P92138 drosophila
32	279	21.3	606	5	Q24561	Q24561 drosophila
33	278	21.2	506	5	Q9Y0I3	Q9y0i3 caenorhabdi
34	277	21.1	456	5	Q94900	Q94900 drosophila
35	277	21.1	430	13	Q90590	Q90590 gallus gall
36	276	21.0	470	13	Q9YGQ2	Q9ygq2 morone amer
37	275.5	21.0	444	5	O76472	O76472 musca domes
38	274.5	20.9	452	5	O76773	O76773 lucilia cup
39	271	20.7	657	5	O17547	O17547 caenorhabdi
40	271	20.7	478	5	O17548	O17548 caenorhabdi
41	271	20.7	478	5	P92023	P92023 caenorhabdi
42	268.5	20.5	686	5	Q24352	Q24352 drosophila
43	268	20.4	461	5	Q17327	Q17327 caenorhabdi
44	267.5	20.4	545	5	O18276	O18276 caenorhabdi
45	267	20.4	453	5	O77295	O77295 drosophila

ALIGNMENTS

RESULT 1
O15346
ID O15346 PRELIMINARY; PRT; 506 AA.
AC O15346;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE GABA RECEPTOR EPSILON SUBUNIT.
GN GABRE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 97480709.
RA WILKE K., GAUL R., KLAUCK S.M., POUSTKA A.;
RT "A gene in human chromosome band Xq28 (GABRE) defines a putative new
RT subunit class of the GABAA neurotransmitter receptor.";
RL Genomics 45:1-10(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA HANNA M.C., HALES T.G., KIRKNESS E.F.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Y09765; CAA70904.1; -.
DR EMBL; U92283; AAB94645.1; -.
DR EMBL; U92281; AAB94645.1; JOINED.
DR EMBL; U92282; AAB94645.1; JOINED.
DR PFAM; PF00065; neur_chan; 2.
DR PRINTS; PR00253; GABAARECEPTR.
SQ SEQUENCE 506 AA; 57971 MW; 95B5B1C4 CRC32;

Query Match 100.0%; Score 1312; DB 4; Length 506;
Best Local Similarity 100.0%; Pred. No. 2.1e-124;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     265 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 324

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     325 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 384

Qy     121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 444
```

```
Qy    181 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 504

Qy    241 NL 242
          ||
Db    505 NL 506
```

```
RESULT   2
Q99520
ID   Q99520      PRELIMINARY;      PRT;   505 AA.
AC   Q99520;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   PUTATIVE GABA-GATED CHLORIDE CHANNEL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97238072.
RA   GARRET M., BASCLES L., BOUE-GRABOT E., SARTOR P., CHARRON G.,
RA   BLOCH B., MARGOLSKEE R.F.;
RT   "An mRNA encoding a putative GABA-gated chloride channel is expressed
RT   in the human cardiac conduction system.";
RL   J. Neurochem. 68:1382-1389(1997).
DR   EMBL; Y07637; CAA68914.1; -.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00253; GABAARECEPTR.
SQ   SEQUENCE   505 AA;  57856 MW;  1E6B104C CRC32;
```

```
  Query Match            100.0%;  Score 1312;  DB 4;  Length 505;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-124;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    264 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 323

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 383

Qy    121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 443

Qy    181 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 503

Qy    241 NL 242
          ||
Db    504 NL 505
```

```
RESULT   3
O55209
ID   O55209      PRELIMINARY;      PRT;   384 AA.
AC   O55209;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   GABA-A RECEPTOR EPSILON SUBUNIT (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   HANNA M.C., HALES T.G., KIRKNESS E.F.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U92284; AAB93879.1; -.
DR   PFAM; PF00065; neur_chan; 2.
FT   NON_TER       1      1
SQ   SEQUENCE   384 AA;  45465 MW;  E5D0E1B9 CRC32;
```

```
  Query Match            64.5%;  Score 846.5;  DB 11;  Length 384;
  Best Local Similarity  65.7%;  Pred. No. 1.3e-77;
  Matches  163;  Conservative   26;  Mismatches   46;  Indels   13;  Gaps    4;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          |||| |||||||||:: ||||:||||||||||||||| |:| || |:|::||||| |||
Db    144 MVMTFFFNVSRRFGFIVFQNYIPSSVTTMLSWVSFWIKIEAAAARASVGVSSVLTMATLG 203

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
          ||||||||||||:|||||||||||| ||| |||| ||||| ||  :  ||||      ||
Db    204 TFSRKNFPRVSYLTALDFYIAICFVLCFCTLLEFTVLNFLTYNNIERQASPKFYQFPTNS 263

Qy    121 RAH------ARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPR 174
          ||:      |||||:|| ||| || |||:||| |  : ||       |  |    |: |
Db    264 RANARTRARARTRARARARQQQEVFVCEIVTYE-ENAEE----GYQWSPRSRRPQCPW 318

Qy    175 SLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVL 234
            | :   |   :  :||||||| |||::||:||:|||||||||||||:||:|||||||:
Db    319 RRCGRSYVC--FRVLRKYFCMVPGCEGNSWQRGRICIHVYRLDNYSRVLFPITFFFFNVV 376

Qy    235 YWLVCLNL 242
          ||::||||
Db    377 YWVICLNL 384
```

```
RESULT   4
Q90288
ID   Q90288      PRELIMINARY;      PRT;   438 AA.
AC   Q90288;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   NEUROTRANSMITTER RECEPTOR ALPHA SUBUNIT PRECURSOR.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC   Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC   Cyprinoidea; Cyprinidae; Cyprininae; Carassius.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 96373714.
RA   BAHN S., HARVEY R.J., DARLISON M.G., WISDEN W.;
RT   "Conservation of gamma-aminobutyric acid type A receptor alpha 6
RT   subunit gene expression in cerebellar granule cells.";
RL   J. Neurochem. 66:1810-1818(1996).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; X94342; CAA64068.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
DR   PRINTS; PR01079; GABAARALPHA.
KW   Signal; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW   Transmembrane.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    483       NEUROTRANSMITTER RECEPTOR ALPHA SUBUNIT.
SQ   SEQUENCE   438 AA;  49982 MW;  ED9DBE5C CRC32;
```

```
  Query Match            27.4%;  Score 360;  DB 13;  Length 438;
  Best Local Similarity  35.9%;  Pred. No. 1.4e-28;
  Matches   88;  Conservative   37;  Mismatches   72;  Indels   48;  Gaps    7;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
```

```
          :|||::|:: |: |:   | |:|  :| :|: |||||  || ||||  |||:|||||||
Db    227 IVMTVYFHLQRKMGFFLIQTYIPCIMTVILAQVSFWIDKESVPARTVFGITTVLTMTTLS 286

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
          :| : |:||| ||:|::||:|| | | ||:||| :|:    |
Db    287 ISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFSTLQ-------------- 331

Qy    121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 180
           |:   |  | |||           ||||       |  ||     |   : :
Db    331 -ANKELRRASMACAAVR-----------SDGE-----LVTNPLDPGGVLKKR--LNSV 369

Qy    181 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL-----DNYSRVVFPVTFFFFNVLY 235
          :  :  :|| :     ||      |||     :  |     | |||::||::|  ||::|
Db    370 SQRDAPERFSR--APQPDLH----QQGSTVPAINTLTTSIIDKYSRILFPLSFGAFNLVY 423

Qy    236 WLVCL 240
          |:| |
Db    424 WIVYL 428


RESULT   5
O57430
ID   O57430      PRELIMINARY;      PRT;   453 AA.
AC   O57430;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GAMMA-AMINOBUTYRIC ACID RECEPTOR BETA SUBUNIT (FRAGMENT).
GN   GABAB RECEPTOR.
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC   Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC   Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   RIBOLDI TUNNICLIFFE G.R., NYAKATURA G., PLATZER M., ELGAR G.S.,
RA   BRENNER S., ROSENTHAL A.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; AF016494; AAB94045.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
FT   NON_TER       1      1
SQ   SEQUENCE   453 AA;  52409 MW;  39C0992B CRC32;


  Query Match             26.9%;  Score 353;  DB 13;  Length 453;
  Best Local Similarity   29.1%;  Pred. No. 7.6e-28;
  Matches   85;  Conservative   43;  Mismatches   98;  Indels   66;  Gaps    5;

Qy      3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
          ::: | : |  ||   | |:|| : |:||||||||  ::: || :||:|:||||||: |
Db    175 LSLSFRIKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALGVTTVLTMTTINTH 234

Qy     63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRA 122
           |:  |:: |: |:| |:  |||| | ||||:| :|:: :   :  | |    |:
Db    235 LRETLPKIPYVKAIDVYLMGCFVFVFLALLEYAFVNYVFFG--RGPAQQKKLSERVGKSN 292

Qy    123 HARTRARSRACARQHQEAFVCQ----------------------------IVTTEGSDG 153
          : | |   :    |   :   |                            :||   :
Db    293 NERMRYEEKRLREQDSISVPFQTNTFRSFTQRRNLYLEEQRKVGVDPYGNILLTTLEMNN 352

Qy    154 EERPS----------------CSAQQPPSPGSPEG-------PRSLCSKLACCEWCKRF 189
          |  ||                |  |   |  |          ||     | |   :|
Db    353 EVMPSDVGSSVSDSRNSVMSFDSSGVQFRKPMVPRDGFSHHSLDRSAMRSRANCRLRRRS 412

Qy    190 KKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 241
          |    :|:              |  :| :|||:||:|| |||::|||  :|
Db    413 SKLKLKIPNLS----------DVSTIDKWSRVIFPITFGFFNLIYWLYYVN 453
```

```
RESULT   6
O93430
ID   O93430      PRELIMINARY;      PRT;   444 AA.
AC   O93430;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GLYCINE RECEPTOR, ALPHAZ1 SUBUNIT PRECURSOR.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC   Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC   Cyprinoidea; Cyprinidae; Rasborinae; Danio.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   DAVID-WATINE B., GOBLET C., DE SAINT JAN D., FUCILE S., DEVIGNOT V.,
RA   BREGESTOVSKI P., KORN H.;
RT   "A novel alpha subunit of the glycine receptor from zebrafish: primary
RT   structure and functional expression.";
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED ION
CC       CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHLORIDE
CC       CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF
CC       NEURONAL FIRING).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- DOMAIN: THE N-TERMINAL DOMAIN CARRIES STRUCTURAL DETERMINANTS
CC       ESSENTIAL FOR AGONIST AND ANTAGONIST BINDING. TM2 IS THOUGHT TO
CC       FORM THE INNERT WALL OF THE CHLORIDE CHANNEL. THE CYTOPLASMIC LOOP
CC       MAY BE AN IMPORTANT DETERMINANT OF CHANNEL INACTIVATION KINETICS.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; AJ005812; CAA06711.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        26    444       GLYCINE RECEPTOR, ALPHAZ1 SUBUNIT.
FT   DOMAIN       26    242       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    248    268       PROBABLE.
FT   TRANSMEM    277    294       PROBABLE.
FT   TRANSMEM    311    331       PROBABLE.
FT   DOMAIN      343    346       POLY-ARG.
FT   DOMAIN      332    415       CYTOPLASMIC (PROBABLE).
FT   DOMAIN      381    384       POLY-ASN.
FT   TRANSMEM    416    436       PROBABLE.
FT   DISULFID    162    176       BY SIMILARITY.
FT   DISULFID    222    233       BY SIMILARITY.
SQ   SEQUENCE   444 AA;  50765 MW;  3405DED8 CRC32;


  Query Match             25.6%;  Score 335.5;  DB 13;  Length 444;
  Best Local Similarity   30.6%;  Pred. No. 4.3e-26;
  Matches   78;  Conservative   32;  Mismatches   60;  Indels   85;  Gaps    6;

Qy      7 FNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKN 66
          |:: |: ||   | |:|| :  :|||||||  ::|||  ||||:||||||  : || :
Db    238 FHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRAS 297

Qy     67 FPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHART 126
           |:|||: |:| ::|:| :| | ||||:| :||:
Db    298 LPKVSYVKAIDIWMAVCLLFVFSALLEYAAVNFI------------------------- 332

Qy    127 RARSRACARQHQEAFVCQ-----IVTTEGSDGE-------ERPSC------------SAQ 162
                ||||:|    |      :   |  ||          |:|            :
Db    332 -------ARQHKELLRFQRRRRHLKEDEAGDGRFSFAAYGMGPACLQAKDGMAIKGNNNN 384

Qy    163 QPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 222
          | |   ||             :  :  :| |                      |:|  |||
Db    385 APTSTNPPE------------KTVEEMRKLFIS----------------RAKRIDTVSRV 416

Qy    223 VFPVTFFFFNVLYWL 237
```

```
          ||: |  ||: ||:
Db    417 AFPLVFLIFNIFYWI 431


RESULT   7
Q9YGQ5
ID   Q9YGQ5      PRELIMINARY;      PRT;   479 AA.
AC   Q9YGQ5;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-2A SUBUNIT PRECURSOR.
OS   Morone americana (white perch).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC   Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC   Perciformes; Percoidei; Moronidae; Morone.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=RETINA;
RX   MEDLINE; 99022091.
RA   QIAN H., DOWLING J.E., RIPPS H.;
RT   "Molecular and pharmacological properties of GABA-rho subunits from
RT   white perch retina.";
RL   J. Neurobiol. 37:305-320(1998).
DR   EMBL; AF101034; AAD17893.1; -.
KW   Receptor.
SQ   SEQUENCE   479 AA;  55381 MW;  0CEFE4A0 CRC32;


  Query Match             25.3%;  Score 332;  DB 13;  Length 479;
  Best Local Similarity   33.3%;  Pred. No. 1e-25;
  Matches   83;  Conservative   43;  Mismatches   81;  Indels   42;  Gaps    7;

Qy       5 IFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSR 64
           | | : |   :   | | |:::  |||||||||   : ||| |||||:||||:|: |
Db     256 INFTLRRHIFFFLLQTYFPATLMVMLSWVSFWIDRRAVPARVSLGITTVLTMSTIITGVN 315

Qy      65 KNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHA 124
            : |||||| |:| |: : ||| | ::||:| :|:|   | :     |:|
Db     316 ASMPRVSYIKAVDIYLWVSFVFVFLSVLEYAAVNYLSTVQDRRER--KMRE--------- 365

Qy     125 RTRARSRACARQHQEAFVCQIVTT------EGSDGEERPSCSAQQPPSPGSPEGPRSLCS 178
           | |::|  |         | |  |      :|:  |   :  |     |  ||  |  |:
Db     365 RARSQSLPC--------TCGISQTRTMTMLDGTYSEADTNSLAGYTEEPMVPERSRKSCT 416

Qy     179 KLACCEWCKRFKKYFCMVPDC---EGSTWQQGR------LCIHVYRLDNYSRVVFPVTFF 229
           ::         :|   ||  |   | :| :: :     :  : : :| |||::|| ::
Db     417 EV--------LEKPEHMVVICVSSESTTTKKKKSLRAINIIQNTHAIDKYSRMIFPGSYI 468

Qy     230 FFNVLYWLV 238
           |||::|| |
Db     469 FFNLIYWSV 477


RESULT   8
O75816
ID   O75816 .    PRELIMINARY;      PRT;   449 AA.
AC   O75816;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GLYCINE RECEPTOR ALPHA 3 SUBUNIT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 98344067.
RA   NIKOLIC Z., LAUBE B., WEBER R.G., LICHTER P., KIOSCHIS P., POUSTKA A.,
RA   MULHARDT C., BECKER C.M.;
RT   "The human glycine receptor subunit alpha3. Glra3 gene structure,
RT   chromosomal localization, and functional characterization of
RT   alternative transcripts.";
RL   J. Biol. Chem. 273:19708-19714(1998).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; U93917; AAC39917.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   449 AA;  51963 MW;  3170F74B CRC32;


  Query Match             24.8%;  Score 325.5;  DB 4;  Length 449;
  Best Local Similarity   29.9%;  Pred. No. 4.4e-25;
  Matches   72;  Conservative   41;  Mismatches   67;  Indels   61;  Gaps    5;

Qy       7 FNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKN 66
           |:: |: ||   | |:|| :  :|||||||  ::|||| :||||:||||||  : || :
Db     247 FHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVALGITTVLTMTTQSSGSRAS 306

Qy      67 FPRVSYITALDFYIAICFVFCFCALLEFAVLNF--------LIYNQTKAHASPKLRHPRI 118
            |:||| |:| ::|:| :| | ||||:| :||        | : : : :   ::|  |
Db     307 LPKVSYVKAIDIWMAVCLLFVFSALLEYAAVNFVSRQHKELLRFRRKRKNKDDEVRESRF 366

Qy     119 NSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCS 178
           :  |:                                |   |:   :|  |  |  :
Db     367 SFTAYGM----------------------------GPCLQAKDGMTPKGPNHPVQVMP 396

Qy     179 KLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCI-HVYRLDNYSRVVFPVTFFFPNVLYWL 237
           |                  ||      :  :: |    ::|  ||  ||: |  ||: ||:
Db     397 K----------------SPD------EMRKVFIDRAKKIDTISRACFPLAFLIFNIFYWV 434

Qy     238 V 238
           :
Db     435 I 435


RESULT   9
O17555
ID   O17555      PRELIMINARY;      PRT;   499 AA.
AC   O17555; O18279;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   ZC482.5 PROTEIN.
GN   ZC482.5.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC   Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   MCMURRAY A.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94150718.
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA   GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA   JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA   LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA   THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA   WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; Z93397; CAB07722.1; -.
DR   EMBL; Z93372; CAB07722.1; JOINED.
```

```
DR   EMBL; Z93372; CAB07549.1; -.
DR   EMBL; Z93397; CAB07549.1; JOINED.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   499 AA;  57553 MW;  34743390 CRC32;


  Query Match             24.6%;  Score 322.5;  DB 5;  Length 499;
  Best Local Similarity   29.6%;  Pred. No. 9.8e-25;
  Matches   82;  Conservative   43;  Mismatches   79;  Indels   73;  Gaps    8;

Qy       2 VMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGT 61
           |: ::| : |: ||   | | | ::  ::|||||||  |::||| |||| :||:|:|:|
Db     244 VLNVYFKLQRQQGYYILQIYTPCTLVVVMSWVSFWINKEASPARVSLGIMTVLSMSTIGF 303

Qy      62 FSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNF--LIYNQTKAHASPKLRHPRIN 119
             | : |:||: |||| ||  |||| | |::|:||:|:  ::| : : |    |
Db     304 GLRTDLPKVSHSTALDVYILTCFVFLFAAMVEYAVINYAQIVYIRKQIHDLKGL------ 358

Qy     120 SRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSK 179
                        |   : |: |  |  |  |         :    |      ::
Db     358 ----------------EQNTAMGQMFTA-GLMGARRRDTIQVDDLTVEKEE------AR 393

Qy     180 LACCEWCKR--FKKYFCMVPDCEGST---WQ---------------------------- 206
           |    | |:  ||       | :|:|   ||
Db     394 LKAVPWWKKLCFK-------DEQGNTSSEWQLEKKINFEKNSPVFYRMAVKAAIAKKTLR 446

Qy     206 QGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 242
             |     | ::||:|:: ||  :  ||| ||:  |:|
Db     447 NGDPAEVVNKIDNFSKLAFPTLYIIFNVFYWVAYLHL 483


RESULT  10
Q16323
ID   Q16323      PRELIMINARY;      PRT;   512 AA.
AC   Q16323;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GABAA RECEPTOR BETA 2 SUBUNIT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95223118.
RA   MCKINLEY D.D., LENNON D.J., CARTER D.B.;
RT   "Cloning, sequence analysis and expression of two forms of mRNA coding
RT   for the human beta 2 subunit of the GABAA receptor.";
RL   Brain Res. Mol. Brain Res. 28:175-179(1995).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; S77553; AAB33982.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
DR   PRINTS; PR01160; GABAARBETA.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   512 AA;  59150 MW;  FF0E2B52 CRC32;


  Query Match             24.2%;  Score 317;  DB 4;  Length 512;
  Best Local Similarity   28.9%;  Pred. No. 3.6e-24;
  Matches   85;  Conservative   44;  Mismatches   97;  Indels   68;  Gaps    8;

Qy       3 MTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTF 62
           ::: | : |  ||   | |:|| : |:||||||||  ::: || :||||:||||||: |
Db     232 LSLSFKLKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALGITTVLTMTTINTH 291

Qy      63 SRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYN---QTKAHASPK------- 113
            |:  |:: |: |:| |:  |||| | ||||:|::|:: :    | :  |: |
Db     292 LRETLPKIPYVKAIDMYLMGCFVFVFMALLEYALVNYIFFGRGPQRQKKAAEKAASANNE 351

Qy     113 ----------------------LRHPRINSRAHARTRAR--SRACARQHQEAFVC---- 144
                                 |  |  |     ||     |       |:   :
Db     352 KMRLDVNKIFYKDIKQNGTQYRSLWDPTGNLSPTRRTTNYDFSLYTMDPHENILLSTLEI 411

Qy     144 --QIVTTEGSDGEERP-------SCSAQQPPSPGSPEG-------PRSLCSKLACCEWCK 187
             :: |:|   |   |          |: |    | |           | :  | :     :
Db     412 KNEMATSEAVMGLGDPRSTMLAYDASSIQYRKAGLPRHSFGRNALERHVAQKKSRLR--R 469

Qy     188 RFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 241
           |  :    :||            |  :| :||: ||| | |||::|||  :|
Db     470 RASQLKITIPD-----------LTDVNAIDRWSRIFFPVVFSFFNIVYWLYYVN 512


RESULT  11
Q25035
ID   Q25035      PRELIMINARY;      PRT;   472 AA.
AC   Q25035;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GABA A/GLYCINE RECEPTOR SUBUNIT.
GN   HG1.
OS   Haemonchus contortus.
OC   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Strongylida;
OC   Trichostrongyloidea; Trichostrongylidae; Haemonchinae; Haemonchus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95041083.
RA   LAUGHTON D.L., AMAR M., THOMAS P., TOWNER P., HARRIS P., LUNT G.C.,
RA   WOLSTENHOLME A.J.;
RT   "Cloning of a putative inhibitory amino acid receptor subunit from the
RT   parasitic nematode Haemonchus contortus.";
RL   Recept. Channels 2:155-163(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; X73584; CAA51991.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
FT   VARIANT     231    231       G -> D.
FT   VARIANT     329    329       S -> A.
SQ   SEQUENCE   472 AA;  54732 MW;  7B8A2213 CRC32;


  Query Match             23.6%;  Score 309;  DB 5;  Length 472;
  Best Local Similarity   29.6%;  Pred. No. 2.1e-23;
  Matches   76;  Conservative   47;  Mismatches   78;  Indels   56;  Gaps    6;

Qy       2 VMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGT 61
           |: ::| : |: ||   | | | ::  ::|||||||  |::||| :||| :||:|:|||
Db     236 VLKVYFKLQRQQGYYVLQIYTPCTLLVVMSWVSFWINKEASPARVALGIMTVLSMSTLGF 295

Qy      62 FSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNF--LIYNQTKAHASPKLRHPRIN 119
             | : |:||: |||| ||  || | | |::|::|:|:  ::| : : |    |     :
Db     296 GLRTDLPKVSHSTALDIYILSCFGFVFAAMVEYSVINYAQIVYIRKQVHDLKGLE----S 351

Qy     120 SRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSK 179
           :||  : |  :          :|    |:       : |: |  |
Db     352 NRAMEKMRLFTAGLMGARRETI--QVDDLVLDEEEDLPWYS------------------ 391

Qy     180 LACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIH----------------VYRLDNYSRVV 223
             | : |: ||   |            |: :                  | |:|: |:|:
Db     391 ---CFFRKKTKKQSSMF----------YRMAVKAAKARRKLKMKDPAKVVNRVDDVSKVI 437

Qy     224 FPVTFFFFNVLYWLVCL 240
           ||  :  ||:|||:  |
Db     438 FPSLYVLFNILYWVAFL 454
```

```
RESULT  12
Q9XZW0
ID   Q9XZW0      PRELIMINARY;      PRT;   494 AA.
AC   Q9XZW0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GABA-GATED CHLORIDE CHANNEL.
OS   Heliothis virescens (Noctuid moth) (Owlet moth).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Noctuoidea; Noctuidae; Heliothinae; Heliothis.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 99228868.
RA   WOLFF M.A., WINGATE V.P.;
RT   "Characterization and comparative pharmacological studies of a
RT   functional gamma-aminobutyric acid (GABA) receptor cloned from the
RT   tobacco budworm, Heliothis virescens (Noctuidae:Lepidoptera).";
RL   Invert. Neurosci. 3:305-315(1999).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; AJ224513; CAB41615.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   494 AA;  54866 MW;  AC357B4F CRC32;


  Query Match             23.3%;  Score 305.5;  DB 5;  Length 494;
  Best Local Similarity   29.2%;  Pred. No. 5e-23;
  Matches   75;  Conservative   42;  Mismatches   83;  Indels   57;  Gaps    6;

Qy      14 GYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYI 73
           ||    | |:|| :  ::|||||||:    : ||| |||:|:|||||||| : :    |::||:
Db     252 GYYLIQIYIPSGLIVIISWVSFWLNRNATPARVSLGVTTVLTMTTLMSSTNAALPKISYV 311

Qy      74 TALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRAC 133
           ::| |:  |||  | :|||:| : ::                ||  |    |  :  |
Db     312 KSIDVYLGTCFVMVFTSLLEYATVGYMA-------------KRIQMRKQRFTAVQKMAA 357

Qy     134 ARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEW----CKRF 189
           :: |           ||   |  ||:  | | :    |   |:|:  :     | :
Db     358 EKKMQ------------IDG---PPGSAEPIPPPRTSTLSRPPPSRLSEVRFKVHDPKAY 402

Qy     190 KKYFCMVPDCEGSTWQQGRL------------CIHVYR------------LDNYSRVVFP 225
           |   :     |:  | |                :|  :           :| |||:|||
Db     403 SKGGTLENTINGARGQPGPAPPADEQAGPPPHLVHASKGINKLLGTTPSDIDKYSRIVFP 462

Qy     226 VTFFFFNVLYWLVCLNL 242
           | |  ||:||:: |::
Db     463 VCFVCFNLMYWIIYLHV 479


RESULT  13
O18468
ID   O18468      PRELIMINARY;      PRT;   496 AA.
AC   O18468;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GABA-GATED CHLORIDE CHANNEL ISOFORM A2.
OS   Heliothis virescens (Noctuid moth) (Owlet moth).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Noctuoidea; Noctuidae; Heliothinae; Heliothis.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEADS;
RA   YUHAS D.A., HALLING B.P.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; AF006189; AAB62563.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
DR   PRINTS; PR01160; GABAARBETA.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   496 AA;  55142 MW;  2CDCCF93 CRC32;


  Query Match             23.2%;  Score 304.5;  DB 5;  Length 496;
  Best Local Similarity   26.8%;  Pred. No. 6.4e-23;
  Matches   73;  Conservative   37;  Mismatches   83;  Indels   79;  Gaps    6;

Qy      11 RRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV 70
           |  ||   | |:|| :  ::|||||||:    : ||| |||:|:|||||||| : :    |::
Db     249 RSMGYYLIQIYIPSGLIVIISWVSFWLNRNATPARVSLGVTTVLTMTTLMSSTNAALPKI 308

Qy      71 SYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARS 130
           ||: ::| |:  |||  | :|||:| : ::                ||  |    | :
Db     309 SYVKSIDVYLGTCFVMVFASLLEYATVGYMA-------------KRIQMRKQRFTAVQK 354

Qy     131 RACARQHQEAFVCQIVTTEGSDGEERP-----SCSAQQPPSP----------------- 168
           |  :: |           :| |   |     : :  :|| |
Db     355 MAAEKKMQ---------IDGPPGSAEPIPPPRTSTLSRPPPPSRLSEVRFKVHDPKAYSK 405

Qy     168 -----------GSPEGPRSLCSKLA-----CCEWCKRFKKYFCMVPDCEGSTWQQGRLC 210
                     |   ||     : |          |   |    |
Db     406 GGTLENTINGARGPAPGPAPPADEEAGPPPHLVHASKGINKLLGTTPS----------- 454

Qy     211 IHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 242
                :| |||:|||| |  ||::||:: |::
Db     454 ----DIDKYSRIVFPVCFVCFNLMYWIIYLHV 481


RESULT  14
O42157
ID   O42157      PRELIMINARY;      PRT;   473 AA.
AC   O42157;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GABAC RECEPTOR SUBUNIT RHO-1B.
OS   Morone americana (white perch).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC   Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC   Perciformes; Percoidei; Moronidae; Morone.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=RETINA;
RA   QIAN H., HYATT G., SCHANZER A., HAZRA R., HACKAM A., CUTTING G.R.,
RA   DOWLING J.E.;
RL   Vis. Neurosci. 0:0-0(1997).
DR   EMBL; AF010287; AAB66600.1; -.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
SQ   SEQUENCE   473 AA;  54396 MW;  60C7B97B CRC32;


  Query Match             23.2%;  Score 304;  DB 13;  Length 473;
  Best Local Similarity   30.9%;  Pred. No. 6.8e-23;
  Matches   77;  Conservative   35;  Mismatches   89;  Indels   48;  Gaps    5;

Qy       5 IFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSR 64
           | | : |    :    | | |::: |||||||||    : ||| |||||:||||:|: |
Db     256 INFTLRRHIFFFLLQTYFPATLMVMLSWVSFWIDRRAVPARVSLGITTVLTMSTIITGVN 315

Qy      65 KNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRH--------- 116
            : |||||| |:| |: : ||| | ::||:| :|:|     :     |||
Db     316 ASMPRVSYIKAVDIYLWVSFVFVFLSVLEYAAVNYL--TTVRDGKDRKLREKVREQSQTL 373
```

```
Qy    116 PRINSRAHARTR----ARSRACARQHQEAFVCQIVTTEGSDGEER--PSCSAQQPPSPGS 169
          |     :||||       | | |          :   : |: :||     |    |:
Db    374 PCTCGMSHARTMMLDGTYSEADANSLAGYTRASMAAEDASEKQERMVVHLSLDNEPTGTK 433

Qy    170 PEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFF 229
           :| |                                |:  : : :| |||::||  :
Db    434 KKGIRGF------------------------------RIIQNTHAIDTYSRMIFPGAYI 462

Qy    230 FFNVLYWLV 238
            ||::|| |
Db    463 LFNLIYWCV 471


RESULT  15
Q26409
ID   Q26409      PRELIMINARY;      PRT;   256 AA.
AC   Q26409;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   GABA RECEPTOR RDL 1 SUBUNIT (FRAGMENT).
OS   Blattella germanica (German cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC   Blaberoidea; Blattellidae; Blattellinae; Blattella.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   KAKU K., MATSUMURA F.;
RL   Comp. Biochem. Physiol. 108:367-376(1994).
DR   EMBL; S76550; AAB33733.1; -.
DR   PFAM; PF00065; neur_chan; 2.
FT   NON_TER       1      1
SQ   SEQUENCE   256 AA;  28637 MW;  4E40D171 CRC32;


  Query Match             23.1%;  Score 302.5;  DB 5;  Length 256;
  Best Local Similarity   27.0%;  Pred. No. 5.3e-23;
  Matches   73;  Conservative   39;  Mismatches   67;  Indels   91;  Gaps    7;

Qy     11 RRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV 70
          |  ||    | |:|| :  ::|||||:   : ||| :||:|:|||||| : :    |::
Db     25 RSMGYYLIQIYIPSGLIVIISWVSFWLNRNATPARVALGVTTVLTMTTLMSSTNAALPKI 84

Qy     71 SYITALDFYIAICFVFCFCALLEFAVLNFL----------------IYNQTK-----AHA 109
          ||: ::| |:  |||  | :|||:| : ::                |  | |     |||
Db     85 SYVKSIDVYLGTCFVMVFASLLEYATVGYMAKRIQMRKNRFLAIQKIAEQKKAGMDTAHA 144

Qy    110 SP----------------KLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSD 152
          |                 |:  |: :|:                        |  |
Db    145 PPPGPPGEGDHAPKQTVRFKVHDPKAHSKGGTLEN----------------TINGRA 185

Qy    153 GEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIH 212
          ||  :     |:|    |:             |  | : :|
Db    186 DEEVAA------PAPQHLIHPK-----------KDINKLYGITPS------------- 214

Qy    213 VYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 242
             :| |||:|||| |  ||::||:: |::
Db    214 --DIDKYSRIVFPVCFICFNLMYWIIYLHI 241


Search completed: March 11, 2000, 06:18:26
Job time: 54 sec
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:25:57 ; Search time 22.24 Seconds
(without alignments)
324.968 Million cell updates/sec

Title: US-09-030-832-2
Perfect score: 1312
Sequence: 1 MVMTIFFNVSRRFGYVAFQN.....VFPVTFFFFNVLYWLVCLNL 242

Scoring table: BLOSUM62

Searched: 82229 seqs, 29864866 residues

Database : SwissProt_38:*

Word size : 0

Number of hits that pass the threshold : 82229

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1312	100.0	506	1	GAE_HUMAN	P78334 homo sapien
2	532.5	40.6	457	1	GAC4_CHICK	P34904 gallus gall
3	458.5	34.9	467	1	GAC3_HUMAN	Q99928 homo sapien
4	453	34.5	474	1	GAC2_CHICK	P21548 gallus gall
5	452.5	34.5	467	1	GAC3_MOUSE	P27681 mus musculu
6	452.5	34.5	467	1	GAC3_RAT	P28473 rattus norv
7	452	34.5	475	1	GAC2_BOVIN	P22300 bos taurus
8	447	34.1	467	1	GAC2_HUMAN	P18507 homo sapien
9	447	34.1	466	1	GAC2_RAT	P18508 rattus norv
10	446	34.0	465	1	GAC1_RAT	P23574 rattus norv
11	445	33.9	474	1	GAC2_MOUSE	P22723 mus musculu
12	380	29.0	465	1	GAA6_CHICK	Q90845 gallus gall
13	374.5	28.5	552	1	GAA4_RAT	P28471 rattus norv
14	369	28.1	453	1	GAA6_RAT	P30191 rattus norv
15	364.5	27.8	554	1	GAA4_HUMAN	P48169 homo sapien
16	362.5	27.6	556	1	GAA4_BOVIN	P20237 bos taurus
17	362	27.6	443	1	GAA6_MOUSE	P16305 mus musculu
18	357	27.2	453	1	GAA6_HUMAN	Q16445 homo sapien
19	349	26.6	488	1	GAB4_CHICK	P24045 gallus gall
20	348	26.5	473	1	GAB3_HUMAN	P28472 homo sapien
21	348	26.5	449	1	GRA1_MOUSE	Q64018 mus musculu
22	345	26.3	473	1	GAB3_MOUSE	P15433 mus musculu
23	345	26.3	449	1	GRA1_HUMAN	P23415 homo sapien
24	341.5	26.0	462	1	GAA5_HUMAN	P31644 homo sapien
25	341.5	26.0	464	1	GAA5_RAT	P19969 rattus norv
26	340.5	26.0	452	1	GRA2_HUMAN	P23416 homo sapien
27	340	25.9	449	1	GRA1_RAT	P07727 rattus norv
28	335.5	25.6	444	1	GRAZ_BRARE	O93430 brachydanio
29	335	25.5	474	1	GAB2_HUMAN	P47870 homo sapien
30	334.5	25.5	455	1	GAA1_CHICK	P19150 gallus gall
31	334.5	25.5	492	1	GAA3_MOUSE	P26049 mus musculu
32	334.5	25.5	452	1	GRA2_RAT	P22771 rattus norv
33	333.5	25.4	496	1	GAB3_DROME	Q08832 drosophila
34	333	25.4	456	1	GAA1_BOVIN	P08219 bos taurus
35	333	25.4	456	1	GAA1_HUMAN	P14867 homo sapien
36	333	25.4	455	1	GAA1_MOUSE	P18504 mus musculu
37	333	25.4	465	1	GRA3_HUMAN	O75311 homo sapien
38	332	25.3	474	1	GAB2_MOUSE	P15432 mus musculu
39	331.5	25.3	474	1	GAB1_BOVIN	P08220 bos taurus
40	331.5	25.3	499	1	GAB_LYMST	P26714 lymnaea sta
41	330.5	25.2	476	1	GAB3_CHICK	P19019 gallus gall
42	329.5	25.1	474	1	GAB1_HUMAN	P18505 homo sapien
43	329.5	25.1	474	1	GAB1_RAT	P15431 rattus norv
44	329	25.1	451	1	GAA2_BOVIN	P10063 bos taurus
45	329	25.1	451	1	GAA2_HUMAN	P47869 homo sapien

ALIGNMENTS

```
RESULT   1
GAE_HUMAN
ID   GAE_HUMAN      STANDARD;      PRT;   506 AA.
AC   P78334; O15345;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR EPSILON SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97192095.
RA   DAVIES P.A., HANNA M.C., HALES T.G., KIRKNESS E.F.;
RT   "Insensitivity to anaesthetic agents conferred by a class of GABA(A)
RT   receptor subunit.";
RL   Nature 385:820-823(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97480709.
RA   WILKE K., GAUL R., KLAUCK S.M., POUSTKA A.;
RT   "A gene in human chromosome band Xq28 (GABRE) defines a putative new
RT   subunit class of the GABAA neurotransmitter receptor.";
RL   Genomics 45:1-10(1997).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. ASSOCIATES WITH ALPHA AND BETA
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: FOUND IN MANY TISSUE. HIGHEST LEVELS OF
CC       EXPRESSION IN ADULT HEART AND PLACENTA.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U66661; AAB49284.1; -.
DR   EMBL; Y09763; CAA70903.1; -.
DR   EMBL; Y09764; CAA70903.1; JOINED.
DR   MIM; 300093; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane.
FT   SIGNAL        1      ?       POTENTIAL.
FT   CHAIN         ?    506       GAMMA-AMINOBUTYRIC-ACID RECEPTOR EPSILON
FT                                SUBUNIT.
FT   DOMAIN        ?    253       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    254    274       POTENTIAL.
FT   TRANSMEM    281    301       POTENTIAL.
FT   TRANSMEM    344    364       POTENTIAL.
FT   DOMAIN      365    485       CYTOPLASMIC (PROBABLE).
```

```
FT   TRANSMEM    486    506       POTENTIAL.
FT   CARBOHYD    134    134       POTENTIAL.
FT   CARBOHYD    252    252       POTENTIAL.
FT   DISULFID    195    209       BY SIMILARITY.
FT   CONFLICT    102    102       A -> S (IN REF. 2).
FT   CONFLICT    245    245       F -> L (IN REF. 2).
FT   CONFLICT    471    471       G -> A (IN REF. 2).
FT   CONFLICT    502    502       V -> F (IN REF. 2).
SQ   SEQUENCE   506 AA;  57955 MW;  6BC8394B CRC32;
```

```
  Query Match             100.0%;  Score 1312; DB 1;  Length 506;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-109;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     265 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 324

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     325 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 384

Qy     121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 444

Qy     181 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     445 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCL 504

Qy     241 NL 242
           ||
Db     505 NL 506
```

```
RESULT   2
GAC4_CHICK
ID   GAC4_CHICK     STANDARD;      PRT;   457 AA.
AC   P34904;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG4.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93387470.
RA   HARVEY R.J., KIM H.-C., DARLISON M.G.;
RT   "Molecular cloning reveals the existence of a fourth gamma subunit of
RT   the vertebrate brain GABAA receptor.";
RL   FEBS Lett. 331:211-216(1993).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: ABUNDANT IN SEVERAL BRAIN REGIONS, INCLUDING
CC       THE ECTOSTRIATUM, NUCLEUS ROTUNDUS AND HYPERSTRIATUM VENTRALE.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X73533; CAA51939.1; -.
DR   PIR; S38296; S38296.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    457       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4
FT                                SUBUNIT.
FT   DOMAIN       22    256       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    257    279       PROBABLE.
FT   TRANSMEM    283    305       PROBABLE.
FT   TRANSMEM    317    339       PROBABLE.
FT   DOMAIN      340    433       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    434    457       PROBABLE.
FT   CARBOHYD     35     35       POTENTIAL.
FT   CARBOHYD    112    112       POTENTIAL.
FT   CARBOHYD    230    230       POTENTIAL.
FT   DISULFID    173    187       BY SIMILARITY.
SQ   SEQUENCE   457 AA;  53183 MW;  1571332B CRC32;
```

```
  Query Match             40.6%;  Score 532.5;  DB 1;  Length 457;
  Best Local Similarity   41.5%;  Pred. No. 4.1e-40;
  Matches  107;  Conservative   36;  Mismatches   56;  Indels   59;  Gaps    5;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           ||||: |::||| || | | |:|  :| :|||||||| :| ||||||||||:|||||||
Db     243 MVMTVSFDLSRRMGYFAIQTYIPCILTVVLSWVSFWIKRDSTPARTSLGITTVLTMTTLS 302

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTK-AHASPKLRHP--- 117
           | |||: |||||||||:| ::::||:| | ||:|:| ||:|: |:    |:| | | |
Db     303 TISRKHLPRVSYITAMDLFVSVCFIFVFAALMEYATLNYLVGNKKPLEHSSRKARLPPAG 362

Qy     117 ------------RINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQP 164
                        ||:  |                        |      :
Db     363 AQVMPSFTAININNNIMH----------------------------WPPEIEEDED 391

Qy     165 PSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVF 224
             ||||           | |  |  :::|| : ||:   |::||: ||: |||:|||| |
Db     392 DDPGSP-----------CLEG-KECERFFCCIEDCQTGMWREGRVRIHISRLDSYSRVFF 439

Qy     225 PVTFFFFNVLYWLVCLNL 242
           |  |  ||::||:  | |
Db     440 PTAFLLFNIVYWIAYLYL 457
```

```
RESULT   3
GAC3_HUMAN
ID   GAC3_HUMAN     STANDARD;      PRT;   467 AA.
AC   Q99928;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=FETAL BRAIN;
RX   MEDLINE; 96360042.
RA   HADINGHAM K.L., WAFFORD K.A., THOMPSON S.A., PALMER K.J.,
RA   WHITING P.J.;
RT   "Expression and pharmacology of human GABAA receptors containing
RT   gamma 3 subunits.";
RL   Eur. J. Pharmacol. 291:301-309(1995).
```

```
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S82769; AAB39369.1; -.
DR   MIM; 600233; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL       1     17       POTENTIAL.
FT   CHAIN       18    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3
FT                               SUBUNIT.
FT   DOMAIN      18    254       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM   255    277       PROBABLE.
FT   TRANSMEM   281    303       PROBABLE.
FT   TRANSMEM   315    337       PROBABLE.
FT   DOMAIN     338    443       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM   444    467       PROBABLE.
FT   CARBOHYD   110    110       POTENTIAL.
FT   CARBOHYD   228    228       POTENTIAL.
FT   DISULFID   171    185       BY SIMILARITY.
SQ   SEQUENCE   467 AA;  54284 MW;  EAB28EEC CRC32;


  Query Match             34.9%;  Score 458.5;  DB 1;  Length 467;
  Best Local Similarity   37.3%;  Pred. No. 1.5e-33;
  Matches   97;  Conservative   44;  Mismatches   68;  Indels   51;  Gaps    6;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           :||||:| :||| ||   | |:|  :| :|||||||| :: ||||:||||:|||||||
Db     241 VVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFWIKKDATPARTALGITTVLTMTTLS 300

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPK----LRHP 116
           | :||: |||||:||:| :: :||:| | ||:|:| ||:  |:  :   : |    | ||
Db     301 TIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEYATLNY--YSSCRKPTTTKKTTSLLHP 358

Qy     117 --------RINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPG 168
                   ||: :| :                                |    :|| |
Db     359 DSSRWIPERISLQAPSNY------------------------------SLLDMRPPPPA 387

Qy     169 SPEGPRSLC---SKLACCEWC---KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 222
                 |:     :  |   |   |  : :||   :|:  :|::||: | :  ||:||||
Db     388 MITLNNSVYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSWRKGRIHIDILELDSYSRV 447

Qy     223 VFPVTFFFFNVLYWLVCLNL 242
           || :|  ||::||:  | |
Db     448 FFPTSFLLFNLVYWVGYLYL 467


RESULT   4
GAC2_CHICK
ID   GAC2_CHICK     STANDARD;      PRT;   474 AA.
AC   P21548;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COMMERCIAL RHODE ISLAND CROSS; TISSUE=BRAIN;
RX   MEDLINE; 91088318.
RA   GLENCORSE T.A., BATESON A.N., DARLISON M.G.;
RT   "Sequence of the chicken GABAA receptor gamma 2-subunit cDNA.";
RL   Nucleic Acids Res. 18:7157-7157(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X54944; CAA38704.1; -.
DR   PIR; S13086; S13086.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane; Phosphorylation.
FT   SIGNAL       1     38       POTENTIAL.
FT   CHAIN       39    474       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                               SUBUNIT.
FT   DOMAIN      39    272       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM   273    295       PROBABLE.
FT   TRANSMEM   299    321       PROBABLE.
FT   TRANSMEM   333    355       PROBABLE.
FT   DOMAIN     356    450       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM   451    474       PROBABLE.
FT   CARBOHYD    51     51       POTENTIAL.
FT   CARBOHYD   128    128       POTENTIAL.
FT   CARBOHYD   246    246       POTENTIAL.
FT   CARBOHYD   266    266       POTENTIAL.
FT   DISULFID   189    203       BY SIMILARITY.
FT   MOD_RES    411    411       PHOSPHORYLATION.
FT   DOMAIN     376    383       INSERTION, SIMILAR TO HUMAN GAMMA-2
FT                               SEQUENCE WHICH IS PROPOSED TO BE CAUSED
FT                               BY ALTERNATIVE SPLICING.
SQ   SEQUENCE   474 AA;  54969 MW;  F3975109 CRC32;


  Query Match             34.5%;  Score 453;  DB 1;  Length 474;
  Best Local Similarity   34.8%;  Pred. No. 4.6e-33;
  Matches   89;  Conservative   50;  Mismatches   63;  Indels   54;  Gaps    6;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           :||:::||:||| ||   | |:| ::  :|||||||  :: |||||||||:|||||||
Db     259 VVMSVYFNLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLS 318

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYN------QTKAHASPKLR 114
           | :||: |:|||:||:| ::::||:| | ||:|:  |:: : |      : |   :| ||
Db     319 TIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPLLR 378

Qy     115 -----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPS 166
                | |: |  : |   : |     |  :  : |        ||::   |::
Db     379 MFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD---CAS----- 424
```

```
Qy    167 PGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPV 226
                                :||   ||    |: ||: | : ::|:|:|: ||
Db    424 -------------------------FFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPT 458

Qy    227 TFFFFNVLYWLVCLNL 242
          |  ||::||:  | |
Db    459 AFCLFNLVYWVSYLYL 474


RESULT   5
GAC3_MOUSE
ID   GAC3_MOUSE     STANDARD;      PRT;   467 AA.
AC   P27681;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C C57; TISSUE=BRAIN;
RX   MEDLINE; 91285135.
RA   WILSON-SHAW D., ROBINSON M., ALALJEV B., SIEGEL R.E., SIKELA J.M.;
RT   "A novel gamma subunit of the GABAA receptor identified using the
RT   polymerase chain reaction.";
RL   FEBS Lett. 284:211-215(1991).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X59300; CAA41988.1; -.
DR   PIR; S16915; S16915.
DR   MGD; MGI:95624; GABRG3.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN        18    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3
FT                                SUBUNIT.
FT   DOMAIN       18    254       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    255    277       PROBABLE.
FT   TRANSMEM    281    303       PROBABLE.
FT   TRANSMEM    315    337       PROBABLE.
FT   DOMAIN      338    443       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    444    467       PROBABLE.
FT   CARBOHYD    110    110       POTENTIAL.
FT   CARBOHYD    228    228       POTENTIAL.
FT   DISULFID    171    185       BY SIMILARITY.
SQ   SEQUENCE   467 AA;  54303 MW;  A332B008 CRC32;


  Query Match            34.5%;  Score 452.5;  DB 1;  Length 467;
  Best Local Similarity   38.7%;  Pred. No. 5e-33;
  Matches   96;  Conservative   44;  Mismatches   81;  Indels   27;  Gaps    5;

Qy      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
          :||||:| :||| ||    | |:|  :| :|||||||| :: ||||:||||:|||||||
Db    241 VVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFWIKKDATPARTTLGITTVLTMTTLS 300

Qy     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
          | :||: |||||:||:| :: :||:| | ||:|:| ||:  |:  :    | :|  : :
Db    301 TIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEYATLNY--YSSCR---KPTIRKKKTSL 355

Qy    121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLC--- 178
             ||      : |   :                |    :|| |       |:
Db    356 LHPDSTRWIPDRISLQAPSNY---------------SLLDMRPPPPVMITLNNSMYWQE 399

Qy    178 SKLACCEWC---KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVL 234
           :  |   |   |  : :||   :|:  :|::||: | |  ||:|||| || :|  ||::
Db    400 FEDTCVYECLDGKDCQSFFCCYEECKSGSWRRGRIHIDVSELDSYSRVFFPTSFLLFNLV 459

Qy    235 YWLVCLNL 242
          ||:  | |
Db    460 YWVGYLYL 467


RESULT   6
GAC3_RAT
ID   GAC3_RAT       STANDARD;      PRT;   467 AA.
AC   P28473;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 92159063.
RA   HERB A., WISDEN W., LUEDDENS H., PUIA G., VICINI S., SEEBURG P.H.;
RT   "The third gamma subunit of the gamma-aminobutyric acid type A
RT   receptor family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:1433-1437(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZUR-SIV; TISSUE=BRAIN;
RX   MEDLINE; 92070559.
RA   KNOFLACH F., RHYNER T., VILLA M., KELLENBERGER S., DRESCHER U.,
RA   MALHERBE P., SIGEL E., MOEHLER H.;
RT   "The gamma 3-subunit of the GABAA-receptor confers sensitivity to
RT   benzodiazepine receptor ligands.";
RL   FEBS Lett. 293:191-194(1991).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
```

```
DR   EMBL; M81142; AAA41181.1; -.
DR   EMBL; X63324; CAA44930.1; -.
DR   PIR; S19317; S19317.
DR   PIR; A40221; A40221.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN        18    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3
FT                                SUBUNIT.
FT   DOMAIN       18    254       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    255    277       PROBABLE.
FT   TRANSMEM    281    303       PROBABLE.
FT   TRANSMEM    315    337       PROBABLE.
FT   DOMAIN      338    443       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    444    467       PROBABLE.
FT   CARBOHYD    110    110       POTENTIAL.
FT   CARBOHYD    228    228       POTENTIAL.
FT   DISULFID    171    185       BY SIMILARITY.
FT   CONFLICT    416    416       S -> T (IN REF. 2).
SQ   SEQUENCE   467 AA;  54292.MW;  B7263D44 CRC32;


  Query Match             34.5%;  Score 452.5;  DB 1;  Length 467;
  Best Local Similarity   38.7%;  Pred. No. 5e-33;
  Matches   96;  Conservative   44;  Mismatches   81;  Indels   27;  Gaps    5;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           :||||:| :||| ||   | |:|  :| :|||||||||| :: ||||:||||:|||||||
Db     241 VVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFWIKKDATPARTTLGITTVLTMTTLS 300

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
           | :||: |||||:||:| :: :||:| | ||:|:| ||:  |:  :    | :|  : :
Db     301 TIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEYATLNY--YSSCR---KPTIRKKKTSL 355

Qy     121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLC--- 178
                ||      : |    :                |    :|| |       |:
Db     356 LHPDSTRWIPDRISLQAPSNY---------------SLLDMRPPPPVMITLNNSMYWQE 399

Qy     178 SKLACCEWC---KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVL 234
             :  |   |   |  : :||   :|:  :|:::||: | |  ||:|||| || :|  ||::
Db     400 FEDTCVYECLDGKDCQSFFCCYEECKSGSWRRGRIHIDVSELDSYSRVFFPTSFLLFNLV 459

Qy     235 YWLVCLNL 242
           ||:  | |
Db     460 YWVGYLYL 467


RESULT   7
GAC2_BOVIN
ID   GAC2_BOVIN     STANDARD;      PRT;   475 AA.
AC   P22300;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC   Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN CORTEX;
RX   MEDLINE; 91088632.
RA   WHITING P.J., MCKERNAN R.M., IVERSEN L.L.;
RT   "Another mechanism for creating diversity in gamma-aminobutyrate type
RT   A receptors: RNA splicing directs expression of two forms of gamma 2
RT   phosphorylation site.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:9966-9970(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: ALTERNATIVE RNA SPLICING DIRECTS EXPRESSION
CC       OF TWO FORMS OF GAMMA-2 SUBUNITS (2S AND 2L), ONE (2L) CONTAINS A
CC       PROTEIN KINASE C PHOSPHORYLATION SITE.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M55563; AAA30531.1; -.
DR   PIR; A39272; A39272.
DR   PIR; B39272; B39272.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane; Phosphorylation;
KW   Alternative splicing.
FT   SIGNAL        1     39       POTENTIAL.
FT   CHAIN        40    475       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                                SUBUNIT.
FT   DOMAIN       40    273       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    274    296       PROBABLE.
FT   TRANSMEM    300    322       PROBABLE.
FT   TRANSMEM    334    356       PROBABLE.
FT   DOMAIN      357    451       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    452    475       PROBABLE.
FT   CARBOHYD     52     52       POTENTIAL.
FT   CARBOHYD    129    129       POTENTIAL.
FT   CARBOHYD    247    247       POTENTIAL.
FT   DISULFID    190    204       BY SIMILARITY.
FT   MOD_RES     382    382       PHOSPHORYLATION (BY PKC) (PROBABLE).
FT   VARSPLIC    377    384       MISSING (IN ISOFORM GAMMA-2S).
FT   VARIANT     230    230       S -> G.
SQ   SEQUENCE   475 AA;  55264 MW;  EEBD5FCE CRC32;


  Query Match             34.5%;  Score 452;  DB 1;  Length 475;
  Best Local Similarity   34.8%;  Pred. No. 5.6e-33;
  Matches   89;  Conservative   50;  Mismatches   63;  Indels   54;  Gaps    6;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           :|||::|::||| ||   | |:| ::  :|||||||  :: ||||||||||:|||||||
Db     260 VVMTVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLS 319

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYN------QTKAHASPKLR 114
           | :||: |:|||:||:| ::::||:| | ||:|:  |:: : |      : |   :| ||
Db     320 TIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPLLR 379

Qy     115 -----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPS 166
                | |: |  : |   : |     |  :  : |        ||::   |::
Db     380 MFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD---CAS----- 425

Qy     167 PGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPV 226
                                  :||   ||    |: ||: | : ::|:|:|: ||
Db     425 -------------------------FFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPT 459

Qy     227 TFFFFNVLYWLVCLNL 242
             |  ||::||:  | |
Db     460 AFCLFNLVYWVSYLYL 475
```

```
RESULT   8
GAC2_HUMAN
ID   GAC2_HUMAN     STANDARD;      PRT;   467 AA.
AC   P18507;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 89181956.
RA   PRITCHETT D.B., SONTHEIMER H., SHIVERS B.D., YMER S., KETTENMANN H.,
RA   SCHOFIELD P.R., SEEBURG P.H.;
RT   "Importance of a novel GABAA receptor subunit for benzodiazepine
RT   pharmacology.";
RL   Nature 338:582-585(1989).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X15376; CAA33437.1; -.
DR   PIR; S03905; S03905.
DR   MIM; 137164; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     39       POTENTIAL.
FT   CHAIN        40    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                                SUBUNIT.
FT   DOMAIN       40    273       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    274    296       PROBABLE.
FT   TRANSMEM    300    322       PROBABLE.
FT   TRANSMEM    334    356       PROBABLE.
FT   DOMAIN      357    443       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    444    466       PROBABLE.
FT   CARBOHYD     52     52       POTENTIAL.
FT   CARBOHYD    129    129       POTENTIAL.
FT   CARBOHYD    247    247       POTENTIAL.
FT   DISULFID    190    204       BY SIMILARITY.
SQ   SEQUENCE   467 AA;  54178 MW;  E78E8090 CRC32;


  Query Match             34.1%;  Score 447;  DB 1;  Length 467;
  Best Local Similarity   34.3%;  Pred. No. 1.5e-32;
  Matches   85;  Conservative   52;  Mismatches   65;  Indels   46;  Gaps    5;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           :||:::|::||| ||   | |:| ::  :||||||||  :: |||||||||:|||||||
Db     260 VVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLS 319

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRH---PR 117
           | :||: |:|||:||:| ::::||:| | ||:|:  |:: : |:  :    | :    |
Db     320 TIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPAPT 379

Qy     118 INSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPR 174
           |: |  : |   : |     |  :  : |        ||::   |::
Db     380 IDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD---CAS------------ 417

Qy     175 SLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVL 234
                         :||   ||    |: ||: | : ::|:|:|: ||  |  ||::
Db     417 ----------------FFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLV 459

Qy     235 YWLVCLNL 242
           ||:  | |
Db     460 YWVSYLYL 467


RESULT   9
GAC2_RAT
ID   GAC2_RAT       STANDARD;      PRT;   466 AA.
AC   P18508;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 90380375.
RA   SHIVERS B.D., KILLISCH I., SPRENGEL R., SONTHEIMER H., KOEHLER M.,
RA   SCHOFIELD P.R., SEEBURG P.H.;
RT   "Two novel GABAA receptor subunits exist in distinct neuronal
RT   subpopulations.";
RL   Neuron 3:327-337(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90331051.
RA   MALHERBE P., SIGEL E., BAUR R., PERSOHN E., RICHARDS J.G., MOHLER H.;
RT   "Functional characteristics and sites of gene expression of the alpha
RT   1, beta 1, gamma 2-isoform of the rat GABAA receptor.";
RL   J. Neurosci. 10:2330-2337(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L08497; AAC42036.1; -.
DR   PIR; A37164; A37164.
DR   PIR; JQ0077; JQ0077.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     38       POTENTIAL.
FT   CHAIN        39    466       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
```

```
FT                                SUBUNIT.
FT   DOMAIN       39    272       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    273    295       PROBABLE.
FT   TRANSMEM    299    321       PROBABLE.
FT   TRANSMEM    333    355       PROBABLE.
FT   DOMAIN      356    442       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    443    465       PROBABLE.
FT   CARBOHYD     51     51       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    246    246       POTENTIAL.
FT   DISULFID    189    203       BY SIMILARITY.
FT   CONFLICT     22     22       M -> I (IN REF. 2).
SQ   SEQUENCE   466 AA;  54077 MW;  EDDEFFEF CRC32;


  Query Match             34.1%;  Score 447;  DB 1;  Length 466;
  Best Local Similarity   34.3%;  Pred. No. 1.5e-32;
  Matches   85;  Conservative   52;  Mismatches   65;  Indels   46;  Gaps    5;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           :||:::|::||| ||   | |:| ::  :|||||||  :: |||||||||:|||||||
Db     259 VVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLS 318

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRH---PR 117
           | :||: |:|||:||:| ::::||:| | ||:|:  |:: : |:  :    | :    |
Db     319 TIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPAPT 378

Qy     118 INSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPR 174
           |: |  : |   : |    |  :  : |          ||::   |::
Db     379 IDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD---CAS------------- 416

Qy     175 SLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVL 234
                       :||   ||    |: ||: | : ::|:|:|: ||  |  ||::
Db     416 ----------------FFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLV 458

Qy     235 YWLVCLNL 242
           ||:  | |
Db     459 YWVSYLYL 466


RESULT  10
GAC1_RAT
ID   GAC1_RAT       STANDARD;      PRT;   465 AA.
AC   P23574;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 91006020.
RA   YMER S., DRAGUHN A., WISDEN W., WERNER P., KEINAENEN K.,
RA   SCHOFIELD P.R., SPRENGEL R., PRITCHETT D.B., SEEBURG P.H.;
RT   "Structural and functional characterization of the gamma 1 subunit of
RT   GABAA/benzodiazepine receptors.";
RL   EMBO J. 9:3261-3267(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X57514; CAA40739.1; -.
DR   PIR; S12056; S12056.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36    465       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1
FT                                SUBUNIT.
FT   DOMAIN       36    272       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    273    294       PROBABLE.
FT   TRANSMEM    299    320       PROBABLE.
FT   TRANSMEM    332    354       PROBABLE.
FT   DOMAIN      355    444       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    445    465       PROBABLE.
FT   CARBOHYD     50     50       POTENTIAL.
FT   CARBOHYD    127    127       POTENTIAL.
FT   CARBOHYD    245    245       POTENTIAL.
FT   DISULFID    188    202       BY SIMILARITY.
SQ   SEQUENCE   465 AA;  53550 MW;  963AF632 CRC32;


  Query Match             34.0%;  Score 446;  DB 1;  Length 465;
  Best Local Similarity   35.2%;  Pred. No. 1.9e-32;
  Matches   89;  Conservative   46;  Mismatches   62;  Indels   56;  Gaps    5;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           ::|||||::||| ||   | |:|  :| :|||||||  :: |||||||||:|||||||
Db     258 IIMTIFFDLSRRMGYFTIQTYIPCILTVVLSWVSFWINKDAVPARTSLGITTVLTMTTLS 317

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYN----------QTKAHA 109
           | :||: |:|||:||:| ::::||:| | ||:|:  |::   |          ::|
Db     318 TIARKSLPKVSYVTAMDLFVSVCFIFVFAALMEYGTLHYFTSNNKGKTTRDRKLKSKTSV 377

Qy     110 SPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGS 169
           || |       | :     :     | :: :  | :  || |      |:
Db     378 SPGL-------HAGSTLIPMNNISMPQGEDDYGYQCL--EGKD------CAT-------- 415

Qy     170 PEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFF 229
                              :||   ||   :|::||: | : ::|:|||: ||  |
Db     415 ----------------------FFCCFEDCRTGSWREGRIHIRIAKIDSYSRIFFPTAFA 452

Qy     230 FFNVLYWLVCLNL 242
            ||::||:  | |
Db     453 LFNLVYWVGYLYL 465


RESULT  11
GAC2_MOUSE
ID   GAC2_MOUSE     STANDARD;      PRT;   474 AA.
AC   P22723;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91108470.
RA   KOFUJI P., WANG J.B., MOSS S.J., HUGANIR R.L., BURT D.R.;
RT   "Generation of two forms of the gamma-aminobutyric acidA receptor
```

```
RT   gamma 2-subunit in mice by alternative splicing.";
RL   J. Neurochem. 56:713-715(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   SIKELA J.M., SHAW W.D., KHAN A.S., LIN L.-H., LEIDENHEIMER G.,
RA   SIEGEL R.E.;
RL   Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: ALTERNATIVE RNA SPLICING DIRECTS EXPRESSION
CC       OF TWO FORMS OF GAMMA2 SUBUNIT (2S AND 2L), ONE (2L) CONTAINS A
CC       PROTEIN KINASE C PHOSPHORYLATION SITE.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M86572; AAB59635.1; -.
DR   EMBL; M62374; AAA37653.1; -.
DR   PIR; JH0317; JH0317.
DR   PIR; JH0316; JH0316.
DR   MGD; MGI:95623; GABRG2.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane; Phosphorylation;
KW   Alternative splicing.
FT   SIGNAL        1     38       POTENTIAL.
FT   CHAIN        39    474       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                                 SUBUNIT.
FT   DOMAIN       39    272       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    273    295       PROBABLE.
FT   TRANSMEM    299    321       PROBABLE.
FT   TRANSMEM    333    355       PROBABLE.
FT   DOMAIN      356    450       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    451    474       PROBABLE.
FT   CARBOHYD     51     51       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    246    246       POTENTIAL.
FT   DISULFID    189    203       BY SIMILARITY.
FT   MOD_RES     381    381       PHOSPHORYLATION (BY PKC) (PROBABLE).
FT   VARSPLIC    376    383       MISSING (IN ISOFORM GAMMA-2S).
FT   CONFLICT     49     49       T -> A (IN REF. 2).
FT   CONFLICT    414    414       Q -> E (IN REF. 2).
FT   CONFLICT    443    443       M -> I (IN REF. 2).
SQ   SEQUENCE   474 AA;  55145 MW;  A3049225 CRC32;
```

```
  Query Match             33.9%;  Score 445;  DB 1;  Length 474;
  Best Local Similarity   34.0%;  Pred. No. 2.3e-32;
  Matches   87;  Conservative   52;  Mismatches   63;  Indels   54;  Gaps    6;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           :||:::|::||| ||   | |:| ::  :|||||||| :: ||||||||||:|||||||
Db     259 VVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLS 318

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYN------QTKAHASPKLR 114
           | :||: |:|||:||:| ::::||:| | ||:|:  |:: : |      : |   :| ||
Db     319 TIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPLLR 378

Qy     115 -----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPS 166
                | |: |  : |   : |     |  :  : |        ||::   |::
Db     379 MFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYQC-------LDGKD---CAS----- 424

Qy     167 PGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPV 226
                                    :||   ||    |: ||: : : ::|:|:|: ||
Db     424 -----------------------FFCCFEDCRTGAWRHGRIHMRIAKMDSYARIFFPT 458

Qy     227 TFFFFNVLYWLVCLNL 242
             |  ||::||:  | |
Db     459 AFCLFNLVYWVSYLYL 474
```

```
RESULT  12
GAA6_CHICK
ID   GAA6_CHICK     STANDARD;      PRT;   465 AA.
AC   Q90845;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRA6.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EMBRYONIC BRAIN;
RX   MEDLINE; 96373714.
RA   BAHN S., HARVEY R.J., DARLISON M.G., WISDEN W.;
RT   "Conservation of gamma-aminobutyric acid type A receptor alpha 6
RT   subunit gene expression in cerebellar granule cells.";
RL   J. Neurochem. 66:1810-1818(1996).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X94343; CAA64069.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    465       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6
FT                                 SUBUNIT.
FT   DOMAIN       20    242       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    243    264       PROBABLE.
FT   TRANSMEM    269    290       PROBABLE.
FT   TRANSMEM    302    324       PROBABLE.
FT   DOMAIN      325    421       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    422    443       PROBABLE.
FT   CARBOHYD     31     31       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    141    141       POTENTIAL.
FT   DISULFID    156    170       BY SIMILARITY.
SQ   SEQUENCE   465 AA;  51717 MW;  B74B26D1 CRC32;
```

```
  Query Match             29.0%;  Score 380;  DB 1;  Length 465;
  Best Local Similarity   35.2%;  Pred. No. 1.3e-26;
```

```
  Matches   92;  Conservative   38;  Mismatches   67;  Indels   64;  Gaps    7;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           ::||::|:: |: ||   | | |  :| :|| |||||  || ||||  |||:|||||||
Db     228 VIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPARTVFGITTVLTMTTLS 287

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
             :| : |:||| ||:|::||:|| | | ||:||| :|:    ||:       |  |  :
Db     288 ISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQTQ-------RAMRKAA 340

Qy     121 RAHARTRARSRACARQHQEAFV-----CQI---VTTEGSDGEERP-----SCSAQQ---- 164
           || |   | | |      |        | :   | :  |  :: |     | || |
Db     341 RAAALAAALSAATVPAEDEIVSHSDSNCNLKKRVNSVTSQADQSPEASIVSNSASQCQPV 400

Qy     164 ---PPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYS 220
              ||:| :|                          |   |::           ::| ||
Db     401 SAPPPAPPAP-------------------------PPVGGTS----------KIDQYS 423

Qy     221 RVVFPVTFFFFNVLYWLVCLN 241
           |::||| |  ||::||:| |:
Db     424 RILFPVAFAGFNLVYWVVYLS 444


RESULT  13
GAA4_RAT
ID   GAA4_RAT       STANDARD;      PRT;   552 AA.
AC   P28471;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRA4.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92008629.
RA   WISDEN W., HERB A., WIELAND H., KEINAENEN K., LUEDDENS H.,
RA   SEEBURG P.H.;
RT   "Cloning, pharmacological characteristics and expression pattern of
RT   the rat GABAA receptor alpha 4 subunit.";
RL   FEBS Lett. 289:227-230(1991).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L08493; AAC42032.1; -.
DR   EMBL; S55933; AAB19902.1; -.
DR   PIR; S17551; S17551.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36    552       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4
FT                                SUBUNIT.
FT   DOMAIN       36    258       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    259    280       PROBABLE.
FT   TRANSMEM    285    306       PROBABLE.
FT   TRANSMEM    318    340       PROBABLE.
FT   DOMAIN      341    521       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    522    541       PROBABLE.
FT   CARBOHYD     47     47       POTENTIAL.
FT   CARBOHYD    144    144       POTENTIAL.
FT   CARBOHYD    157    157       POTENTIAL.
FT   DISULFID    172    186       BY SIMILARITY.
SQ   SEQUENCE   552 AA;  60951 MW;  62956C8F CRC32;


  Query Match           28.5%;  Score 374.5;  DB 1;  Length 552;
  Best Local Similarity   31.1%;  Pred. No. 4.7e-26;
  Matches   96;  Conservative   39;  Mismatches   95;  Indels   79;  Gaps    7;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           :|||::|:: |: ||   | |:|  :| :|| |||||  || ||||  |||:|||||||
Db     244 IVMTVYFHLRRKMGYFMIQTYIPCIMTVILSQVSFWINKESVPARTVFGITTVLTMTTLS 303

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ-----------TKAH 108
             :| : |:||| ||:|::||:|| | | ||:||| :|:    |             :
Db     304 ISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNIQMQKAKKKISKPPPEVP 363

Qy     109 ASPKLRHPRINS---RAHARTRARSRACARQHQEAFV---------CQIVTTEGSDGEER 156
           |:| |:     :     ||    | |  |  | |: |              |      |
Db     364 AAPVLKEKHTETSLQNTHANLNMRKRTNALVHSESDVNSRTEVGNHSSKTTAAQESSETT 423

Qy     157 PSCSAQQPPSP----------------------GSPEG---PRSLCSKLACCEWCKRFKK 191
           |       |:|                      || |   |  | |' |   :  |  :
Db     424 PKAHLASSPNPFSRANAAETISAAARGLSSAASPSPHGTLQPAPLRSASARPAFGARLGR 483

Qy     192 YFCMV------------------PDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFN 232
               |                  |   |::           ::| |:|::|||||  ||
Db     484 IKTTVNTTGVPGNVSATPPPSAPPPSGSGTS----------KIDKYARILFPVTFGAFN 532

Qy     233 VLYWLVCLN 241
           ::||:| |:
Db     533 MVYWVVYLS 541


RESULT  14
GAA6_RAT
ID   GAA6_RAT       STANDARD;      PRT;   453 AA.
AC   P30191;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRA6 OR GABRA-6.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 90348963.
RA   LUEDDENS H., PRITCHETT D., KHLER M., KILLISCH I., KEINAENEN K.,
RA   MONYER H., SPRENGEL R., SEEBURG P.H.;
RT   "Cerebellar GABAA receptor selective for a behavioural alcohol
RT   antagonist.";
RL   Nature 346:648-651(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: ONLY FOUND IN CEREBELLAR GRANULE CELLS.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
```

```
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; L08495; AAC42034.1; -.
DR   EMBL; X55742; CAA39273.1; -.
DR   PIR; S11087; S11087.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    453       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6
FT                                SUBUNIT.
FT   DOMAIN       20    242       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    243    264       PROBABLE.
FT   TRANSMEM    269    290       PROBABLE.
FT   TRANSMEM    301    324       PROBABLE.
FT   DOMAIN      325    419       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    420    441       PROBABLE.
FT   CARBOHYD     31     31       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    141    141       POTENTIAL.
FT   DISULFID    156    170       BY SIMILARITY.
SQ   SEQUENCE   453 AA;  51184 MW;  0ED8616E CRC32;
```

```
  Query Match             28.1%;  Score 369;  DB 1;  Length 453;
  Best Local Similarity   32.3%;  Pred. No. 1.2e-25;
  Matches   83;  Conservative   42;  Mismatches   74;  Indels   58;  Gaps    4;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           ::|||::|:: |: ||   | | |  :| :|| ||||| || |||| |||:|||||||
Db     228 VIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPARTVFGITTVLTMTTLS 287

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120
             :| : |:||| ||:|::||:|| | | ||:||| :|:    |::           :
Db     288 ISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQSQ-----------KA 335

Qy     121 RAHARTRARSRACARQHQEAFVCQIVTTEGS---------------DGEERPSCSAQQP 164
             |:| |:       :  |:   :||    |                |     :: |
Db     336 ERQAQTAAKPPVAKSKTTESLEAEIVVHSDSKYHLKKRISSLTLPIVPSSEASKVLSRTP 395

Qy     165 PSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVF 224
           | :|  |  |                   :|   |::          ::| |||::|
Db     396 ILPSTPVTPPLL-----------------LPAIGGTS----------KIDQYSRILF 425

Qy     225 PVTFFFFNVLYWLVCLN 241
           || |  ||::||:| |:
Db     426 PVAFAGFNLVYWIVYLS 442
```

```
RESULT  15
GAA4_HUMAN
ID   GAA4_HUMAN     STANDARD;      PRT;   554 AA.
AC   P48169;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRA4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN CORTEX;
RA   YANG W., DREWE J.A., LAN N.C.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
```

```
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; U30461; AAB52519.1; -.
DR   MIM; 137141; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36    554       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4
FT                                SUBUNIT.
FT   DOMAIN       36    258       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    259    280       PROBABLE.
FT   TRANSMEM    285    306       PROBABLE.
FT   TRANSMEM    318    340       PROBABLE.
FT   DOMAIN      341    523       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    524    543       PROBABLE.
FT   CARBOHYD     47     47       POTENTIAL.
FT   CARBOHYD    144    144       POTENTIAL.
FT   CARBOHYD    157    157       POTENTIAL.
FT   DISULFID    172    186       BY SIMILARITY.
SQ   SEQUENCE   554 AA;  61640 MW;  49E8E56A CRC32;
```

```
  Query Match             27.8%;  Score 364.5;  DB 1;  Length 554;
  Best Local Similarity   29.5%;  Pred. No. 3.6e-25;
  Matches   93;  Conservative   46;  Mismatches   87;  Indels   89;  Gaps    8;

Qy       1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60
           :|||::|:: |: ||   | |:|  :| :|| |||||  || ||||  |||:|||||||
Db     244 IVMTVYFHLRRKMGYFMIQTYIPCIMTVILSQVSFWINKESVPARTVFGITTVLTMTTLS 303

Qy      61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ-----------TKAH 108
             :| : |:|||:||:|::||:|| | | ||:||| :|:    |           :
Db     304 ISARHSLPKVSYLTAMDWFIAVCFAFVFSALIEFAAVNYFTNIQMEKAKRKTSKPPQEVP 363

Qy     109 ASP--KLRHPRINSR-AHARTRARSRACARQHQEAFV-----------CQIVTTEGSDG 153
           |:|  : :||    :  :|   | |  |  | |: |                |  | | |
Db     364 AAPVQREKHPEAPLQDTNANLNMRKRTNALVHSESDVGNRTEVGNHSSKSSTVVQESSKG 423

Qy     154 EERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRL---- 210
             |   ::   |:| |        |                  :|    :: : | :
Db     424 TPRSYLASS--PNPFSRANAAETISAARA-----------LPSASPTSIRTGHMPRKA 468

Qy     210 ------CIHVY-----------------------------------RLDNYSRVVFPV 226
                  ||:                                    ::| |:|::|||
Db     469 SVGSASTRHVFGSRLQRIKTTVNTIGATGKLSATPPPSAPPPSGSGTSKIDKYARILFPV 528

Qy     227 TFFFFNVLYWLVCLN 241
           ||  ||::||:| |:
Db     529 TFGAFNMVYWVVYLS 543
```

```
Search completed: March 11, 2000, 06:26:38
Job time: 41 sec
```

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2000, 13:38:51 ; Search time 147.28 Seconds
(without alignments)
2563.855 Million cell updates/sec

Title: US-09-030-832-41
Perfect score: 3154
Sequence: 1 CGCGACCTCCGCGCAGGTGG.....AGCAAAAAGAAAAAAAAAAA 3154

Scoring table: IDENTITY_NUC

Searched: 214294 seqs, 59861208 residues

Database : Issued_Patents_NA:*

Word size : 0

Number of hits that pass the threshold : 428588
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	264.6	8.4	1732	2	US-08-417-330A-17	Sequence 17, Appl
2	261.8	8.3	2310	2	US-08-417-330A-15	Sequence 15, Appl
3	237.6	7.5	1638	2	US-08-417-330A-13	Sequence 13, Appl
4	224.4	7.1	2191	2	US-08-417-330A-11	Sequence 11, Appl
5	169	5.4	1866	2	US-08-417-330A-19	Sequence 19, Appl
6	129.6	4.1	2635	3	US-08-768-301-3	Sequence 3, Appli
7	122	3.9	1491	1	US-08-137-614A-3	Sequence 3, Appli
8	122	3.9	1491	3	US-08-768-301-1	Sequence 1, Appli
9	119.2	3.8	1542	1	US-08-249-112-1	Sequence 1, Appli
10	119.2	3.8	1542	6	PCT-US95-06556-1	Sequence 1, Appli
11	112	3.6	3958	2	US-08-435-933-5	Sequence 5, Appli
12	112	3.6	1657	2	US-08-554-659-1	Sequence 1, Appli
13	112	3.6	3958	6	PCT-US96-06035-5	Sequence 5, Appli
14	110.4	3.5	1657	2	US-08-554-659-3	Sequence 3, Appli
15	108.2	3.4	1650	1	US-08-459-100A-1	Sequence 1, Appli
16	108.2	3.4	1650	6	PCT-US94-09589-1	Sequence 1, Appli
17	76.6	2.4	1479	1	US-08-249-112-2	Sequence 2, Appli
18	76.6	2.4	1479	6	PCT-US95-06556-2	Sequence 2, Appli
19	76	2.4	2066	5	US-08-072-064-3	Sequence 3, Appli
20	76	2.4	2066	5	US-08-072-064-5	Sequence 5, Appli
21	74.4	2.4	2066	5	US-08-072-064-2	Sequence 2, Appli
22	72.8	2.3	2066	5	US-08-072-064-7	Sequence 7, Appli
23	72	2.3	7218	1	US-08-232-463-14	Sequence 14, Appl
24	65.6	2.1	1970	5	US-08-072-064-9	Sequence 9, Appli
25	65.6	2.1	2059	6	PCT-US92-08558-2	Sequence 2, Appli
26	65.6	2.1	1970	6	PCT-US92-08558-3	Sequence 3, Appli
27	39.2	1.2	152	2	US-08-435-933-4	Sequence 4, Appli
28	39.2	1.2	152	6	PCT-US96-06035-4	Sequence 4, Appli
29	37.4	1.2	575	2	US-08-554-659-11	Sequence 11, Appl
30	36.6	1.2	1345	2	US-08-525-654A-134	Sequence 134, App
31	36.6	1.2	8779	3	US-08-750-703-4	Sequence 4, Appli
32	36	1.1	1813	6	PCT-US94-12883-3	Sequence 3, Appli
33	34.4	1.1	2370	1	US-08-117-907-1	Sequence 1, Appli
34	34.4	1.1	1898	1	US-08-342-411A-1	Sequence 1, Appli
35	34.4	1.1	2254	2	US-08-153-848-27	Sequence 27, Appl
36	34.4	1.1	1161	2	US-08-153-848-31	Sequence 31, Appl
37	34.4	1.1	2254	6	PCT-US93-11153-27	Sequence 27, Appl
38	34.4	1.1	1161	6	PCT-US93-11153-31	Sequence 31, Appl
c 39	34.2	1.1	300	7	5218100-5	Patent No. 5218100
c 40	33	1.0	2791	4	US-09-016-000-8	Sequence 8, Appli
41	33	1.0	1166	6	PCT-US96-12129B-1	Sequence 1, Appli
c 42	32.8	1.0	234	3	US-08-623-906A-2	Sequence 2, Appli
c 43	32.8	1.0	790	7	5194596-8	Patent No. 5194596
c 44	32.8	1.0	789	7	5219739-8	Patent No. 5219739
c 45	32.6	1.0	2313	1	US-08-133-248-7	Sequence 7, Appli

ALIGNMENTS

```
RESULT   1
US-08-417-330A-17
; Sequence 17, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1732 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  27...1385
;      OTHER INFORMATION:
US-08-417-330A-17


  Query Match                 8.4%;  Score 264.6;  DB 2;  Length 1732;
```

```
  Best Local Similarity   56.5%;  Pred. No. 7.2e-68;
  Matches  514;  Conservative    0;  Mismatches  389;  Indels    6;  Gaps    1;

Qy     247 AGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGG 306
           | | | |  ||| ||||||  |||   | ||       ||||||  |    ||||| || ||
Db     116 AAACGTCAGTCGGATCCTGGACAACTTGCTTGAAGGCTATGACAATCGGCTGCGGCCGGG 175

Qy     307 CATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCT 366
           ||||||      |||||  ||||     || ||    || | |||  |||| ||  |
Db     176 ATTTGGAGGTGCTGTCACTGAAGTCAAAACAGACATTTATGTGACCAGTTTTGGGCCCGT 235

Qy     367 CTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGA 426
           ||     | || ||||| || || || ||  |  | ||   |||||||||   || ||
Db     236 GTCAGATGTGGAGATGGAGTATACGATGGATGTTTTTTTTCGCCAGACCTGGACTGATGA 295

Qy     427 ACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCA 486
           | |    |     |   |  |||| |||  |||||||       |||| ||  |
Db     296 GAGGTTGAAGTTTGGGGGGCCAACTGAGATTCTGAGTCTGAATAATTTGATGGTCAGTAA 355

Qy     487 GCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCAC 546
           | ||||  || ||||||||||| || |||  ||| | | ||   |  ||  | || ||
Db     356 AATCTGGACGCCTGACACCTTTTTCAGAAATGGTAAAAAGTCCATTGCTCACAACATGAC 415

Qy     547 CATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGAT 606
           |  || ||  |  |  || | ||     || |||| |   | || ||||| || ||| |
Db     416 AACTCCTAATAAACTCTTCAGAATAATGCAGAATGGAACCATTTTATACACCATGAGGCT 475

Qy     607 GACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTG 666
           |||||  |||| |  ||  | |     || | |  ||||| ||||||   ||  ||||
Db     476 TACCATCAATGCTGACTGTCCCATGAGGCTGGTTAACTTTCCTATGGATGGGCATGCTTG 535

Qy     667 CCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA 726
           || ||    ||   |||| | | |||||  | | ||| || || || | |||| ||||
Db     536 TCCACTCAAGTTTGGGAGCTATGCTTATCCCAAAAGTGAAATCATATATACGTGGAAAAA 595

Qy     727 TTTCAAGCTTGAAATCAATGA------GAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 780
           |||  |       ||        |  | || |  |  ||  |||||| |||| |
Db     596 AGGACCACTTTACTCAGTAGAAGTCCCAGAAGAATCTTCAAGCCTTCTCCAGTATGATCT 655

Qy     781 TACAGGAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCAT 840
           |  |||   |        | ||| | ||| | | |       |||||  | | |  | ||
Db     656 GATTGGACAAACAGTATCTAGTGAGACAATTAAATCTAACACAGGTGAATACGTTATAAT 715

Qy     841 GACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCC 900
           |||  ||| |||| |  ||   |||  | | |||||  |    | || |  ||    ||
Db     716 GACAGTTTACTTCCACTTGCAAAGGAAGATGGGCTACTTCATGATACAGATATACACTCC 775

Qy     901 TTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCC 960
           ||      ||||    || || |||  ||| || || ||||| || |  |||||  |  ||
Db     776 TTGCATTATGACAGTCATTCTTTCCCAGGTGTCTTTCTGGATTAATAAGGAGTCCGTCCC 835

Qy     961 AGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTC 1020
           |||  | ||   ||| ||||||||| |||||  | || |||||||| ||| |||  |  | |
Db     836 AGCAAGAACTGTTCTTGGGATCACCACTGTTTTAACTATGACCACTTTGAGCATCAGTGC 895

Qy    1021 TCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTG 1080
           ||  |   ||| ||    || || |||  ||| ||| ||||||  |  || ||  | ||
Db     896 CCGGCACTCTTTGCCAAAAGTGTCATATGCCACTGCCATGGATTGGTTCATAGCTGTTTG 955

Qy    1081 CTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAA 1140
           ||| |  |||  ||||| |||||  | ||||| || |   ||||||  | | | | |
Db     956 CTTTGCATTCGTCTTCTCTGCTCTTATCGAGTTCGCAGCTGTCAACTACTTTACCAATCT 1015

Qy    1141 CCAGACAAA 1149
           |||||| |
Db    1016 TCAGACACA 1024


RESULT   2
US-08-417-330A-15
; Sequence 15, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;     APPLICANT:  HADINGHAM, KAREN
;     APPLICANT:  LE BOURDELLES, BEATRICE
;     APPLICANT:  WHITING, PAUL
;     APPLICANT:  WINGROVE, PETER
;     TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;     TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;     TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;     NUMBER OF SEQUENCES:  20
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;       STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;       CITY:  RAHWAY
;       STATE:  NJ
;       COUNTRY:  US
;       ZIP:  07065-0900
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/417,330A
;       FILING DATE:  05-APR-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  HAND, MARK
;       REGISTRATION NUMBER:  36,545
;       REFERENCE/DOCKET NUMBER:  T1109IA
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  908-594-3905
;       TELEFAX:  908-594-4720
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  15:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2310 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  Coding Sequence
;       LOCATION:  298...1683
;       OTHER INFORMATION:
US-08-417-330A-15


  Query Match             8.3%;  Score 261.8;  DB 2;  Length 2310;
  Best Local Similarity   55.7%;  Pred. No. 5.7e-67;
  Matches  525;  Conservative    0;  Mismatches  412;  Indels    6;  Gaps    1;

Qy     203 AAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATC 262
           | | ||||     | | ||  |     |    || |||  |  |   |    | | |||
Db     394 ATGCCAACCAGTTCAGTGAAAGATGAGACCAATGACAACATCACGATATTTACCAGGATC 453

Qy     263 CTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCC 322
           || |      || ||  |   || ||| ||| ||| || || ||  | |||||      |
Db     454 TTGGATGGGCTCTTGGATGGCTACGACAACAGACTTCGGCCCGGGCTGGGAGAGCGCATC 513

Qy     323 ACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATG 382
           |||  |||  |      || |||  ||||| |||| | || ||  | ||   |  || |||
Db     514 ACTCAGGTGAGGACCGACATCTACGTCACCAGCTTCGGCCCGGTGTCCGACACGGAAATG 573

Qy     383 GAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAAC 442
           || |||||||| ||| |  | |||   || | |||| | || ||| | ||  | |  ||
Db     574 GAGTACACCATAGACGTGTTTTTCCGACAAAGCTGGAAAGATGAAAGGCTTCGGTTTAAG 633

Qy     443 GACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGAC 502
           |   || | ||   ||   ||| ||    |    | |  ||| || | |||| ||| |||
Db     634 GGGCCCATGCAGCGCCTCCCTCTCAACAACCTCCTTGCCAGCAAGATCTGGACCCCAGAC 693
```

```
Qy     503 ACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATG 562
           || || ||    ||    |||| | ||  ||  ||  | || |||| ||||||| || ||
Db     694 ACGTTCTTCCACAACGGGAAGAAGTCCATCGCTCACAACATGACCACGCCCAACAAGCTG 753

Qy     563 GTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGA 622
           | ||  |  |  | || ||||   || | ||||| ||  |  |||||||   ||| |
Db     754 CTGCGGCTGGAGGACGACGGCACCCTGCTCTACACCATGCGCTTGACCATCTCTGCAGAG 813

Qy     623 TGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCT 682
           ||| |  | ||  |       || || |||||| | ||| ||||||||||    ||
Db     814 TGCCCCATGCAGCTTGAGGACTTCCCGATGGATGCGCACGCTTGCCCTCTGAAATTTGGC 873

Qy     683 AGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA------TTTCAAGCTT 736
           |||| | | || ||| |   |||  |  | |||   |||   ||         ||||
Db     874 AGCTATGCGTACCCTAATTCTGAAGTCGTTTACGTCTGGACCAACGGCTCCACCAAGTCG 933

Qy     737 GAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAAC 796
           |   |   | | |  |   ||  |  ||   |||||   |  | |  ||   ||
Db     934 GTGGTGGTGGCGGAAGATGGCTCCAGACTGAACCAGTACCACCTGATGGGGCAGACGGTG 993

Qy     797 AAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAAT 856
           |||||  |  ||||  |||       || || | ||   |||||||   |  |||| |
Db     994 GGCACTGAGAACATCAGCACCAGCACAGGCGAATACACAATCATGACAGCTCACTTCCAC 1053

Qy     857 GTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACG 916
           |||  |||  | |||||||  ||| | | || | |||  | || |       |||||  |
Db    1054 CTGAAAAGGAAGATTGGCTACTTTGTCATCCAGACCTACCTTCCCTGCATAATGACCGTG 1113

Qy     917 ATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTA 976
           ||  | ||   ||| |||||||||| | ||    || || |  ||||||  ||||   | |
Db    1114 ATCTTATCACAGGTGTCCTTTTGGCTGAACCGGGAATCAGTCCCAGCCAGGACAGTTTTT 1173

Qy     977 GGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCG 1036
           ||| |||||  | ||  |||||||||||  ||  |  ||| |     |  | ||   | | ||
Db    1174 GGGGTCACCACGGTGCTGACCATGACGACCCTCAGCATCAGCGCCAGGAACTCTCTGCCC 1233

Qy    1037 CGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTC 1096
           ||  ||||   ||| ||| |||| |  |  || ||  | ||||  | ||||  ||||
Db    1234 AAAGTGGCCTACGCCACCGCCATGGACTGGTTCATAGCTGTGTGCTATGCCTTCGTCTTC 1293

Qy    1097 TGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACA 1139
           |  || ||| | ||||||||   | |||| | | | | | | |
Db    1294 TCGGCGCTGATAGAGTTTGCCACGGTCAATTACTTTACCAAGA 1336


RESULT   3
US-08-417-330A-13
; Sequence 13, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1638 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  87...1562
;      OTHER INFORMATION:
US-08-417-330A-13


  Query Match             7.5%;  Score 237.6;  DB 2;  Length 1638;
  Best Local Similarity   54.4%;  Pred. No. 5.9e-60;
  Matches  502;  Conservative    0;  Mismatches  414;  Indels    6;  Gaps    1;

Qy     222 CTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTA 281
           |||    |||   || |||  |  |      | |  | ||| || |   | | |||
Db     256 CTGATGACAGCACTGACAACATCACTATCTTCACCAGAATCTTGGATCGTCTTCTGGACG 315

Qy     282 ATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGA 341
           ||||||  ||   ||||| |||||  |||||||       ||||  || |    ||| |
Db     316 GCTATGACAACCGGCTGCGACCTGGGCTTGGAGATGCAGTGACTGAAGTGAAGACTGACA 375

Qy     342 TCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCA 401
           ||  ||| | |||  |||| ||| | ||   |  |||||||| ||||| |||||  |
Db     376 TCTACGTGACCAGTTTTGGCCCTGTGTCAGACACTGACATGGAGTACACTATTGATGTAT 435

Qy     402 TCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTG 461
           | ||    ||||| ||| | || ||| | ||    |   | | | || |  ||   |||
Db     436 TTTTTCGGCAGACATGGCATGATGAAAGACTGAAATTTGATGGCCCCATGAAGATCCTTC 495

Qy     462 TTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTA 521
           |||||        |||  ||  || | ||||  |||||||||||  ||    |||   |
Db     496 CACTGAACAATCTCCTGGCTAGTAAGATCTGGACACCGGACACCTTCTTCCACAATGGCA 555

Qy     522 AGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATG 581
           |||   |   | ||| | || |||| |||||| || || || |  |   |  | | |
Db     556 AGAAATCAGTGGCTCATAACATGACCACGCCCAACAAGCTGCTCAGATTGGTGGACAACG 615

Qy     582 GCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCA 641
           | |   |  | || ||||| ||| | || ||| |||| |  ||  |  | | ||  ||
Db     616 GAACCCTCCTCTATACAATGAGGTTAACAATTCATGCTGAGTGTCCCATGCATTTGGAAG 675

Qy     642 GATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGA 701
           |||||  ||||||   ||  | |||||  ||    ||    |||| | |||||  |
Db     676 ATTTTCCCATGGATGTGCATGCCTGCCCACTGAAGTTTGGAAGCTATGCCTATACAACAG 735

Qy     702 ATGAGATGATCTACAAGTGG------GAAAATTTCAAGCTTGAAATCAATGAGAAGAACT 755
           |||  || | ||    |||       | |||   |||     |         |   || |
Db     736 CTGAAGTGGTTTATTCTTGGACTCTCGGAAAGAACAAATCCGTGGAAGTGGCACAGGATG 795

Qy     756 CCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACAA 815
           |       |   ||||| |||  ||   ||                  || || ||||||
Db     796 GTTCTCGCTTGAACCAGTATGACCTTTTGGGCCATGTTGTTGGGACAGAGATAATCCGGT 855

Qy     816 CCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCT 875
           |       || || |   | ||||||||  |    |||| || | |   |     ||||||
Db     856 CTAGTACAGGAGAATATGTCGTCATGACAACCCACTTCCATCTCAAGCGAAAAATTGGCT 915
```

```
Qy    876 ATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCT 935
Db    916 ACTTTGTGATCCAGACCTACTTGCCATGTATCATGACTGTCATTCTGTCACAAGTGTCGT 975

Qy    936 TTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGA 995
Db    976 TCTGGCTCAACAGAGAGTCTGTTCCTGCCCGTACAGTCTTTGGTGTCACCACTGTGCTTA 1035

Qy    996 CCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAG 1055
Db   1036 CCATGACCACCTTGAGTATCAGTGCCAGAAATTCCTTACCTAAAGTGGCATATGCGACGG 1095

Qy   1056 CCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTG 1115
Db   1096 CCATGGACTGGTTCATAGCCGTCTGTTATGCCTTTGTATTTTCTGCACTGATTGAATTTG 1155

Qy   1116 CTGTGCTCAACTTCCTGATCTA 1137
Db   1156 CCACTGTCAACTATTTCACCAA 1177
```

```
RESULT   4
US-08-417-330A-11
; Sequence 11, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2191 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  214...1566
;      OTHER INFORMATION:
```

US-08-417-330A-11

Query Match 7.1%; Score 224.4; DB 2; Length 2191;
Best Local Similarity 54.2%; Pred. No. 5.3e-56;
Matches 481; Conservative 0; Mismatches 401; Indels 6; Gaps 1;

```
Qy    258 GCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGA 317
Db    344 GAATTCTTGACAGACTTCTGGATGGTTACGATAATCGGCTTAGACCAGGACTGGGAGACA 403

Qy    318 AGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAG 377
Db    404 GTATTACTGAAGTCTTCACTAACATCTACGTGACCAGTTTTGGCCCTGTCTCAGATACAG 463

Qy    378 ACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTT 437
Db    464 ATATGGAATATACAATTGATGTTTTCTTTCGACAAAAATGGAAAGATGAACGTTTAAAAT 523

Qy    438 ACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCC 497
Db    524 TTAAAGGTCCTATGAATATCCTTCGACTAAACAATTTAATGGCTAGCAAAATCTGGACTC 583

Qy    498 CGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACC 557
Db    584 CAGATACCTTTTTTCACAATGGGAAGAAATCAGTAGCTCATAATATGACAATGCCAAATA 643

Qy    558 AGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATG 617
Db    644 AGTTGCTTCGAATTCAGGATGATGGGACTCTGCTGTATACCATGAGGCTTACAGTTCAAG 703

Qy    618 CCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTT 677
Db    704 CTGAATGCCCAATGCACTTGGAGGATTTCCCAATGGATGCTCATTCATGTCCTCTGAAAT 763

Qy    678 TCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTG 737
Db    764 TTGGCAGCTATGCATATACAACTTCAGAGGTCACTTATATTTGGACTTACAATGCATCTG 823

Qy    738 A------AATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGA 791
Db    824 ATTCAGTACAGGTTGCTCCTGATGGCTCTAGGTTAAATCAATATGACCTGCTGGGCCAAT 883

Qy    792 GCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCT 851
Db    884 CAATCGGAAAGGAGACAATTAAATCCAGTACAGGTGAATATACTGTAATGACAGCTCATT 943

Qy    852 TCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGA 911
Db    944 TCCACCTGAAAAGAAAAATTGGGTATTTTGTGATTCAAACCTATCTGCCTTGCATCATGA 1003

Qy    912 CCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCT 971
Db   1004 CTGTCATTCTCTCCCAAGTTTCATTCTGGCTTAACAGAGAATCTGTGCCTGCAAGAACTG 1063

Qy    972 CTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATT 1031
Db   1064 TGTTTGGAGTAACAACTGTCCTAACAATGACAACTCTAAGCATCAGTGCTCGGAATTCTC 1123

Qy   1032 TCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCT 1091
Db   1124 TCCCCAAAGTGGCTTATGCAACTGCCATGGACTGGTTTATTGCTGTTTGTTATGCATTTG 1183

Qy   1092 GCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACA 1139
Db   1184 TGTTCTCTGCCCTAATTGAATTTGCAACTGTTAATTACTTCACCAAAA 1231
```

```
RESULT   5
US-08-417-330A-19
; Sequence 19, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1866 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  225...1646
;      OTHER INFORMATION:
US-08-417-330A-19


  Query Match             5.4%;  Score 169;  DB 2;  Length 1866;
  Best Local Similarity   49.6%;  Pred. No. 9.1e-40;
  Matches  433;  Conservative    0;  Mismatches  440;  Indels    0;  Gaps    0;

Qy    264 TGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCA 323
Db    343 TGGATAGACTCCTGAAAGGCTATGACATTCGTCTGAGACCAGATTTTGGAGGTCCCCCCG 402

Qy    324 CTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGG 383
Db    403 TGGCTGTGGGGATGAACATTGACATTGCCAGCATCGATATGGTTTCTGAAGTCAATATGG 462

Qy    384 AATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACG 443
Db    463 ATTATACCTTGACAATGTACTTTCAACAAGCCTGGAGAGATAAGAGGCTGTCCTATAATG 522

Qy    444 ACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACA 503
Db    523 TAATACCTTTAAACTTGACTCTGGACAACAGAGTGGCAGACCAGCTCTGGGTGCCTGATA 582

Qy    504 CCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGG 563
Db    583 CCTATTTCCTGAACGATAAGAAGTCATTTGTGCACGGAGTGACTGTTAAGAACCGCATGA 642

Qy    564 TCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGAT 623
Db    643 TTCGCCTGCATCCTGATGGCACCGTCCTTTATGGACTCAGAATCACAACCACAGCTGCCT 702

Qy    624 GCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTA 683
Db    703 GCATGATGGACCTAAGGAGGTACCCACTGGATGAACAAAACTGCACCTTGGAAATTGAGA 762

Qy    684 GCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCA 743
Db    763 GCTATGGATACACAACTGATGACATTGAGTTTTACTGGCGTGGCGATGATAATGCAGTAA 822

Qy    744 ATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTG 803
Db    823 CAGGAGTAACGAAAATTGAACTTCCACAGTTCTCTATTGTAGATTACAAACTTATCACCA 882

Qy    804 AAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCA 863
Db    883 AGAAGGTTGTTTTTTCCACAGGTTCCTATCCCAGGTTATCCCTCAGCTTTAAGCTTAAGA 942

Qy    864 GGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCT 923
Db    943 GAAACATTGGCTACTTTATCCTGCAAACATACATGCCTTCCATCCTGATTACCATCCTCT 1002

Qy    924 CCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCA 983
Db   1003 CCTGGGTCTCCTTCTGGATTAATTACGATGCTTCAGCTGCAAGGGTGGCATTAGGAATCA 1062

Qy    984 CCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCT 1043
Db   1063 CAACTGTCCTCACAATGACCACAATCAACACCCACCTCCGGGAAACTCTCCCTAAAATCC 1122

Qy   1044 CCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTC 1103
Db   1123 CCTATGTGAAGGCCATTGACATGTACCTGATGGGGTGCTTTGTCTTCGTTTTCATGGCCC 1182

Qy   1104 TGTTGGAGTTTGCTGTGCTCAACTTCCTGATCT 1136
Db   1183 TTCTGGAATATGCCCTAGTCAACTACATCTTCT 1215


RESULT   6
US-08-768-301-3
; Sequence 3, Application US/08768301
; Patent No. 5854002
;  GENERAL INFORMATION:
;    APPLICANT:  Tomalski, Michael D.
;    APPLICANT:  Gant, Daniel B.
;    TITLE OF INVENTION:  METHOD OF IDENTIFYING COMPOUNDS THAT BIND
;    TITLE OF INVENTION:  TO THE INSECT GABA RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brumbaugh, Graves, Donohue & Raymond
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  10112-0228
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/768,301
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacLeod, Janet M
;      REGISTRATION NUMBER:  35,263
```

```
;      REFERENCE/DOCKET NUMBER:  A30693
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-408-2500
;      TELEFAX:  212-765-2519
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2635 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
US-08-768-301-3


  Query Match             4.1%;  Score 129.6;  DB 3;  Length 2635;
  Best Local Similarity   53.1%;  Pred. No. 4.2e-28;
  Matches  276;  Conservative    0;  Mismatches  244;  Indels    0;  Gaps    0;

Qy     261 TCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGC 320
           | ||| ||| | | ||| |    |||||| | |   | || || |   | || |      |
Db     693 TACTGGACAATCTGCTGCGCGGCTATGACAATAGCATACGTCCGGATTTCGGTGGACCTC 752

Qy     321 CCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACA 380
           |  |     |    || || ||    ||   |||| | || ||  | ||      | || |
Db     753 CAGCCACTATTGAAGTGGATATAATGGTTCGCAGCATGGGCCCAATATCAGAGGTCGATA 812

Qy     381 TGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACA 440
           ||   ||| | || |||      |||  |||  |||||   ||  |||| |||   | |
Db     813 TGACCTACTCGATGGACTGTTATTTCCGCCAATCCTGGGTGGATAAACGTCTCGCATTCG 872

Qy     441 ACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGG 500
           | | | ||   ||  | || |  ||||  | |    || ||   | | | ||||  ||||
Db     873 AGGGCGCCCAGGACACGCTGGCACTGAGCGTCTCGATGTTGGCACGGATTTGGAAGCCGG 932

Qy     501 ACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGA 560
           | || |  |||   ||    |||  || | |   |||  ||| |||| ||| ||  ||
Db     933 ATACGTACTTTTACAACGGCAAGCAGAGCTATTTGCACACGATTACCACGCCAAATAAGT 992

Qy     561 TGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCG 620
           | ||  | |||||  || | ||    ||| ||||| | |   || |||| ||| | ||||
Db     993 TTGTGAGGATCTATCAGAACGGACGCGTGCTGTACTCCAGCCGGCTGACAATTAAAGCCG 1052

Qy     621 GATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCT 680
           | ||| |  |  |  ||  |   ||||||||||||   ||    || |||||    |||
Db    1053 GCTGCCCCATGAATCTGGCCGATTTTCCAATGGATATACAAAAGTGTCCTCTGAAATTCG 1112

Qy     681 CTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAA 740
           |   |||  |||  |   |   ||  | ||||||   ||| | ||    |  |
Db    1113 GTTCATTTGGCTACACAACGTCGGATGTCATCTACCGTTGGAACAAAGAAAGACCACCCG 1172

Qy     741 TCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 780
           ||          |   |  |||||| | ||| || |||||
Db    1173 TCGCCATTGCCGAGGACATGAAGCTGTCCCAATTCGATTT 1212


RESULT   7
US-08-137-614A-3
; Sequence 3, Application US/08137614A
; Patent No. 5487976
;  GENERAL INFORMATION:
;    APPLICANT:  Soderlund, David M.
;    APPLICANT:  Knipple, Douglas C.
;    APPLICANT:  Henderson, Joseph E.
;    TITLE OF INVENTION:  Gene Encoding An Insect
;    TITLE OF INVENTION:  Gamma-Aminobutyric Acid (GABA) Receptor Subunit
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,614A
;      FILING DATE:  15-OCT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716)263-1636
;      TELEFAX:  (716)263-1600
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-137-614A-3


  Query Match             3.9%;  Score 122;  DB 1;  Length 1491;
  Best Local Similarity   51.6%;  Pred. No. 5.1e-26;
  Matches  331;  Conservative    0;  Mismatches  305;  Indels    6;  Gaps    2;

Qy     486 AGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCA 545
           || ||||| | ||||| || || ||    |||   || | |        ||| ||  |||
Db     389 AGATATGGGTACCGGATACGTTCTTCGCCAATGACAAAAACAGTTTTCTGCACGATGTCA 448

Qy     546 CCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGA 605
           ||       ||| |  |||| ||  |   |  |||||    ||    ||    || ||
Db     449 CCGAAAGGAACAAACTGGTGCGACTTGGCGGCGATGGAGCTGTTACTTATGGCATGAGAT 508

Qy     606 TGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTT 665
           | ||||        ||  |||    |  |  ||| |   | |||| |||| || ||   ||
Db     509 TCACCACGACCCTCGCCTGCATGATGGATCTGCACTACTATCCATTGGACTCGCAGAATT 568

Qy     666 GCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAA 725
           || || |     |    |||| |   ||  | |  |  ||  || ||     | ||| |
Db     569 GCACTGTGGAAATTGAGAGCTATGGATACACGGTCAGCGATGTGGTCATGTACTGGAA-- 627

Qy     726 ATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAG 785
           |  | |   |   |  |||  ||      |||    |  |   |    |     |
Db     627 ---GCCAACGCCAGTGCGCGGAGTGGAGGATGCGGAGCTGCCGCAGTTCACCATCATTGG 683

Qy     786 GAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGA 845
           |  ||||    |  || |||| | |       |||  ||| | ||    |  | |  ||
Db     684 GTATGAGACCAATGACCGAAAGGAGCGGCTGGCCAC-TGGAGTCTATCAGCGCCTCTCGC 742

Qy     846 TTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTT 905
           | |  |||||  ||    ||    | || ||  |||  || ||||  ||| | ||
Db     743 TCTCATTCAAACTGCAACGGAATATCGGATACTTTGTATTCCAAACTTATCTGCCCAGCA 802

Qy     906 CCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCC 965
           |||  |  ||||| || ||||| || || ||||| ||    ||| |  |    ||||
Db     803 TTCTGATCGTAATGCTGTCGTGGGTCTCGTTCTGGATTAACCACGAGGCGACGAGTGCCC 862

Qy     966 GGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTA 1025
           ||    |  | || |||||| | || || ||||||||||||  |  ||||   |  ||| |
Db     863 GGGTTGCATTGGGCATCACCACGGTGCTCACCATGACCACCATTAGCACGGGTGTTCGCA 922

Qy    1026 AGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCG 1085
              | |||||  | || ||| | |  ||  | ||  | ||| | | ||| |||||||
```

```
Db    923 GCTCACTGCCGCGCATATCGTATGTGAAGGCGATCGACATTTATCTGGTCATGTGCTTCG 982

Qy   1086 TCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACT 1127
          | |||   |||   || || ||||| |  ||||   | ||||
Db    983 TTTTCGTGTTCGCAGCCCTCTTGGAATACGCTGCCGTTAACT 1024


RESULT   8
US-08-768-301-1
; Sequence 1, Application US/08768301
; Patent No. 5854002
;  GENERAL INFORMATION:
;    APPLICANT:  Tomalski, Michael D.
;    APPLICANT:  Gant, Daniel B.
;    TITLE OF INVENTION:  METHOD OF IDENTIFYING COMPOUNDS THAT BIND
;    TITLE OF INVENTION:  TO THE INSECT GABA RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brumbaugh, Graves, Donohue & Raymond
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  10112-0228
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/768,301
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacLeod, Janet M
;      REGISTRATION NUMBER:  35,263
;      REFERENCE/DOCKET NUMBER:  A30693
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-408-2500
;      TELEFAX:  212-765-2519
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
US-08-768-301-1


  Query Match             3.9%;  Score 122;  DB 3;  Length 1491;
  Best Local Similarity   51.6%;  Pred. No. 5.1e-26;
  Matches  331;  Conservative    0;  Mismatches  305;  Indels    6;  Gaps    2;

Qy    486 AGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCA 545
          || ||||| | ||||| || || ||    |||   || |  |       ||| ||  |||
Db    389 AGATATGGGTACCGGATACGTTCTTCGCCAATGACAAAAACAGTTTTCTGCACGATGTCA 448

Qy    546 CCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGA 605
          ||      ||| |  |||| ||  |    |   |||||    ||     ||    || ||
Db    449 CCGAAAGGAACAAACTGGTGCGACTTGGCGGCGATGGAGCTGTTACTTATGGCATGAGAT 508

Qy    606 TGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTT 665
          | ||||       ||  |||    |  |  ||| |   | |||| |||| || ||   ||
Db    509 TCACCACGACCCTCGCCTGCATGATGGATCTGCACTACTATCCATTGGACTCGCAGAATT 568

Qy    666 GCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAA 725
          || || |      |    |||| |   ||  | |  |  ||  || ||    | ||| |
Db    569 GCACTGTGGAAATTGAGAGCTATGGATACACGGTCAGCGATGTGGTCATGTACTGGAA-- 627

Qy    726 ATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAG 785
          |  | |   |   |   |||  ||       |||    |  |   |      |     |
Db    627 ---GCCAACGCCAGTGCGCGGAGTGGAGGATGCGGAGCTGCCGCAGTTCACCATCATTGG 683

Qy    786 GAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGA 845
          |  ||||    |  || ||||  | |       |||  ||| | ||    |  | |  ||
Db    684 GTATGAGACCAATGACCGAAAGGAGCGGCTGGCCAC-TGGAGTCTATCAGCGCCTCTCGC 742

Qy    846 TTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTT 905
          | |  |||||  ||     ||    | || ||  |||  || ||||  ||| | ||
Db    743 TCTCATTCAAACTGCAACGGAATATCGGATACTTTGTATTCCAAACTTATCTGCCCAGCA 802

Qy    906 CCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCC 965
          |||  |   ||||| || ||||| || || ||||| ||    ||| |  |    ||||
Db    803 TTCTGATCGTAATGCTGTCGTGGGTCTCGTTCTGGATTAACCACGAGGCGACGAGTGCCC 862

Qy    966 GGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTA 1025
          ||    |  | || |||||| | || || |||||||||||  |  ||||   |  ||| |
Db    863 GGGTTGCATTGGGCATCACCACGGTGCTCACCATGACCACCATTAGCACGGGTGTTCGCA 922

Qy   1026 AGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCG 1085
          |  |||||  | || ||| | |  ||  | ||  | ||| | | ||| |||||||
Db    923 GCTCACTGCCGCGCATATCGTATGTGAAGGCGATCGACATTTATCTGGTCATGTGCTTCG 982

Qy   1086 TCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACT 1127
          | |||   |||   || || ||||| |  ||||   | ||||
Db    983 TTTTCGTGTTCGCAGCCCTCTTGGAATACGCTGCCGTTAACT 1024


RESULT   9
US-08-249-112-1
; Sequence 1, Application US/08249112
; Patent No. 5527703
;  GENERAL INFORMATION:
;    APPLICANT:  Cully, Doris F.
;    APPLICANT:  Arena, Joseph P.
;    APPLICANT:  Liu, Ken K.
;    APPLICANT:  Vassilatis, Demetrios
;    TITLE OF INVENTION:  DNA ENCODING GLUTAMATE GATED CHLORIDE
;    TITLE OF INVENTION:  CHANNELS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wallen, John W.
;      STREET:  126 E. Lincoln Ave., P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/249,112
;      FILING DATE:  25-MAY-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wallen, John W.
;      REGISTRATION NUMBER:  35,403
;      REFERENCE/DOCKET NUMBER:  19194
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-3905
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1542 base pairs
;      TYPE:  nucleic acid
```

```
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-249-112-1


  Query Match             3.8%;  Score 119.2;  DB 1;  Length 1542;
  Best Local Similarity   48.2%;  Pred. No. 3.5e-25;
  Matches  402;  Conservative    0;  Mismatches  423;  Indels    9;  Gaps    2;

Qy     320 CCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGAC 379
           ||   ||||||  | ||| | ||   | |     |   ||        |   | | |  |
Db     312 CCAGTTGTGGTTTCAGTTAACATGCTCCTTCGAACTATTTCAAAGATAGATGTTGTGAAT 371

Qy     380 ATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTAC 439
           |||||  || |     | |  | |  ||      |||  |||   ||| |  | ||| | |||
Db     372 ATGGAGTATAGTGCTCAATTGACATTGCGAGAGAGTTGGATTGACAAGAGACTCAGCTAC 431

Qy     440 ------AACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGG 493
                 || |       | || |   | || ||| |  || ||| |     ||  | |||
Db     432 GGAGTAAAAGGAGATGGTCAGCCAGATTTTGTGATTCTCACTGTTGGACATCAAATTTGG 491

Qy     494 ATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCC 553
           || || ||||| |||||    ||||   ||      |  || ||||||  |||    | |||
Db     492 ATGCCCGACACGTTTTTCCCGAATGAGAAACAAGCTTACAAGCATACGATTGATAAGCCG 551

Qy     554 AACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATT 613
           ||      || | || ||  |||| ||||| |  || ||||||  |  || | ||  |  |
Db     552 AATGTATTGATTCGAATACACAATGATGGTACAGTATTGTACTCTGTTCGTATTTCACTA 611

Qy     614 GATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTA 673
           |    |   ||| || |  |  | |     | ||||||||||  |||    ||  |  |
Db     612 GTCCTCTCTTGCCCAATGTATCTACAGTACTATCCAATGGATGTTCAACAGTGTTCCATT 671

Qy     674 TCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGG---GAAAATTTC 730
             | |  |    | | ||||  ||   || || ||    ||   ||||  ||  |||
Db     672 GATCTTGCATCGTATGCCTACACTACAAAAGATATCGAATATTTGTGGAAAGAGCATTCA 731

Qy     731 AAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTG 790
           |||  |  | ||  |          ||  |   | |       ||  | || ||
Db     732 CCACTTCAGTTAAAGGTTGGATTATCAAGCTCGTTGCCTTCATTCCAGTTGACTAATACT 791

Qy     791 AGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTC 850
             | | |  |   |  |    |||      |||   |          ||   | |
Db     792 TCAACGACATATTGCACCAGTGTAACAAACACTGGCATTTATTCCTGTTTGCGAACTACT 851

Qy     851 TTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTG 910
           |  | | |  ||   |||  | | |        | |||  |||  |||| || | | ||
Db     852 ATTCAGTTAAAGAGAGAGTTCAGTTTTACCTTCTCCAACTCTACATCCCGTCATGCATG 911

Qy     911 ACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACC 970
             ||  | ||||||||||| |||||| |  |   |    |    || || ||   |
Db     912 CTAGTCATCGTATCCTGGGTTTCATTTTGGTTTGATCGAACTGCAATCCCGGCTCGTGTC 971

Qy     971 TCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAAT 1030
           | || ||  ||||| |  | || || |||||  |         ||  |      |    |
Db     972 ACCCTCGGAGTCACCACGCTGCTTACAATGACAGCTCAATCAGCCGGTATCAATTCACAA 1031

Qy    1031 TTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTC 1090
           | || |  || |||||||||  ||  | ||| |||  || |     ||  |   |||
Db    1032 CTACCTCCAGTTTCCTATATCAAGGCGATTGATGTCTGGATTGGTGCATGTATGACATTC 1091

Qy    1091 TGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAACCAG 1144
           |||||||  ||||||||||||  || | ||      |    |||| |||
Db    1092 ATTTTCTGCGCGTTGTTGGAGTTTGCATTGGTAAATCATATAGCTAACAAGCAG 1145


RESULT  10
PCT-US95-06556-1
; Sequence 1, Application PC/TUS9506556
;  GENERAL INFORMATION:
;    APPLICANT:  Cully, Doris F.
;    APPLICANT:  Arena, Joseph P.
;    APPLICANT:  Liu, Ken K.
;    APPLICANT:  Vassilatis, Demetrios
;    TITLE OF INVENTION:  DNA ENCODING GLUTAMATE GATED CHLORIDE
;    TITLE OF INVENTION:  CHANNELS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wallen, John W.
;      STREET:  126 E. Lincoln Ave., P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06556
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/249,112
;      FILING DATE:  25-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wallen, John W.
;      REGISTRATION NUMBER:  35,403
;      REFERENCE/DOCKET NUMBER:  19194
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-3905
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1542 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US95-06556-1


  Query Match             3.8%;  Score 119.2;  DB 6;  Length 1542;
  Best Local Similarity   48.2%;  Pred. No. 3.5e-25;
  Matches  402;  Conservative    0;  Mismatches  423;  Indels    9;  Gaps    2;

Qy     320 CCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGAC 379
           ||   ||||||  | ||| | ||   | |     |   ||        |   | | |  |
Db     312 CCAGTTGTGGTTTCAGTTAACATGCTCCTTCGAACTATTTCAAAGATAGATGTTGTGAAT 371

Qy     380 ATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTAC 439
           |||||  || |     | |  | |  ||      |||  |||   ||| |  | ||| | |||
Db     372 ATGGAGTATAGTGCTCAATTGACATTGCGAGAGAGTTGGATTGACAAGAGACTCAGCTAC 431

Qy     440 ------AACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGG 493
                 || |       | || |   | || ||| |  || ||| |     ||  | |||
Db     432 GGAGTAAAAGGAGATGGTCAGCCAGATTTTGTGATTCTCACTGTTGGACATCAAATTTGG 491

Qy     494 ATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCC 553
           || || ||||| |||||    ||||   ||      |  || ||||||  |||    | |||
Db     492 ATGCCCGACACGTTTTTCCCGAATGAGAAACAAGCTTACAAGCATACGATTGATAAGCCG 551

Qy     554 AACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATT 613
           ||      || | || ||  |||| ||||| |  || ||||||  |  || | ||  |  |
Db     552 AATGTATTGATTCGAATACACAATGATGGTACAGTATTGTACTCTGTTCGTATTTCACTA 611

Qy     614 GATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTA 673
           |    |   ||| || |  |  | |     | ||||||||||  |||    ||  |  |
Db     612 GTCCTCTCTTGCCCAATGTATCTACAGTACTATCCAATGGATGTTCAACAGTGTTCCATT 671

Qy     674 TCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGG---GAAAATTTC 730
             | |  |    | | ||||  ||   || || ||    ||   ||||  ||  |||
Db     672 GATCTTGCATCGTATGCCTACACTACAAAAGATATCGAATATTTGTGGAAAGAGCATTCA 731
```

```
Qy     731 AAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTG 790
Db     732 CCACTTCAGTTAAAGGTTGGATTATCAAGCTCGTTGCCTTCATTCCAGTTGACTAATACT 791

Qy     791 AGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTC 850
Db     792 TCAACGACATATTGCACCAGTGTAACAAACACTGGCATTTATTCCTGTTTGCGAACTACT 851

Qy     851 TTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTG 910
Db     852 ATTCAGTTAAAGAGAGAGTTCAGTTTTTACCTTCTCCAACTCTACATCCCGTCATGCATG 911

Qy     911 ACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACC 970
Db     912 CTAGTCATCGTATCCTGGGTTTCATTTTGGTTTGATCGAACTGCAATCCCGGCTCGTGTC 971

Qy     971 TCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAAT 1030
Db     972 ACCCTCGGAGTCACCACGCTGCTTACAATGACAGCTCAATCAGCCGGTATCAATTCACAA 1031

Qy    1031 TTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTC 1090
Db    1032 CTACCTCCAGTTTCCTATATCAAGGCGATTGATGTCTGGATTGGTGCATGTATGACATTC 1091

Qy    1091 TGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAACCAG 1144
Db    1092 ATTTTCTGCGCGTTGTTGGAGTTTGCATTGGTAAATCATATAGCTAACAAGCAG 1145
```

```
RESULT  11
US-08-435-933-5
; Sequence 5, Application US/08435933
; Patent No. 5693492
;  GENERAL INFORMATION:
;    APPLICANT:  Cully, Doris F.
;    APPLICANT:  Arena, Joseph P.
;    APPLICANT:  Paress, Philip S.
;    APPLICANT:  Liu, Ken K.
;    TITLE OF INVENTION:  DNA ENCODING GLUTAMATE GATED CHLORIDE
;    TITLE OF INVENTION:  CHANNELS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  John W. Wallen III
;      STREET:  126 East Lincoln Avenue
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  US
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,933
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wallen, III John W.
;      REGISTRATION NUMBER:  35,403
;      REFERENCE/DOCKET NUMBER:  19264
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-3905
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3958 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-435-933-5
```

```
  Query Match             3.6%;  Score 112;  DB 2;  Length 3958;
  Best Local Similarity   48.5%;  Pred. No. 7.9e-23;
  Matches  397;  Conservative    0;  Mismatches  415;  Indels    6;  Gaps    3;

Qy     313 AGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTAT 372
Db     578 AGATGGTCCCGCCATAGTCAGAATCAATCTATTCGTTCGCAGTATTATGACGATTAGTGA 637

Qy     373 CCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCT 432
Db     638 TATTAAAATGGAGTACAGTGTGCAGTTAACCTTCCGTGAACAGTGGACGGATGAACGCCT 697

Qy     433 CTGTTACAACGACACCTTTGAGTCTCT---TGTTCTGAATGGCAATGTGGTGAGCCAGCT 489
Db     698 CAAGTTCGACGATATCCAGGGTCGCCTAAAGTATCTGACCCTGACGGAGGCGAACCGCGT 757

Qy     490 ATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCAT 549
Db     758 GTGGATGCCCGATCTTTTCTTCTCGAACGAGAAGGAGGGACACTTCCACAACATCATCAT 817

Qy     550 GCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGAC 609
Db     818 GCCCAATGTGTATATTCGCATCTTCCCCAACGGATCTGTGCTATATAGTATACGTATCTC 877

Qy     610 CATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCC 669
Db     878 GCTGACATTGGCCTGCCCAATGAACCTAAAGCTGTATCCGCTGGATAGACAGATCTGCTC 937

Qy     670 TCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTT 729
Db     938 ACTACGGATGGCCAGCTATGGCTGGACCACCAACGACTTGGTCTTCCTGTGGAAGGAGGG 997

Qy     730 CAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGT 789
Db     998 CGATCCCGTACAGGTGGTAAAGAACT--TACACCTACCTCGCTTCACACTGGAGAAGTTT 1055

Qy     790 GAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTT 849
Db    1056 CTGACTGATTACTGTAACAGTAAAACCAACACCGGTGAATACAGTTGCCTCAAAGTCGAT 1115

Qy     850 CTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGT 909
Db    1116 CTACTAT-TCAGGCGAGAATTCTCATATTACTTAATACAAATTTATATACCATGCTGTAT 1174

Qy     910 GACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGAC 969
Db    1175 GTTGGTCATTGTATCATGGGTATCATTCTGGCTGGATCAAGGAGCAGTACCGGCGCGAGT 1234

Qy     970 CTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAA 1029
Db    1235 GTCACTGGGTGTCACCACCCTGCTGACCATGGCCACCCAGACGTCGGGCATAAACGCCTC 1294

Qy    1030 TTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTT 1089
Db    1295 CCTGCCGCCCGTTTCCTATACGAAGGCCATCGATGTGTGGACAGGCGTGTGTCTGACGTT 1354

Qy    1090 CTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACT 1127
Db    1355 CGTGTTCGGGGCCCTGCTCGAGTTCGCCCTGGTGAACT 1392
```

```
RESULT  12
US-08-554-659-1
; Sequence 1, Application US/08554659
; Patent No. 5767261
;  GENERAL INFORMATION:
;    APPLICANT:  Wingate, Vincent
;    APPLICANT:  Wolff, Mark
;    TITLE OF INVENTION:  LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
;    TITLE OF INVENTION:  AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  Scully, Scott, Murphy & Presser
;       STREET:  400 Garden City Plaza
;       CITY:  Garden City
;       STATE:  New York
;       COUNTRY:  USA
;       ZIP:  11530-0299
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/554,659
;       FILING DATE:
;       CLASSIFICATION:  436
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DiGiglio, Frank S
;       REGISTRATION NUMBER:  31,346
;       REFERENCE/DOCKET NUMBER:  9732
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (516) 742-4343
;       TELEFAX:  (516) 742-4366
;       TELEX:  230 901 SANS UR
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1657 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  115..1581
US-08-554-659-1


  Query Match             3.6%;  Score 112;  DB 2;  Length 1657;
  Best Local Similarity   46.3%;  Pred. No. 4.7e-23;
  Matches  410;  Conservative    0;  Mismatches  470;  Indels    6;  Gaps    1;

Qy     253 CTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGG 312
           |||   |||  || |  |  |       |  || ||| | | | || | ||   |  |||
Db     243 CTCAGCCATTTTGGATTCGCTAAGTGTAAGCTACGACAAAAGAGTGAGGCCGAACTATGG 302

Qy     313 AGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTAT 372
           ||    |||    |  ||    ||  | ||   |||   |  | |  |  |  | |||
Db     303 AGGACCGCCAGTGGATGTGGGAGTCAACATGTACGTGCTCTCCATCAGCTCCTTATCTGA 362

Qy     373 CCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCT 432
           |  | |||||  | |||| | ||  ||  ||||   ||    |||   |||    | ||
Db     363 AGTGAAAATGGATTTCACCCTGGATTTCTACTTCAGACAATTTTGGACAGACCCCAGGCT 422

Qy     433 CTGTTACAACGACACCT------TTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCA 486
           ||||||  | | |       | ||| ||||     |       |  |  | ||  |
Db     423 TGCTTACAAAAAAAGCACGGGTGTGGAGACTCTGTCCGTCGGCTCGGAATTTATTAGAAA 482

Qy     487 GCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCAC 546
           |||||  | || ||||||||  |||   ||   ||  | |  |   ||       ||
Db     483 CATATGGGTACCCGACACCTTCTTTGTTAACGAAAAACAGTCATATTTCCACATAGCTAC 542

Qy     547 CATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGAT 606
           |    |||| |  |  | |||||  |  |   |||      |       |  || ||  |
Db     543 TACAAGCAACGAATTCATACGCATTCATCATTCTGGATCTATTACTAGGAGTATAAGACT 602

Qy     607 GACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTG 666
           |||  ||    ||   ||  |  |  |||     ||||| |||||   |||  |  ||
Db     603 GACTATCACCGCTTCTTGTCCGATGGATTTGCAGTATTTTCCGATGGACCGTCAATTATG 662

Qy     667 CCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA 726
           |  | |      ||   || |||  |||  |   |   ||  ||    |||||||||  |  |
Db     663 CAATATTGAAATCGAAAGTTTTGGCTACACCATGCGGGACATCCGATACAAGTGGAATGA 722

Qy     727 TTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGG 786
                   | |   || |  || |      |    |    || ||  |  |    ||
Db    723 GGGGCCCAACTCAGTGGGTGTGTCGAGCGAAGTGTCTTTGCCGCAATTCAAGGTGCTGGG 782

Qy    787 AGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGAT 846
          |  |      |          ||  |      |    ||  |||  |        || |
Db    783 CCACCGGCAGCGGGCCATGGAGATTTCTCTTACGACAGGAAACTACTCTCGTCTGGCATG 842

Qy    847 TTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTC 906
          |    |  |  |      |   | | || ||   |    ||||  |  |||  | ||  |||
Db    843 TGAAATTCAATTTGTAGGCTCGATGGGATACTATTTAATTCAGATTTATATTCCGTCTGG 902

Qy    907 CGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCG 966
          | | |      ||  | || ||||| || |||||| | ||   | |  |  | || ||  |
Db    903 CCTAATTGTCATTATATCTTGGGTATCATTTTGGTTGAATCGAAATGCGACACCTGCAAG 962

Qy    967 GACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAA 1026
          |   || |||||  ||||  ||||  |||| ||||| ||| |      | |   |   |
Db    963 GGTATCACTAGGTGTCACAACTGTATTGACGATGACGACGCTCATGTCGTCCACGAATGC 1022

Qy    1027 GAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGT 1086
           |  | | ||      |||| ||| |||   || | ||| ||||| | |   |  || |||||
Db    1023 GGCTCTGCCCAAGATCTCATATGTCAAGTCCATCGATGTCTATCTGGGAACTTGTTTCGT 1082

Qy    1087 CTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTG 1132
           | |   ||||  |  | |  | || | |||   | |   ||   ||
Db    1083 CATGGTCTTCACCAGTTTACTAGAATATGCCACGGTTGGCTATATG 1128


RESULT  13
PCT-US96-06035-5
; Sequence 5, Application PC/TUS9606035
;  GENERAL INFORMATION:
;     APPLICANT:  Cully, Doris F.
;     APPLICANT:  Arena, Joseph P.
;     APPLICANT:  Paress, Philip S.
;     APPLICANT:  Liu, Ken K.
;     TITLE OF INVENTION:  DNA ENCODING GLUTAMATE GATED CHLORIDE
;     TITLE OF INVENTION:  CHANNELS
;     NUMBER OF SEQUENCES:  6
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Jody M. Giesser
;       STREET:  126 East Lincoln Avenue - P.O. BOX 2000-0907
;       CITY:  Rahway
;       STATE:  New Jersey
;       COUNTRY:  US
;       ZIP:  07065-0907
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US96/06035
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Giesser, Jody M.
;       REGISTRATION NUMBER:  32,838
;       REFERENCE/DOCKET NUMBER:  19264 PCT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (908) 594-3046
;       TELEFAX:  (908) 594-4720
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3958 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
PCT-US96-06035-5


  Query Match             3.6%;  Score 112;  DB 6;  Length 3958;
```

```
  Best Local Similarity   48.5%;  Pred. No. 7.9e-23;
  Matches  397;  Conservative    0;  Mismatches  415;  Indels    6;  Gaps    3;

Qy     313 AGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTAT 372
           |||    ||| |  | ||||   |  |  |   |||   |||  ||     |  |  |
Db     578 AGATGGTCCCGCCATAGTCAGAATCAATCTATTCGTTCGCAGTATTATGACGATTAGTGA 637

Qy     373 CCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCT 432
             |  | ||||| ||||   |  |  | | ||||    |    |||   || ||||||||
Db     638 TATTAAAATGGAGTACAGTGTGCAGTTAACCTTCCGTGAACAGTGGACGGATGAACGCCT 697

Qy     433 CTGTTACAACGACACCTTTGAGTCTCT---TGTTCTGAATGGCAATGTGGTGAGCCAGCT 489
           |   | | |||| | |    |      ||       |||||     |  | || || ||   |
Db     698 CAAGTTCGACGATATCCAGGGTCGCCTAAAGTATCTGACCCTGACGGAGGCGAACCGCGT 757

Qy     490 ATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCAT 549
           |||||  || ||    || ||   |||    |||  |   |||   ||  | |||| |||
Db     758 GTGGATGCCCGATCTTTTCTTCTCGAACGAGAAGGAGGGACACTTCCACAACATCATCAT 817

Qy     550 GCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGAC 609
           ||||||   |    | |||||||| |    | ||    ||| | || |  ||  | ||  |
Db     818 GCCCAATGTGTATATTCGCATCTTCCCCAACGGATCTGTGCTATATAGTATACGTATCTC 877

Qy     610 CATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCC 669
             |       |  ||| || |  || |       | |||  |||||   ||    ||| |
Db     878 GCTGACATTGGCCTGCCCAATGAACCTAAAGCTGTATCCGCTGGATAGACAGATCTGCTC 937

Qy     670 TCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTT 729
           |||    |  | |||| |  ||   |    || ||  || ||| |  |||| |  |
Db     938 ACTACGGATGGCCAGCTATGGCTGGACCACCAACGACTTGGTCTTCCTGTGGAAGGAGGG 997

Qy     730 CAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGT 789
           | | |  | |      |  |||||||  |  |    | ||   |   | |  | | |  |
Db     998 CGATCCCGTACAGGTGGTAAAGAACT--TACACCTACCTCGCTTCACACTGGAGAAGTTT 1055

Qy     790 GAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTT 849
             |    | |||| || | | | | |  ||   |   |      | | |   | |    |
Db    1056 CTGACTGATTACTGTAACAGTAAAACCAACACCGGTGAATACAGTTGCCTCAAAGTCGAT 1115

Qy     850 CTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGT 909
           || | ||  | ||  |    ||    |||        | ||||  ||| | || |  |   |
Db    1116 CTACTAT-TCAGGCGAGAATTCTCATATTACTTAATACAAATTTATATACCATGCTGTAT 1174

Qy     910 GACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGAC 969
           |      ||  | || ||||| || || ||| |  |   ||   | |  || || ||
Db    1175 GTTGGTCATTGTATCATGGGTATCATTCTGGCTGGATCAAGGAGCAGTACCGGCGCGAGT 1234

Qy     970 CTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAA 1029
           || || ||  ||||| |  | |||||||| ||||   |    |
Db    1235 GTCACTGGGTGTCACCACCCTGCTGACCATGGCCACCCAGACGTCGGGCATAAACGCCTC 1294

Qy    1030 TTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTT 1089
           | ||||  || |||||||  |  ||| | ||| | |  |  | | | ||  |    ||
Db    1295 CCTGCCGCCCGTTTCCTATACGAAGGCCATCGATGTGTGGACAGGCGTGTGTCTGACGTT 1354

Qy    1090 CTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACT 1127
           |   ||| | || ||| | ||||| ||  || | ||||
Db    1355 CGTGTTCGGGGCCCTGCTCGAGTTCGCCCTGGTGAACT 1392


RESULT  14
US-08-554-659-3
; Sequence 3, Application US/08554659
; Patent No. 5767261
;  GENERAL INFORMATION:
;    APPLICANT:  Wingate, Vincent
;    APPLICANT:  Wolff, Mark
;    TITLE OF INVENTION:  LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
;    TITLE OF INVENTION:  AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/554,659
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9732
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1657 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  115..1581
US-08-554-659-3


  Query Match             3.5%;  Score 110.4;  DB 2;  Length 1657;
  Best Local Similarity   46.2%;  Pred. No. 1.4e-22;
  Matches  409;  Conservative    0;  Mismatches  471;  Indels    6;  Gaps    1;

Qy     253 CTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGG 312
           |||   |||  || |  |  |         |  || ||| | | | || | ||   |  |||
Db     243 CTCAGCCATTTTGGATTCGCTAAGTGTAAGCTACGACAAAAGAGTGAGGCCGAACTATGG 302

Qy     313 AGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTAT 372
           ||    |||    |  ||    ||  | ||   |||    | | |  |   |  | |||
Db     303 AGGACCGCCAGTGGATGTGGGAGTCAACATGTACGTGCTCTCCATCAGCTCCTTATCTGA 362

Qy     373 CCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCT 432
             |  | |||||  | ||||  | ||  ||  ||||    ||     |||    |||     | ||
Db     363 AGTGAAAATGGATTTCACCCTGGATTTCTACTTCAGACAATTTTGGACAGACCCCAGGCT 422

Qy     433 CTGTTACAACGACACCT------TTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCA 486
             ||||||  | | |       | |||  ||||      |          |  |  | ||  |
Db     423 TGCTTACAAAAAAAGCACGGGTGTGGAGACTCTGTCCGTCGGCTCGGAATTTATTAGAAA 482

Qy     487 GCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCAC 546
             |||||  | ||  ||||||||  |||   ||    ||    | |  |    ||       ||
Db     483 CATATGGGTACCCGACACCTTCTTTGTTAACGAAAAACAGTCATATTTCCACATAGCTAC 542

Qy     547 CATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGAT 606
           |    |||| |  |  | |||||  |  |  |||      |        |  || ||  |
Db     543 TACAAGCAACGAATTCATACGCATTCATCATTCTGGATCTATTACTAGGAGTATAAGACT 602

Qy     607 GACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTG 666
           ||| ||    ||    ||  |  |  | |||     ||||| |||||   ||| |  ||
Db     603 GACTATCACCGCTTCTTGTCCGATGGATTTGCAGTATTTTCCGATGGACCGTCAATTATG 662

Qy     667 CCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA 726
           |  | |    ||   || |||  |||  |   |    || ||    |||||||||  |  |
Db     663 CAATATTGAAATCGAAAGTTTTGGCTACACCATGCGGGACATCCGATACAAGTGGAATGA 722

Qy     727 TTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGG 786
                 | |   || |  || |      |    |    || ||  |  |    ||
Db     723 GGGGCCCAACTCAGTGGGTGTGTCGAGCGAAGTGTCTTTGCCGCAATTCAAGGTGCTGGG 782
```

```
Qy    787 AGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGAT 846
Db    783 CCACCGGCAGCGGGCCATGGAGATTTCTCTTACGACAGGAAACTACTCTCGTCTGGCATG 842

Qy    847 TTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTC 906
Db    843 TGAAATTCAATTTGTAGGCTCGATGGGATACTATTTAATTCAGATTTATATTCCGTCTGG 902

Qy    907 CGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCG 966
Db    903 CCTAATTGTCATTATATCTTGGGTATCATTTTGGTTGAATCGAAATGCGACACCTGCAAG 962

Qy    967 GACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAA 1026
Db    963 GGTAGCACTAGGTGTCACAACTGTATTGACGATGACGACGCTCATGTCGTCCACGAATGC 1022

Qy   1027 GAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGT 1086
Db   1023 GGCTCTGCCCAAGATCTCATATGTCAAGTCCATCGATGTCTATCTGGGAACTTGTTTCGT 1082

Qy   1087 CTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTG 1132
Db   1083 CATGGTCTTCACCAGTTTACTAGAATATGCCACGGTTGGCTATATG 1128
```

```
RESULT  15
US-08-459-100A-1
; Sequence 1, Application US/08459100A
; Patent No. 5654172
;  GENERAL INFORMATION:
;    APPLICANT:  Li, ET AL.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,100A
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09589
;      FILING DATE:  26 AUG 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-325
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1650 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
US-08-459-100A-1
```

```
Query Match             3.4%;  Score 108.2;  DB 1;  Length 1650;
Best Local Similarity   47.9%;  Pred. No. 6.2e-22;
```

```
  Matches  376;  Conservative    0;  Mismatches  403;  Indels    6;  Gaps    2;

Qy    378 ACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTT 437
Db    392 ACATGGACTACACAGCCACCATATACCTCCGACAGCGCTGGATGGACCAGCGGCTGGTGT 451

Qy    438 ACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCC 497
Db    452 TTGAAGGCAAC---AAGAGCTTCACTCTGGATGCCCGCCTCGTGGAGTTCCTCTGGGTGC 508

Qy    498 CGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACC 557
Db    509 CAGATACTTACATTGTGGAGTCCAAGAAGTCCTTCCTCCATGAAGTCACTGTGGGAAACA 568

Qy    558 AGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATG 617
Db    569 GGCTCATCCGCCTCTTCTCCAATGGCACGGTCCTGTATGCCCTCAGAATCACGACAACTG 628

Qy    618 CCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTT 677
Db    629 TTGCATGTAACATGGATCTGTCTAAATACCCCATGGACACACAGACATGCAAGTTGCAGC 688

Qy    678 TCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTG 737
Db    689 TGGAAAGCTGGGGCTATGATGGAAATGATGTGGAGTTCACCTGGCTGAGAGGGAACGACT 748

Qy    738 AAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACA 797
Db    749 CTGTGCGTGGACTGGAACACCTGCGGCTTGCTCAGTACACCATAGAGCGGTATTTCACCT 808

Qy    798 AAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATG 857
Db    809 TAGTCACCAGATCGCAGCAGGAGACAGGAAATTACACTAGATTGGTCTTACAGTTTGAGC 868

Qy    858 TGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGA 917
Db    869 TTCGGAGGAATGTTCTGTATTTCATTTTGGAAACCTACGTTCCTTCCACTTTCCTGGTGG 928

Qy    918 TGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAG 977
Db    929 TGTTGTCCTGGGTTCTGTATTTCATTTTGGAAGATTCAGTCCCTGCAAGAACCTGCATTG 988

Qy    978 GGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCC-- 1036
Db    989 GAGTGACGACCGTGTTATCAATGACCACACTGATGATCGGGTCCCGCACTTCTCTTCCCA 1048

Qy   1036 -GCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCT 1094
Db   1049 ACACCAACTGCTTCATCAAGGCCATCGATGTGTACCTGGGGATCTGCTTTAGCTTTGTGT 1108

Qy   1095 TCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAACCAGACAAAAGCCC 1154
Db   1109 TTGGGGCCTTGCTAGAATATGCAGTTGCTCACTACAGTTCCTTACAGCAGATGGCAGCCA 1168

Qy   1155 ATGCT 1159
Db   1169 AAGAT 1173
```

```
Search completed:  March  9, 2000, 13:39:48
Job time:  936 sec
```

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2000, 22:43:31 ; Search time 235.59 Seconds
(without alignments)
3349.488 Million cell updates/sec

Title: US-09-030-832-41
Perfect score: 3154
Sequence: 1 CGCGACCTCCGCGCAGGTGG.....AGCAAAAAGAAAAAAAAAAA 3154

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3054.2	96.8	3123	1	V11776	GABA-A receptor ep
2	2852.2	90.4	3026	1	V11777	Variant of GABA-A
3	1943.6	61.6	10697	1	V11778	GABA-A receptor ep
4	1536.2	48.7	1552	1	V36319	Human GABA recepto
5	352.8	11.2	1565	1	T02334	GABA-A receptor ga
6	278.8	8.8	1707	1	T28988	Human GABA-A recep
7	264.6	8.4	1408	1	Q33130	GABA-A receptor al
8	264.6	8.4	1408	1	Q69142	Human GABA recepto
9	261.8	8.3	2310	1	Q33129	GABA-A receptor al
10	261.8	8.3	2310	1	Q69141	Human GABA recepto
11	239.2	7.6	1638	1	Q69140	Human GABA recepto
12	237.6	7.5	1638	1	Q33128	GABA-A receptor al
13	224.4	7.1	2189	1	Q33127	GABA-A receptor al
14	224.4	7.1	2189	1	Q69139	Human GABA recepto
15	196.8	6.2	1555	1	T28989	Human GABA-A recep
16	186	5.9	187	1	T21715	Human gene signatu
17	176	5.6	1884	1	V83111	Human GABA-A recep
18	176	5.6	1884	1	V83112	Human GABA-A recep
19	169	5.4	1866	1	Q33131	GABA-A receptor be
20	169	5.4	1866	1	Q69143	Human GABA recepto
21	139.4	4.4	675	1	Q25720	OmpF signal peptid
22	129.6	4.1	2635	1	V84686	Insect GABA recept
23	122	3.9	1491	1	Q99330	GABA receptor subu
24	122	3.9	1491	1	V84685	Insect GABA recept
25	119.2	3.8	1542	1	T09695	Caenorhabditis ele
26	114.6	3.6	1650	1	T10500	Human GABA-A recep
27	114.6	3.6	1650	1	T84630	Human GABA-A recep
28	112	3.6	3958	1	T43596	Glutamate-gated ch
29	112	3.6	1657	1	V55007	GABA gated chlorid
30	110.4	3.5	1657	1	V55008	GABA gated chlorid
31	108.8	3.4	1844	1	V64372	GABA-gated chlorid
32	106.8	3.4	657	1	Q25722	GABA-A receptor be
33	105.8	3.4	1368	1	X24372	Cat flea glutamate
34	105.4	3.3	660	1	Q25721	GABA-A receptor al
35	104.6	3.3	1519	1	V64373	GABA-gated chlorid
36	102.4	3.2	1297	1	X24373	Cat flea glutamate
37	93.4	3.0	669	1	V64374	GABA-gated chlorid
38	92	2.9	1823	1	X16065	DNA sequence of Lu
39	76.6	2.4	1479	1	T09696	Caenorhabditis ele
40	65.6	2.1	2059	1	Q40045	Sequence of cDNA N
41	45	1.4	45	1	V36324	Human GABA recepto
42	43.4	1.4	45	1	V36325	Human GABA recepto
43	39.2	1.2	152	1	T43599	Glutamate-gated ch
44	37.4	1.2	575	1	V55016	Fragment of GABA g
c 45	36.8	1.2	50000	1	X23517	Human kidney amino

ALIGNMENTS

RESULT 1
V11776
ID V11776 standard; cDNA; 3123 BP.
AC V11776;
DT 25-SEP-1998 (first entry)
DE GABA-A receptor epsilon sub-unit related gene.
KW ss; GABA-A receptor; diagnosis; therapy; drug screening.
OS Mammalia.
FH Key Location/Qualifiers
FT CDS 55. .1573
FT /*tag= a
FT /product= "GABA-A receptor epsilon sub-unit related
FT protein"
PN DE19644501-A1.
PD 30-APR-1998.
PF 25-OCT-1996; 044501.
PR 25-OCT-1996; DE-044501.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR WPI; 98-252096/23.
DR P-PSDB; W59048.
PT Protein related to GABA-A receptor sub-unit epsilon - useful for
PT diagnosis, therapy or drug screening
PS Example 1; Fig 1; 12pp; German.
CC The GABA-A receptor sub-unit epsilon related protein is used for the
CC diagnosis and/or therapy of related disorders. It can also be used to
CC screen for substances that modulate the activity of the protein.
SQ Sequence 3123 BP; 710 A; 877 C; 686 G; 849 T;

Query Match 96.8%; Score 3054.2; DB 1; Length 3123;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 3105; Conservative 0; Mismatches 3; Indels 29; Gaps 2;

```
Qy       1 CGCGACCTCCGCGCAGGTGGTCGCGCCGGTCTCCGCGGAAATGTTGTCCAAAGTTCTTCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      15 CGCGACCTCCGCGCAGGTGGTCGCGCCGGTCTCCGCGGAAATGTTGTCCAAAGTTCTTCC 74

Qy      61 AGTCCTCCTAGGCATCTTATTGATCCTCCAGTCGAGGGTCGAGGGACCTCAGACTGAATC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      75 AGTCCTCCTAGGCATCTTATTGATCCTCCAGTCGAGGGTCGAGGGACCTCAGACTGAATC 134

Qy     121 AAAGAATGAAGCCTCTTCCCGTGATGTTGTCTATGGCCCCCAGCCCCAGCCTCTGGAAAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     135 AAAGAATGAAGCCTCTTCCCGTGATGTTGTCTATGGCCCCCAGCCCCAGCCTCTGGAAAA 194

Qy     181 TCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     195 TCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAA 254

Qy     241 ACTGCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     255 ACTGCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCG 314

Qy     301 CCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGG 360
           ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db     315 CCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCTCCGTCAACAGCCTTGG 374

Qy     361 TCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     375 TCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTA 434
```

```
Qy    421 CGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    435 CGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGT 494

Qy    481 GAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    495 GAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGA 554

Qy    541 GATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAAT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    555 GATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAAT 614

Qy    601 TAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    615 TAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCA 674

Qy    661 CTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    675 CTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTG 734

Qy    721 GGAAAATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    735 GGAAAATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 794

Qy    781 TACAGGAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCAT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    795 TACAGGAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCAT 854

Qy    841 GACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    855 GACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCC 914

Qy    901 TTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    915 TTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCC 974

Qy    961 AGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    975 AGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTC 1034

Qy   1021 TCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1035 TCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTG 1094

Qy   1081 CTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1095 CTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAA 1154

Qy   1141 CCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1155 CCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCA 1214

Qy   1201 TGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1215 TGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTG 1274

Qy   1261 CCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1275 CCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCA 1334

Qy   1321 GCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1335 GCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTG 1394

Qy   1381 TGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTAC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1395 TGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTAC 1454

Qy   1441 CTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1455 CTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGT 1514

Qy   1501 TTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1515 TTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTA 1574

Qy   1561 GGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1575 GGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTT 1634

Qy   1621 GCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1635 GCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCC 1694

Qy   1681 CATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGC 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1695 CATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGC 1754

Qy   1741 CCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1755 CCATTCACTGAGTTTTCTCAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCT 1814

Qy   1801 CTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1815 CTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGC 1874

Qy   1861 TCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1875 TCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCA 1934

Qy   1921 GACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1935 GACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGCAGTGCTTTCGGCCCAGTT 1994

Qy   1981 CTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAG 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1995 CTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAG 2054

Qy   2041 ATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGT 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2055 ATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGT 2114

Qy   2101 TCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2115 TCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCC 2174

Qy   2161 CTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTG 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2175 CTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCT------- 2228

Qy   2221 CTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAAT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2228 ----------------------CTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAAT 2266

Qy   2281 GCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2267 GCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTA 2326

Qy   2341 TATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGAC 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2327 TATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGAC 2386

Qy   2401 TTCCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAG 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2387 TTCCCCTAGCCCTGA-CCAGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAG 2445

Qy   2461 GAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACT 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2446 GAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACT 2505

Qy   2521 GTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2506 GTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCG 2565

Qy   2581 GGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   2566 GGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAA 2625

Qy   2641 CTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGAC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2626 CTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGAC 2685

Qy   2701 ATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2686 ATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTC 2745

Qy   2761 TGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCAC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2746 TGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCAC 2805

Qy   2821 ATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACAC 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2806 ATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACAC 2865

Qy   2881 CAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2866 CAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTC 2925

Qy   2941 AGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGAC 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2926 AGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGAC 2985

Qy   3001 ATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2986 ATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGA 3045

Qy   3061 TAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAAT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3046 TAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAAT 3105

Qy   3121 AAATATATCAGCAAAGC 3137
          |||||||||||||||||
Db   3106 AAATATATCAGCAAAGC 3122


RESULT   2
V11777
ID   V11777 standard; DNA; 3026 BP.
AC   V11777;
DT   25-SEP-1998  (first entry)
DE   Variant of GABA-A receptor epsilon sub-unit related gene.
KW   ss; GABA-A receptor; diagnosis; therapy; drug screening.
OS   Mammalia.
FH   Key             Location/Qualifiers
FT   CDS             55. .1479
FT                   /*tag= a
FT                   /product= "Variant of GABA-A receptor epsilon sub-unit
FT                            related protein"
PN   DE19644501-A1.
PD   30-APR-1998.
PF   25-OCT-1996; 044501.
PR   25-OCT-1996; DE-044501.
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI   Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR   WPI; 98-252096/23.
DR   P-PSDB; W59048.
PT   Protein related to GABA-A receptor sub-unit epsilon - useful for
PT   diagnosis, therapy or drug screening
PS   Disclosure; Fig 2; 12pp; German.
CC   The GABA-A receptor sub-unit epsilon related protein is used for the
CC   diagnosis and/or therapy of related disorders.  It can also be used to
CC   screen for substances that modulate the activity of the protein.
SQ   Sequence   3026 BP;    689 A;    853 C;    663 G;    821 T;


  Query Match            90.4%;  Score 2852.2;  DB 1;  Length 3026;
  Best Local Similarity  95.9%;  Pred. No. 0;
  Matches 3009;  Conservative    0;  Mismatches    3;  Indels  125;  Gaps    3;

Qy      1 CGCGACCTCCGCGCAGGTGGTCGCGCCGGTCTCCGCGGAAATGTTGTCCAAAGTTCTTCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     15 CGCGACCTCCGCGCAGGTGGTCGCGCCGGTCTCCGCGGAAATGTTGTCCAAAGTTCTTCC 74

Qy     61 AGTCCTCCTAGGCATCTTATTGATCCTCCAGTCGAGGGTCGAGGGACCTCAGACTGAATC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     75 AGTCCTCCTAGGCATCTTATTGATCCTCCAGTCGAGGGTCGAGGGACCTCAGACTGAATC 134

Qy    121 AAAGAATGAAGCCTCTTCCCGTGATGTTGTCTATGGCCCCCAGCCCCAGCCTCTGGAAAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    135 AAAGAATGAAGCCTCTTCCCGTGATGTTGTCTATGGCCCCCAGCCCCAGCCTCTGGAAAA 194

Qy    181 TCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    195 TCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAA 254

Qy    241 ACTGCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    255 ACTGCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCG 314

Qy    301 CCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGG 360
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    315 CCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCTCCGTCAACAGCCTTGG 374

Qy    361 TCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    375 TCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCT---- 431

Qy    421 CGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGT 480

Db    431 ------------------------------------------------------------ 431

Qy    481 GAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGA 540
                                                ||||||||||||||||||||||||||
Db    431 ------------------------------GGAATTCTAAGAGGACCCACGAGCATGA 458

Qy    541 GATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAAT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    459 GATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAAT 518

Qy    601 TAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    519 TAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCA 578

Qy    661 CTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    579 CTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTG 638

Qy    721 GGAAAATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    639 GGAAAATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 698

Qy    781 TACAGGAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCAT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    699 TACAGGAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCAT 758

Qy    841 GACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    759 GACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCC 818

Qy    901 TTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    819 TTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCC 878

Qy    961 AGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    879 AGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTC 938

Qy   1021 TCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    939 TCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTG 998

Qy   1081 CTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAA 1140
```

```
Db    999 CTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAA 1058
Qy   1141 CCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCA 1200
Db   1059 CCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCA 1118
Qy   1201 TGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTG 1260
Db   1119 TGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTG 1178
Qy   1261 CCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCA 1320
Db   1179 CCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCA 1238
Qy   1321 GCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTG 1380
Db   1239 GCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTG 1298
Qy   1381 TGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTAC 1440
Db   1299 TGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTAC 1358
Qy   1441 CTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGT 1500
Db   1359 CTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGT 1418
Qy   1501 TTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTA 1560
Db   1419 TTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTA 1478
Qy   1561 GGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTT 1620
Db   1479 GGTACCAGCTGGTACCCTGTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTT 1538
Qy   1621 GCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCC 1680
Db   1539 GCCAAGGGAGTTGGGGGAAAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCC 1598
Qy   1681 CATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGC 1740
Db   1599 CATTCCCCAAACAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGC 1658
Qy   1741 CCATTCACTGAGTCTTCTCAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCT 1800
Db   1659 CCATTCACTGAGTTTTCTCAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCT 1718
Qy   1801 CTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGC 1860
Db   1719 CTTCTTCAAGGAGCATCCGTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGC 1778
Qy   1861 TCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCA 1920
Db   1779 TCCCTAAAACCATGCCTAAGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCA 1838
Qy   1921 GACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTT 1980
Db   1839 GACAATTACTGCATTTTTCCAGAAGCCCACTATTGCCTTTGCAGTGCTTTCGGCCCAGTT 1898
Qy   1981 CTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAG 2040
Db   1899 CTGGCCTCAGCCTCAAAGTGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAG 1958
Qy   2041 ATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGT 2100
Db   1959 ATGCTGGGCAGCAGTATAACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGT 2018
Qy   2101 TCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCC 2160
Db   2019 TCTCAGTTCTCTCTCCCTGCTACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCC 2078
Qy   2161 CTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTG 2220
Db   2079 CTTTAGGAAGAGGGGGGGGCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCT------- 2132
Qy   2221 CTGCTGTGACATCTCCCTCTCCTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAAT 2280
Db   2132 ----------------------CTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAAT 2170
Qy   2281 GCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTA 2340
Db   2171 GCCCTTCATCCAATGGGTATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTA 2230
Qy   2341 TATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGAC 2400
Db   2231 TATGCCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGAC 2290
Qy   2401 TTCCCCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAG 2460
Db   2291 TTCCCCTAGCCCTGA-CCAGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAG 2349
Qy   2461 GAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACT 2520
Db   2350 GAAACTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACT 2409
Qy   2521 GTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCG 2580
Db   2410 GTCGGAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCG 2469
Qy   2581 GGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAA 2640
Db   2470 GGGCACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAA 2529
Qy   2641 CTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGAC 2700
Db   2530 CTTTGGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGAC 2589
Qy   2701 ATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTC 2760
Db   2590 ATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTC 2649
Qy   2761 TGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCAC 2820
Db   2650 TGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCAC 2709
Qy   2821 ATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACAC 2880
Db   2710 ATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACAC 2769
Qy   2881 CAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTC 2940
Db   2770 CAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTC 2829
Qy   2941 AGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGAC 3000
Db   2830 AGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGAC 2889
Qy   3001 ATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGA 3060
Db   2890 ATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGA 2949
Qy   3061 TAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAAT 3120
Db   2950 TAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAAT 3009
Qy   3121 AAATATATCAGCAAAGC 3137
Db   3010 AAATATATCAGCAAAGC 3026
```

RESULT 3
V11778
ID V11778 standard; DNA; 10697 BP.
AC V11778;
DT 25-SEP-1998 (first entry)
DE GABA-A receptor epsilon sub-unit related genomic sequence.

```
KW   ss; GABA-A receptor; diagnosis; therapy; drug screening.
OS   Mammalia.
FH   Key             Location/Qualifiers
FT   exon            1. .110
FT                   /*tag= a
FT                   /number= 1
FT   intron          111. .1217
FT                   /*tag= b
FT                   /number= 1
FT   exon            1218. .1435
FT                   /*tag= c
FT                   /number= 2
FT   intron          1436. .1883
FT                   /*tag= d
FT                   /number= 2
FT   exon            1884. .2172
FT                   /*tag= e
FT                   /number= 3
FT   intron          2173. .3169
FT                   /*tag= f
FT                   /number= 3
FT   exon            3170. .3252
FT                   /*tag= g
FT                   /number= 4
FT   intron          3253. .4559
FT                   /*tag= h
FT                   /number= 4
FT   exon            4560. .4697
FT                   /*tag= i
FT                   /number= 5
FT   intron          4698. .7962
FT                   /*tag= j
FT                   /number= 5
FT   exon            7963. .8115
FT                   /*tag= k
FT                   /number= 6
FT   intron          8116. .8255
FT                   /*tag= l
FT                   /number= 6
FT   exon            8256. .8455
FT                   /*tag= m
FT                   /number= 7
FT   intron          8456. .8738
FT                   /*tag= n
FT                   /number= 7
FT   exon            8739. .10697
FT                   /*tag= o
FT                   /number= 8
PN   DE19644501-A1.
PD   30-APR-1998.
PF   25-OCT-1996; 044501.
PR   25-OCT-1996; DE-044501.
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI   Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR   WPI; 98-252096/23.
PT   Protein related to GABA-A receptor sub-unit epsilon - useful for
PT   diagnosis, therapy or drug screening
PS   Disclosure; Fig 3; 12pp; German.
CC   The GABA-A receptor sub-unit epsilon related protein is used for the
CC   diagnosis and/or therapy of related disorders.  It can also be used to
CC   screen for substances that modulate the activity of the protein.
SQ   Sequence   10697 BP;    2524 A;    2704 C;    2471 G;    2991 T;

  Query Match            61.6%;  Score 1943.6;  DB 1;  Length 10697;
  Best Local Similarity  99.0%;  Pred. No. 0;
  Matches 1966;  Conservative    0;  Mismatches   19;  Indels    1;  Gaps    1;

Qy   1152 CCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 1211
            ||||    | ||||    |       | ||||||||||||||||||||||||||||||||||
Db   8713 CCCACTTCTTTCCTTGTCCATTTTAGCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 8772

Qy   1212 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 1271
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8773 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 8832

Qy   1272 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 1331
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8833 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 8892

Qy   1332 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 1391
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8893 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 8952

Qy   1392 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 1451
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8953 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 9012

Qy   1452 GCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 1511
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9013 CCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 9072

Qy   1512 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTG 1571
            |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   9073 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTTTTTGCCTTAACTTGTAGGTACCAGCTG 9132

Qy   1572 GTACCCTGTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGT 1631
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9133 GTACCCTGTGGGGCAACCTCTCCAGTTCCCCAGGAGGTCCAAGCCCCTTGCCAAGGGAGT 9192

Qy   1632 TGGGGGAAAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAA 1691
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9193 TGGGGGAAAGCAGCAGCAGCAGGAGCGACTAGAGTTTTTCCTGCCCCATTCCCCAAA 9252

Qy   1692 CAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGA 1751
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9253 CAGAAGCTTGCAGAGGGTTTGTCTTTGCTGCCCCTCTCCCCTACCTGGCCCATTCACTGA 9312

Qy   1752 GTCTTCTCAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGG 1811
            || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9313 GTTTTCTCAGCAGACCATTTCAAATTATTAATAAATGGGCCACCTCCCTCTTCTTCAAGG 9372

Qy   1812 AGCATCCGTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACC 1871
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9373 AGCATCCGTGATGCTCAGTGTTCAAAACCACAGCCACTTAGTGATCAGCTCCCTAAAACC 9432

Qy   1872 ATGCCTAAGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTG 1931
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9433 ATGCCTAAGTACAGGCGGATTAGCTATCTTCCAACAATGCTGACCACCAGACAATTACTG 9492

Qy   1932 CATTTTTCCAGAAGCCCACTATTGCCTTTGTAGTGCTTTCGGCCCAGTTCTGGCCTCAGC 1991
            |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   9493 CATTTTTCCAGAAGCCCACTATTGCCTTTGCAGTGCTTTCGGCCCAGTTCTGGCCTCAGC 9552

Qy   1992 CTCAAAGTGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAG 2051
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9553 CTCAAAGTGCACCGACTAGTTGCTTGCCTATACCTGGCACCTCATTAAGATGCTGGGCAG 9612

Qy   2052 CAGTATAACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTC 2111
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9613 CAGTATAACAGGAGGAAGAGATCCCTCTCCTTTGGTCAGATTATTATGTTCTCAGTTCTC 9672

Qy   2112 TCTCCCTGCTACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCCCTTTAGGAAGA 2171
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9673 TCTCCCTGCTACCCCTTTCTCTGCAGATAGATAGACACTGGCATTATCCCTTTAGGAAGA 9732

Qy   2172 GGGGGGGGCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACA 2231
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9733 GGGGGGGGCAGCAAGAGAGCCTATTTGGGACAGCATTCCTCTCTCTCTGCTGCTGTGACA 9792

Qy   2232 TCTCCCTCTCCTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCC 2291
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9793 TCTCCCTCTCCTTGCTGGCTCCATCTTTCGTCTGCACTACCAATTCAATGCCCTTCATCC 9852

Qy   2292 AATGGGTATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCT 2351
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    9853 AATGGGTATCTATTTTTGTGTGTGATTATAGTAACTACTCCCTGCTTTATATGCCACCCT 9912

Qy    2352 CTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCC 2411
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    9913 CTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCC 9972

Qy    2412 CTGACCCAGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCT 2471
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    9973 CTGA-CCAGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCT 10031

Qy    2472 TTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCT 2531
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10032 TTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCT 10091

Qy    2532 ATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAA 2591
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10092 ATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAA 10151

Qy    2592 CCATCACAATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAG 2651
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10152 CCATCACAATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAG 10211

Qy    2652 CACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGC 2711
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10212 CACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGC 10271

Qy    2712 AGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGT 2771
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10272 AGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGT 10331

Qy    2772 GGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCT 2831
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10332 GGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCT 10391

Qy    2832 AGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGG 2891
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10392 AGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGG 10451

Qy    2892 CCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCC 2951
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10452 CCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCC 10511

Qy    2952 AAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATG 3011
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10512 AAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATG 10571

Qy    3012 CTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGT 3071
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10572 CTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGT 10631

Qy    3072 CTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATATCAG 3131
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10632 CTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATATCAG 10691

Qy    3132 CAAAGC 3137
           ||||||
Db   10692 CAAAGC 10697


RESULT   4
V36319
ID   V36319 standard; cDNA; 1552 BP.
AC   V36319;
DT   12-OCT-1998  (first entry)
DE   Human GABA receptor epsilon subunit cDNA.
KW   GABA receptor; gamma-amino butyric acid receptor; human;
KW   appetite; cognition; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             18. .1538
FT                   /*tag= a
PN   WO9823742-A1.
PD   04-JUN-1998.
PF   18-NOV-1997; G03159.
PR   03-OCT-1997; GB-020995.
PR   25-NOV-1996; GB-024442.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Whiting PJ;
DR   WPI; 98-322722/28.
DR   P-PSDB; W61045.
PT   New isolated GABA receptor subunit, epsilon - used to develop
PT   products for the screening and design of drugs, e.g. for modulating
PT   appetite behaviours, hormonal interactions and cognition
PS   Claim 5; Fig 1; 37pp; English.
CC   This cDNA sequence codes for a novel class of subunit (see W61045),
CC   classified as epsilon, within the human GABA receptor gene family.
CC   It was generated from human brain cDNA by PCR using primers (see
CC   V36322-23) derived from the 5' untranslated region (UTR) of an
CC   anchored PCR product (see V36320-21) and from the 3'UTR of EST
CC   R49718 (obtained from an EST database search using a GABA-A
CC   receptor polypeptide).  A stably co-transfected eukaryotic cell
CC   line capable of expressing the GABA epsilon receptor subunit, at
CC   least one alpha receptor subunit and at least one beta receptor
CC   subunit is claimed.  A recombinant expression vector, and protein
CC   and membrane preparations of the GABA receptor obtained from the
CC   co-transfected cells are also claimed.  The new GABA-A receptor
CC   epsilon subunit and products can be used in the screening and
CC   design of drugs which act upon the GABA receptor.  The ligands or
CC   drug candidates identified may be used as therapeutic agents, e.g.
CC   for the modulation of appetite behaviours, hormonal interactions
CC   and cognition.  They can also be used for the study of structure,
CC   pharmacology and function of the various GABA receptor subtypes.
SQ   Sequence   1552 BP;    344 A;    443 C;    349 G;    416 T;


  Query Match             48.7%;  Score 1536.2;  DB 1;  Length 1552;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1538;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      31 CTCCGCGGAAATGTTGTCCAAAGTTCTTCCAGTCCTCCTAGGCATCTTATTGATCCTCCA 90
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8 CTCCGCGGAAATGTTGTCCAAAGTTCTTCCAGTCCTCCTAGGCATCTTATTGATCCTCCA 67

Qy      91 GTCGAGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGT 150
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68 GTCGAGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGT 127

Qy     151 CTATGGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAAC 210
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     128 CTATGGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAAC 187

Qy     211 TGAGACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACAC 270
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     188 TGAGACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACAC 247

Qy     271 TATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGT 330
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     248 TATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGT 307

Qy     331 CACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACAC 390
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     308 CACTGTTGAGATCTCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACAC 367

Qy     391 CATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTT 450
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     368 CATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTT 427

Qy     451 TGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTT 510
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     428 TGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTT 487

Qy     511 TAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCAT 570
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     488 TAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCAT 547

Qy     571 CTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACT 630
```

```
Db    548 CTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACT 607

Qy    631 CCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTC 690
Db    608 CCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTC 667

Qy    691 CTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAA 750
Db    668 CTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAA 727

Qy    751 GAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAAT 810
Db    728 GAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAAT 787

Qy    811 CACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTT 870
Db    788 CACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTT 847

Qy    871 TGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGT 930
Db    848 TGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGT 907

Qy    931 TTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGT 990
Db    908 TTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGT 967

Qy    991 TCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATAT 1050
Db    968 TCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATAT 1027

Qy   1051 CACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGA 1110
Db   1028 CACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGA 1087

Qy   1111 GTTTGCTGTGCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACT 1170
Db   1088 GTTTGCTGTGCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACT 1147

Qy   1171 CCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTG 1230
Db   1148 CCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTG 1207

Qy   1231 TGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGG 1290
Db   1208 TGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGG 1267

Qy   1291 AGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCC 1350
Db   1268 AGAGGAGCGCCCGTCTTGCTCTGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCC 1327

Qy   1351 CCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTT 1410
Db   1328 CCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTT 1387

Qy   1411 CTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGT 1470
Db   1388 CTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGT 1447

Qy   1471 CTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGT 1530
Db   1448 CTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGT 1507

Qy   1531 GCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCTG 1571
Db   1508 GCTCTACTGGCTTGTTTGCCTTAACTTGTAGGTACCAGCGG 1548
```

RESULT 5
T02334
ID T02334 standard; cDNA; 1565 BP.
AC T02334;
DT 02-FEB-1996 (first entry)
DE GABA-A receptor gamma-3 subunit cDNA.
KW GABA-A receptor; gamma-aminobutyric acid receptor; gamma-3 subunit;
KW ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 33. .1436
FT /*tag= a
PN WO9529234-A1.
PD 02-NOV-1995.
PF 12-APR-1995; G00834.
PR 22-APR-1994; GB-008064.
PA (MERI) MERCK SHARP & DOHME LTD.
PI Whiting PJ;
DR WPI; 95-382983/49.
DR P-PSDB; R83968.
PT New cell line expressing human GABA-A receptor sub-units - useful in
PT drug screening and design
PS Claim 5; Page 18-20; 30pp; English.
CC A rat GABA-A receptor gamma-3 subunit cDNA probe was used to screen
CC a human foetal brain cDNA library. The single isolated clone
CC lacked the 5' and 3' ends of the gamma-3 subunit coding region.
CC These were obtd. by further PCR using primers based on the
CC truncated sequence, giving a complete cDNA sequence (T02334).
CC This can be used to express gamma-3 in transfected eukaryotic
CC (pref. rodent fibroblast) cell lines for prodn. of hybrid GABA-A
CC receptors having novel subunit compositions.
SQ Sequence 1565 BP; 430 A; 397 C; 339 G; 399 T;

Query Match 11.2%; Score 352.8; DB 1; Length 1565;
Best Local Similarity 62.4%; Pred. No. 1.5e-93;
Matches 552; Conservative 0; Mismatches 332; Indels 0; Gaps 0;

```
Qy    246 CAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTG 305
Db    166 CCGACGTGACTCTTATTCTCAACAAGTTGCTAAGAGAGTATGATAAAAAGCTGAGGCCAG 225

Qy    306 GCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTC 365
Db    226 ATATTGGAATAAAACCGACCGTAATTGACGTTGACATTTATGTTAACAGCATTGGTCCTG 285

Qy    366 TCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACG 425
Db    286 TGTCATCAATAAACATGGAATACCAAATTGACATATTTTTTGCTCAGACCTGGACAGATA 345

Qy    426 AACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCC 485
Db    346 GTCGCCTTCGATTCAACAGCACAATGAAAATTCTTACTCTGAACAGCAACATGGTGGGGT 405

Qy    486 AGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCA 545
Db    406 TAATCTGGATCCCAGACACCATCTTCCGCAATTCTAAAACCGCAGAGGCTCACTGGATCA 465

Qy    546 CCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGA 605
Db    466 CCACACCCAATCAGCTCCTCCGGATTTGGAATGACGGGAAAATCCTTTACACTTTGAGGC 525

Qy    606 TGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTT 665
Db    526 TCACCATCAATGCTGAGTGCCAGCTGCAGCTGCACAACTTCCCCATGGACGAACACTCCT 585

Qy    666 GCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAA 725
Db    586 GCCCGCTGATTTTCTCCAGCTATGGCTATCCCAAAGAACAAATGATTTATAGATGGAGAA 645

Qy    726 ATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAG 785
Db    646 AAAATTCAGTGCAGGCAGCTGACCAGAAATCATGGCGGCTTTATCAGTTTGACTTCATGG 705

Qy    786 GAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGA 845
Db    706 GCCTCAGAAACACCACAGAAATCGTGACAACGTCTGCAGGTGATTATGTTGTCATGACTA 765
```

```
Qy    846 TTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTT 905
Db    766 TATATTTTGAATTGAGTACAAGAATGGGATACTTCACCATTCAGACATACATTCCCTGTA 825

Qy    906 CCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCC 965
Db    826 TACTGACTGTGGTTTTATCCTGGGTGTCATTTTGGATCAAAAAAGATGCTACGCCAGCAA 885

Qy    966 GGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTA 1025
Db    886 GAACAGCATTAGGCATCACCACGGTGCTGACCATGACCACCCTGAGCACCATCGCCAGGA 945

Qy   1026 AGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCG 1085
Db    946 AGTCCTTGCCACGCGTGTCCTACGTGACCGCCATGGACCTTTTTGTGACTGTGTGCTTCC 1005

Qy   1086 TCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTC 1129
Db   1006 TGTTTGTCTTCGCCGCGCTGATGGAGTATGCCACCCTCAACTAC 1049


RESULT   6
T28988
ID   T28988 standard; cDNA; 1707 BP.
AC   T28988;
DT   06-JAN-1997  (first entry)
DE   Human GABA-A receptor alpha 4 subunit cDNA.
KW   GABA-A receptor; gamma-aminobutyric acid; alpha-4 subunit; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             39. .1703
FT                   /*tag= a
PN   WO9610637-A1.
PD   11-APR-1996.
PF   29-SEP-1995; G02323.
PR   01-OCT-1994; GB-020010.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Le Bourdelles B,  Whiting PJ;
DR   WPI; 96-209359/21.
DR   P-PSDB; R97298.
PT   DNA encoding alpha-4 and delta subunit(s) of the human GABAa
PT   receptor  - also stably co-transfected eukaryotic cells expressing
PT   receptors contg. these subunit(s), used for screening and designing
PT   drugs
PS   Claim 9; Fig 2; 45pp; English.
CC   A cDNA clone (T28988) codes for the alpha-4 subunit (R97298) of the
CC   human GABA-A receptor.  It was isolated from human brain thalamus
CC   cDNA using primers (see also T28994-95) based on the 5' and 3'
CC   untranslated regions of a partial cDNA clone.  The cDNA can be
CC   incorporated into a vector and used to direct expression of the
CC   alpha-4 subunit in transfected cells, partic. rodent fibroblasts.
CC   Co-transfected host cells capable of expressing the alpha-4, delta
CC   (see also R97299) and beta subunits can be used to screen or design
CC   drugs that act on GABA-A receptors.
SQ   Sequence   1707 BP;    490 A;    373 C;    368 G;    476 T;


  Query Match             8.8%;  Score 278.8;  DB 1;  Length 1707;
  Best Local Similarity   57.6%;  Pred. No. 8.9e-72;
  Matches  521;  Conservative    0;  Mismatches  377;  Indels    6;  Gaps    1;

Qy    253 CTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGG 312
Db    182 CACCCGCATCCTGGACAGTTTGCTCGATGGTTATGACAACAGGCTGCGTCCTGGATTTGG 241

Qy    313 AGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTAT 372
Db    242 GGGTCCTGTTACAGAAGTGAAAACTGACATATATGTCACCAGCTTTGGACCTGTTTCTGA 301

Qy    373 CCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCT 432
Db    302 TGTTGAAGTGGAATACACAATGGATGTGTTCTTCAGGCAGACATGGATTGACAAAAGATT 361

Qy    433 CTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATG 492
Db    362 AAAATATGACGGCCCCATTGAAATTTTGAGATTGAACAATATGATGGTAACGAAAGTGTG 421

Qy    493 GATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCC 552
Db    422 GACCCCTGATACTTTCTTCAGGAATGGAAAGAAATCTGTCTCACATAATATGACAGCTCC 481

Qy    553 CAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCAT 612
Db    482 AAATAAGCTTTTTAGAATTATGAGAAATGGTACTATTTTATACACAATGAGACTCACCAT 541

Qy    613 TGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCT 672
Db    542 AAGTGCGGAGTGTCCCATGAGATTGGTGGATTTTCCCATGGATGGTCATGCATGCCCTGT 601

Qy    673 ATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA------ 727
Db    602 GAAATTCGGGAGTTATGCCTATCCAAAGAGTGAGATGATCTATACCTGGACAAAAGGTCC 661

Qy    727 TTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGG 786
Db    662 TGAGAAATCAGTTGAAGTTCCGAAGGAGTCTTCCAGCTTAGTTCAATATGATTTGATTGG 721

Qy    787 AGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGAT 846
Db    722 GCAAACCGTATCAAGTGAAACCATCAAATCAATTACGGGTGAATATATTGTTATGACGGT 781

Qy    847 TTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTC 906
Db    782 TTACTTCCACCTCAGACGGAAGATGGGTTATTTTATGATTCAGACCTATATTCCGTGCAT 841

Qy    907 CGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCG 966
Db    842 TATGACAGTGATTCTTTCTCAAGTTTCATTTTGGATAAATAAAGAATCAGTTCCCGCTAG 901

Qy    967 GACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAA 1026
Db    902 GACCGTATTTGGAATAACAACTGTCCTCACCATGACCACACTAAGCATCAGTGCACGACA 961

Qy   1027 GAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGT 1086
Db    962 TTCTTTGCCCAAAGTGTCCTATGCTACCGCCATGGACTGGTTCATAGCTGTCTGCTTTGC 1021

Qy   1087 CTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAACCAGAC 1146
Db   1022 TTTTGTATTTTCGGCCCTTATCGAGTTTGCTGCTGTCAACTATTTCACCAATATTCAAAT 1081

Qy   1147 AAAA 1150
Db   1082 GGAA 1085


RESULT   7
Q33130
ID   Q33130 standard; DNA; 1408 BP.
AC   Q33130;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-6 subunit gene.
KW   Primer; human; alpha-6; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             27. .1388
FT                   /*tag= a
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
```

```
DR   WPI; 93-018138/02.
DR   P-PSDB; R31187.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Claim 8; Fig 5; 43pp; English.
CC   The sequence given encodes the human alpha-6 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Rat alpha-6 cDNA was used as a probe
CC   and a human alpha-6 cDNA clone was isolated from a cerebellum cDNA
CC   library.  No full length cDNA's were isolated. To obtain a full length
CC   cDNA 3 clones were joined together using convenient restriction sites.
CC   GABA-A receptor comprises a multimeric protein of molecular size
CC   230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   1408 BP;    392 A;    321 C;    300 G;    395 T;

  Query Match             8.4%;  Score 264.6;  DB 1;  Length 1408;
  Best Local Similarity   56.5%;  Pred. No. 1.2e-67;
  Matches  514;  Conservative    0;  Mismatches  389;  Indels    6;  Gaps    1;

Qy    247 AGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGG 306
Db    116 AAACGTCAGTCGGATCCTGGACAACTTGCTTGAAGGCTATGACAATCGGCTGCGGCCGGG 175

Qy    307 CATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCT 366
Db    176 ATTTGGAGGTGCTGTCACTGAAGTCAAAACAGACATTTATGTGACCAGTTTTGGGCCCGT 235

Qy    367 CTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGA 426
Db    236 GTCAGATGTGGAGATGGAGTATACGATGGATGTTTTTTTTCGCCAGACCTGGACTGATGA 295

Qy    427 ACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCA 486
Db    296 GAGGTTGAAGTTTGGGGGGCCAACTGAGATTCTGAGTCTGAATAATTTGATGGTCAGTAA 355

Qy    487 GCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCAC 546
Db    356 AATCTGGACGCCTGACACCTTTTTCAGAAATGGTAAAAAGTCCATTGCTCACAACATGAC 415

Qy    547 CATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGAT 606
Db    416 AACTCCTAATAAACTCTTCAGAATAATGCAGAATGGAACCATTTTATACACCATGAGGCT 475

Qy    607 GACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTG 666
Db    476 TACCATCAATGCTGACTGTCCCATGAGGCTGGTTAACTTTCCTATGGATGGGCATGCTTG 535

Qy    667 CCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA 726
Db    536 TCCACTCAAGTTTGGGAGCTATGCTTATCCCAAAAGTGAAATCATATATACGTGGAAAAA 595

Qy    727 TTTCAAGCTTGAAATCAATGA------GAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 780
Db    596 AGGACCACTTTACTCAGTAGAAGTCCCAGAAGAATCTTCAAGCCTTCTCCAGTATGATCT 655

Qy    781 TACAGGAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCAT 840
Db    656 GATTGGACAAACAGTATCTAGTGAGACAATTAAATCTAACACAGGTGAATACGTTATAAT 715

Qy    841 GACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCC 900
Db    716 GACAGTTTACTTCCACTTGCAAAGGAAGATGGGCTACTTCATGATACAGATATACACTCC 775

Qy    901 TTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCC 960
Db    776 TTGCATTATGACAGTCATTCTTTCCCAGGTGTCTTTCTGGATTAATAAGGAGTCCGTCCC 835

Qy    961 AGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTC 1020
Db    836 AGCAAGAACTGTTCTTGGGATCACCACTGTTTTAACTATGACCACTTTGAGCATCAGTGC 895

Qy   1021 TCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTG 1080
Db    896 CCGGCACTCTTTGCCAAAAGTGTCATATGCCACTGCCATGGATTGGTTCATAGCTGTTTG 955

Qy   1081 CTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAA 1140
Db    956 CTTTGCATTCGTCTTCTCTGCTCTTATCGAGTTCGCAGCTGTCAACTACTTTACCAATCT 1015

Qy   1141 CCAGACAAA 1149
Db   1016 TCAGACACA 1024


RESULT   8
Q69142
ID   Q69142 standard; DNA; 1408 BP.
AC   Q69142;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha6 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             27. .1388
FT                   /*tag=  a
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   P-PSDB; R59865.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.5; 79pp; English.
CC   This receptor DNA may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   1408 BP;    392 A;    321 C;    300 G;    395 T;

  Query Match             8.4%;  Score 264.6;  DB 1;  Length 1408;
  Best Local Similarity   56.5%;  Pred. No. 1.2e-67;
  Matches  514;  Conservative    0;  Mismatches  389;  Indels    6;  Gaps    1;

Qy    247 AGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGG 306
Db    116 AAACGTCAGTCGGATCCTGGACAACTTGCTTGAAGGCTATGACAATCGGCTGCGGCCGGG 175

Qy    307 CATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCT 366
Db    176 ATTTGGAGGTGCTGTCACTGAAGTCAAAACAGACATTTATGTGACCAGTTTTGGGCCCGT 235

Qy    367 CTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGA 426
Db    236 GTCAGATGTGGAGATGGAGTATACGATGGATGTTTTTTTTCGCCAGACCTGGACTGATGA 295

Qy    427 ACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCA 486
```

```
Db    296 GAGGTTGAAGTTTGGGGGGCCAACTGAGATTCTGAGTCTGAATAATTTGATGGTCAGTAA 355

Qy    487 GCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCAC 546

Db    356 AATCTGGACGCCTGACACCTTTTTCAGAAATGGTAAAAAGTCCATTGCTCACAACATGAC 415

Qy    547 CATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGAT 606

Db    416 AACTCCTAATAAACTCTTCAGAATAATGCAGAATGGAACCATTTTATACACCATGAGGCT 475

Qy    607 GACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTG 666

Db    476 TACCATCAATGCTGACTGTCCCATGAGGCTGGTTAACTTTCCTATGGATGGGCATGCTTG 535

Qy    667 CCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA 726

Db    536 TCCACTCAAGTTTGGGAGCTATGCTTATCCCAAAAGTGAAATCATATATACGTGGAAAAA 595

Qy    727 TTTCAAGCTTGAAATCAATGA------GAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 780

Db    596 AGGACCACTTTACTCAGTAGAAGTCCCAGAAGAATCTTCAAGCCTTCTCCAGTATGATCT 655

Qy    781 TACAGGAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCAT 840

Db    656 GATTGGACAAACAGTATCTAGTGAGACAATTAAATCTAACACAGGTGAATACGTTATAAT 715

Qy    841 GACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCC 900

Db    716 GACAGTTTACTTCCACTTGCAAAGGAAGATGGGCTACTTCATGATACAGATATACACTCC 775

Qy    901 TTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCC 960

Db    776 TTGCATTATGACAGTCATTCTTTCCCAGGTGTCTTTCTGGATTAATAAGGAGTCCGTCCC 835

Qy    961 AGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTC 1020

Db    836 AGCAAGAACTGTTCTTGGGATCACCACTGTTTTAACTATGACCACTTTGAGCATCAGTGC 895

Qy   1021 TCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTG 1080

Db    896 CCGGCACTCTTTGCCAAAAGTGTCATATGCCACTGCCATGGATTGGTTCATAGCTGTTTG 955

Qy   1081 CTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAA 1140

Db    956 CTTTGCATTCGTCTTCTCTGCTCTTATCGAGTTCGCAGCTGTCAACTACTTTACCAATCT 1015

Qy   1141 CCAGACAAA 1149

Db   1016 TCAGACACA 1024
```

RESULT 9
Q33129
ID Q33129 standard; DNA; 2310 BP.
AC Q33129;
DT 10-MAY-1993 (first entry)
DE GABA-A receptor alpha-5 subunit gene.
KW Primer; human; alpha-5; subunit; gamma-amino butyric acid; GABA; -A;
KW receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW ligand; alpha; beta; gamma; delta; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 298. .1686
FT /*tag= a
PN WO9222652-A.
PD 23-DEC-1992.
PF 09-JUN-1992; G01031.
PR 11-JUN-1991; GB-012504.
PA (MERI) MERCK SHARP & DOHME LTD.
PI Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR WPI; 93-018138/02.
DR P-PSDB; R31186.

PT Stably transfected eukaryotic cell line - expresses human GABA-A
PT receptor comprising alpha, beta and gamma sub-units, useful for
PT medicament prepn.
PS Claim 7; Fig 4; 43pp; English.
CC The sequence given encodes the human alpha-5 subunit of gamma-amino
CC butyric acid (GABA)-A receptor. Rat alpha-5 cDNA was used as a probe
CC and a human alpha-5 cDNA clone was isolated from a hippocampal cDNA
CC library. GABA-A receptor comprises a multimeric protein of molecular
CC size 230-370 kD with specific binding sites for various drugs including
CC benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC agonist ligand GABA. The receptor is composed of several distinct
CC types of subunit, which are divided into four classes (alpha, beta,
CC gamma and delta) based on sequence homology. To date six types of
CC alpha, three types of beta, two types of gamma and one type of delta
CC subunit have been identified. It has been found that in addition to
CC an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC required to confer benzodiazipine sensitivity. The benzodiazepine
CC pharmacology of the receptor is largely dependent on the identity of
CC the alpha and gamma subunits present. Receptors containing a delta
CC subunit do not appear to bind benzodiazepines.
SQ Sequence 2310 BP; 655 A; 582 C; 512 G; 561 T;

Query Match 8.3%; Score 261.8; DB 1; Length 2310;
Best Local Similarity 55.7%; Pred. No. 1e-66;
Matches 525; Conservative 0; Mismatches 412; Indels 6; Gaps 1;

```
Qy    203 AAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATC 262

Db    394 ATGCCAACCAGTTCAGTGAAAGATGAGACCAATGACAACATCACGATATTTACCAGGATC 453

Qy    263 CTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCC 322

Db    454 TTGGATGGGCTCTTGGATGGCTACGACAACAGACTTCGGCCCGGGCTGGGAGAGCGCATC 513

Qy    323 ACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATG 382

Db    514 ACTCAGGTGAGGACCGACATCTACGTCACCAGCTTCGGCCCGGTGTCCGACACGGAAATG 573

Qy    383 GAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAAC 442

Db    574 GAGTACACCATAGACGTGTTTTTCCGACAAAGCTGGAAAGATGAAAGGCTTCGGTTTAAG 633

Qy    443 GACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGAC 502

Db    634 GGGCCCATGCAGCGCCTCCCTCTCAACAACCTCCTTGCCAGCAAGATCTGGACCCCAGAC 693

Qy    503 ACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATG 562

Db    694 ACGTTCTTCCACAACGGGAAGAAGTCCATCGCTCACAACATGACCACGCCCAACAAGCTG 753

Qy    563 GTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGA 622

Db    754 CTGCGGCTGGAGGACGACGGCACCCTGCTCTACACCATGCGCTTGACCATCTCTGCAGAG 813

Qy    623 TGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCT 682

Db    814 TGCCCCATGCAGCTTGAGGACTTCCCGATGGATGCGCACGCTTGCCCTCTGAAATTTGGC 873

Qy    683 AGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA------TTTCAAGCTT 736

Db    874 AGCTATGCGTACCCTAATTCTGAAGTCGTTTACGTCTGGACCAACGGCTCCACCAAGTCG 933

Qy    737 GAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAAC 796

Db    934 GTGGTGGTGGCGGAAGATGGCTCCAGACTGAACCAGTACCACCTGATGGGGCAGACGGTG 993

Qy    797 AAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAAT 856

Db    994 GGCACTGAGAACATCAGCACCAGCACAGGCGAATACACAATCATGACAGCTCACTTCCAC 1053

Qy    857 GTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACG 916
```

```
Db   1054 CTGAAAAGGAAGATTGGCTACTTTGTCATCCAGACCTACCTTCCCTGCATAATGACCGTG 1113

Qy    917 ATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTA 976
          ||  | ||   ||| |||||||||| | ||    || || |  |||||| |||   | |
Db   1114 ATCTTATCACAGGTGTCCTTTTGGCTGAACCGGGAATCAGTCCCAGCCAGGACAGTTTTT 1173

Qy    977 GGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCG 1036
          ||| ||||| | || ||||||||||| ||  |  ||| |    |  | ||   | | ||
Db   1174 GGGGTCACCACGGTGCTGACCATGACGACCCTCAGCATCAGCGCCAGGAACTCTCTGCCC 1233

Qy   1037 CGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTC 1096
            ||  ||||   ||| ||| |||| |  |  || ||  | ||||  | ||||  ||||
Db   1234 AAAGTGGCCTACGCCACCGCCATGGACTGGTTCATAGCTGTGTGCTATGCCTTCGTCTTC 1293

Qy   1097 TGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACA 1139
          |  || ||| | |||||||   | |||| | | | | | | |
Db   1294 TCGGCGCTGATAGAGTTTGCCACGGTCAATTACTTTACCAAGA 1336


RESULT  10
Q69141
ID   Q69141 standard; DNA; 2310 BP.
AC   Q69141;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha5 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             298. .1687
FT                   /*tag=  a
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   P-PSDB; R59864.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.4; 79pp; English.
CC   This receptor DNA may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   2310 BP;    654 A;    583 C;    513 G;    560 T;


  Query Match             8.3%;  Score 261.8;  DB 1;  Length 2310;
  Best Local Similarity   55.7%;  Pred. No. 1e-66;
  Matches  525;  Conservative    0;  Mismatches  412;  Indels    6;  Gaps    1;

Qy    203 AAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATC 262
          | | ||||     | | ||  |      |    || |||  |  |    |     |  | |||
Db    394 ATGCCAACCAGTTCAGTGAAAGATGAGACCAATGACAACATCACGATATTTACCAGGATC 453

Qy    263 CTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCC 322
            || |     || ||  |   || ||| ||| ||| || || ||  | ||||||     |
Db    454 TTGGATGGGCTCTTGGATGGCTACGACAACAGACTTCGGCCCGGGCTGGGAGAGCGCATC 513

Qy    323 ACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATG 382
          |||  ||| |      || |||  ||||| |||| | || ||  | ||   |   || |||
Db    514 ACTCAGGTGAGGACCGACATCTACGTCACCAGCTTCGGCCCGGTGTCCGACACGGAAATG 573

Qy    383 GAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAAC 442
          || |||||||| ||| |  | |||   || | |||| | || ||| | ||  | |  ||
Db    574 GAGTACACCATAGACGTGTTTTTCCGACAAAGCTGGAAAGATGAAAGGCTTCGGTTTAAG 633

Qy    443 GACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGAC 502
          |   || |  ||   ||  ||| ||   |    | |  ||| || | |||| ||| |||
Db    634 GGGCCCATGCAGCGCCTCCCTCTCAACAACCTCCTTGCCAGCAAGATCTGGACCCCAGAC 693

Qy    503 ACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATG 562
          || || ||    ||    |||| | ||  ||  ||  | || |||| ||||||| || ||
Db    694 ACGTTCTTCCACAACGGGAAGAAGTCCATCGCTCACAACATGACCACGCCCAACAAGCTG 753

Qy    563 GTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGA 622
          | ||  |  |  | || ||||   || | ||||| ||  |  |||||||   ||| |
Db    754 CTGCGGCTGGAGGACGACGGCACCCTGCTCTACACCATGCGCTTGACCATCTCTGCAGAG 813

Qy    623 TGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCT 682
          ||| |  | ||  |        || || |||||| | ||| ||||||||||    ||
Db    814 TGCCCCATGCAGCTTGAGGACTTCCCGATGGATGCGCACGCTTGCCCTCTGAAATTTGGC 873

Qy    683 AGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA------TTTCAAGCTT 736
          |||| | | || ||| |   |||  |  | |||   |||   ||          ||||
Db    874 AGCTATGCGTACCCTAATTCTGAAGTCGTTTACGTCTGGACCAACGGCTCCACCAAGTCG 933

Qy    737 GAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAAC 796
          |   |    | | |  |   ||  |  ||  |||||   |  | |  ||   ||
Db    934 GTGGTGGTGGCGGAAGATGGCTCCAGACTGAACCAGTACCACCTGATGGGGCAGACGGTG 993

Qy    797 AAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAAT 856
            ||||| |  ||||  |||       || || | ||   |||||||    |  |||| |
Db    994 GGCACTGAGAACATCAGCACCAGCACAGGCGAATACACAATCATGACAGCTCACTTCCAC 1053

Qy    857 GTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACG 916
          |||  |||  | |||||||  ||| | | || | |||  | || |      ||||  |
Db   1054 CTGAAAAGGAAGATTGGCTACTTTGTCATCCAGACCTACCTTCCCTGCATAATGACCGTG 1113

Qy    917 ATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTA 976
          ||  | ||   ||| |||||||||| | ||    || || |  |||||| |||   | |
Db   1114 ATCTTATCACAGGTGTCCTTTTGGCTGAACCGGGAATCAGTCCCAGCCAGGACAGTTTTT 1173

Qy    977 GGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCG 1036
          ||| ||||| | || ||||||||||| ||  |  ||| |    |  | ||   | | ||
Db   1174 GGGGTCACCACGGTGCTGACCATGACGACCCTCAGCATCAGCGCCAGGAACTCTCTGCCC 1233

Qy   1037 CGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTC 1096
            ||  ||||   ||| ||| |||| |  |  || ||  | ||||  | ||||  ||||
Db   1234 AAAGTGGCCTACGCCACCGCCATGGACTGGTTCATAGCTGTGTGCTATGCCTTCGTCTTC 1293

Qy   1097 TGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACA 1139
          |  || ||| | |||||||   | |||| | | | | | | |
Db   1294 TCGGCGCTGATAGAGTTTGCCACGGTCAATTACTTTACCAAGA 1336


RESULT  11
Q69140
ID   Q69140 standard; DNA; 1638 BP.
AC   Q69140;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha3 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             87. .1562
FT                   /*tag=  a
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   P-PSDB; R59863.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.3; 79pp; English.
CC   This receptor DNA may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
```

```
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   1638 BP;    430 A;    437 C;    364 G;    407 T;


  Query Match             7.6%;  Score 239.2;  DB 1;  Length 1638;
  Best Local Similarity   54.6%;  Pred. No. 3.8e-60;
  Matches  503;  Conservative    0;  Mismatches  413;  Indels    6;  Gaps    1;

Qy     222 CTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTA 281
           |||    |||   || |||  |  |      | |  | ||| || |   | | |||
Db     256 CTGATGACAGCACTGACAACATCACTATCTTCACCAGAATCTTGGATCGTCTTCTGGACG 315

Qy     282 ATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGA 341
             |||||| ||   ||||| ||||| |||||||       ||||  || |    ||| |
Db     316 GCTATGACAACCGGCTGCGACCTGGGCTTGGAGATGCAGTGACTGAAGTGAAGACTGACA 375

Qy     342 TCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCA 401
           ||  ||| | |||  |||| ||| | ||   |  |||||||| ||||| |||||  |
Db     376 TCTACGTGACCAGTTTTGGCCCTGTGTCAGACACTGACATGGAGTACACTATTGATGTAT 435

Qy     402 TCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTG 461
           | ||    ||||| ||| | || ||| | ||    |   | | | || |  ||   |||
Db     436 TTTTTCGGCAGACATGGCATGATGAAAGACTGAAATTTGATGGCCCCATGAAGATCCTTC 495

Qy     462 TTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTA 521
           |||||         |||  ||  || | ||||  ||||||||||| ||    |||   |
Db     496 CACTGAACAATCTCCTGGCTAGTAAGATCTGGACACCGGACACCTTCTTCCACAATGGCA 555

Qy     522 AGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATG 581
           |||   |    |  ||| | || |||| |||||| || || || |  |      |  | |
Db     556 AGAAATCAGTGGCTCATAACATGACCACGCCCAACAAGCTGCTCAGATTGGTGGACAACG 615

Qy     582 GCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCA 641
           | |   |  | || ||||| ||| | || ||| |||| |  ||  |  ||||  ||
Db     616 GAACCCTCCTCTATACAATGAGGTTAACAATTCATGCTGAGTGTCCCATCCATTTGGAAG 675

Qy     642 GATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGA 701
           |||||  ||||||   ||  | ||||| ||    ||    |||| | ||||| |
Db     676 ATTTTCCCATGGATGTGCATGCCTGCCCACTGAAGTTTGGAAGCTATGCCTATACAACAG 735

Qy     702 ATGAGATGATCTACAAGTGG------GAAAATTTCAAGCTTGAAATCAATGAGAAGAACT 755
           |||  || | ||    |||       | |||   |||    |          |   || |
Db     736 CTGAAGTGGTTTATTCTTGGACTCTCGGAAAGAACAAATCCGTGGAAGTGGCACAGGATG 795

Qy     756 CCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACAA 815
           |       |  ||||| ||| ||  ||              || || ||||||
Db     796 GTTCTCGCTTGAACCAGTATGACCTTTTGGGCCATGTTGTTGGGACAGAGATAATCCGGT 855

Qy     816 CCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCT 875
           |     || || |   | ||||||| |    |||| || | |    |     ||||||
Db     856 CTAGTACAGGAGAATATGTCGTCATGACAACCCACTTCCATCTCAAGCGAAAAATTGGCT 915

Qy     876 ATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCT 935
           |  |||   | || | |||  | || | |  | ||||    || || ||    || || |
Db     916 ACTTTGTGATCCAGACCTACTTGCCATGTATCATGACTGTCATTCTGTCACAAGTGTCGT 975

Qy     936 TTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGA 995
           | ||| |||| | |||||||| ||| ||||| ||     | ||  ||||| |||| || |
Db     976 TCTGGCTCAACAGAGAGTCTGTTCCTGCCCGTACAGTCTTTGGTGTCACCACTGTGCTTA 1035

Qy     996 CCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAG 1055
           |||||||||| ||| | |  |  | ||    || ||    ||  | |||    || |
Db    1036 CCATGACCACCTTGAGTATCAGTGCCAGAAATTCCTTACCTAAAGTGGCATATGCGACGG 1095

Qy    1056 CCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTG 1115
           || |||| |   |  || ||| |||| |  | |||    || |  || ||| | || ||||
Db    1096 CCATGGACTGGTTCATAGCCGTCTGTTATGCCTTTGTATTTTCTGCACTGATTGAATTTG 1155

Qy    1116 CTGTGCTCAACTTCCTGATCTA 1137
           |     ||||||   | | | |
Db    1156 CCACTGTCAACTATTTCACCAA 1177
```

```
RESULT  12
Q33128
ID   Q33128 standard; DNA; 1638 BP.
AC   Q33128;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-3 subunit gene.
KW   Primer; human; alpha-3; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             87. .1565
FT                   /*tag=  a
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   P-PSDB; R31185.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Claim 6; Fig 3; 43pp; English.
CC   The sequence given encodes the human alpha-3 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Bovine alpha-3 cDNA was used as a
CC   probe and an alpha-3 cDNA clone was isolated from a human foetal
CC   brain cDNA library, which was missing approx. 100 bp of the 5' end.
CC   This missing fragment was isolated by PCR.  The two fragments were
CC   ligated together to give a full length alpha-3 cDNA.    GABA-A
CC   receptor comprises a multimeric protein of molecular size 230-370 kD
CC   with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   1638 BP;    430 A;    436 C;    365 G;    407 T;


  Query Match             7.5%;  Score 237.6;  DB 1;  Length 1638;
  Best Local Similarity   54.4%;  Pred. No. 1.1e-59;
  Matches  502;  Conservative    0;  Mismatches  414;  Indels    6;  Gaps    1;

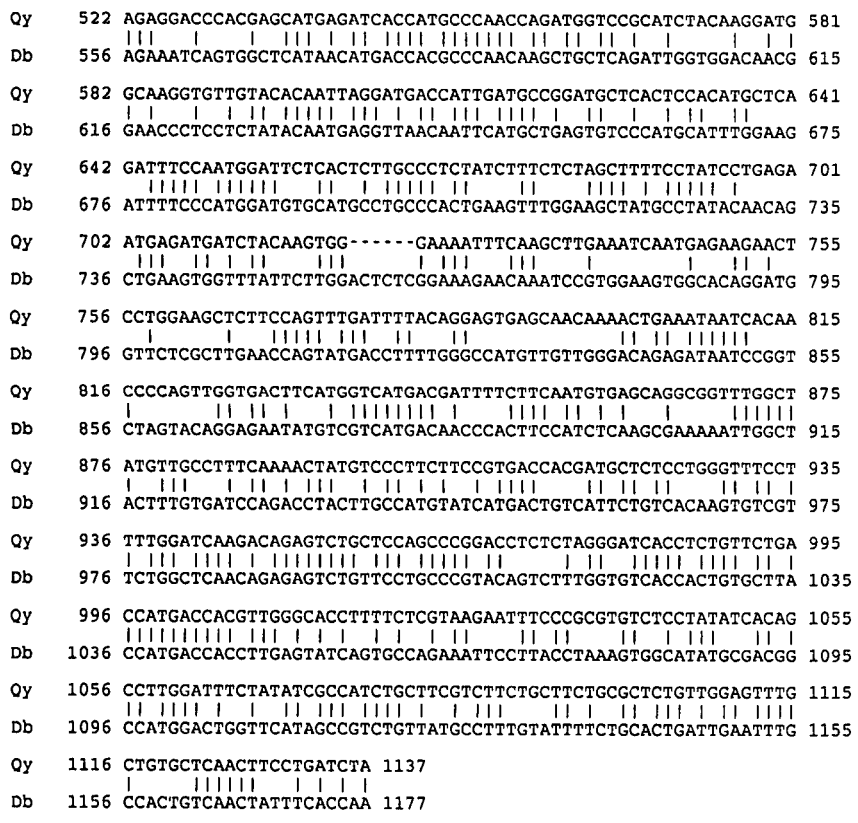
Qy     222 CTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTA 281
           |||    |||   || |||  |  |      | |  | ||| || |   | | |||
Db     256 CTGATGACAGCACTGACAACATCACTATCTTCACCAGAATCTTGGATCGTCTTCTGGACG 315

Qy     282 ATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGA 341
             |||||| ||   ||||| ||||| |||||||       ||||  || |    ||| |
Db     316 GCTATGACAACCGGCTGCGACCTGGGCTTGGAGATGCAGTGACTGAAGTGAAGACTGACA 375

Qy     342 TCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCA 401
           ||  ||| | |||  |||| ||| | ||   |  |||||||| ||||| |||||  |
Db     376 TCTACGTGACCAGTTTTGGCCCTGTGTCAGACACTGACATGGAGTACACTATTGATGTAT 435

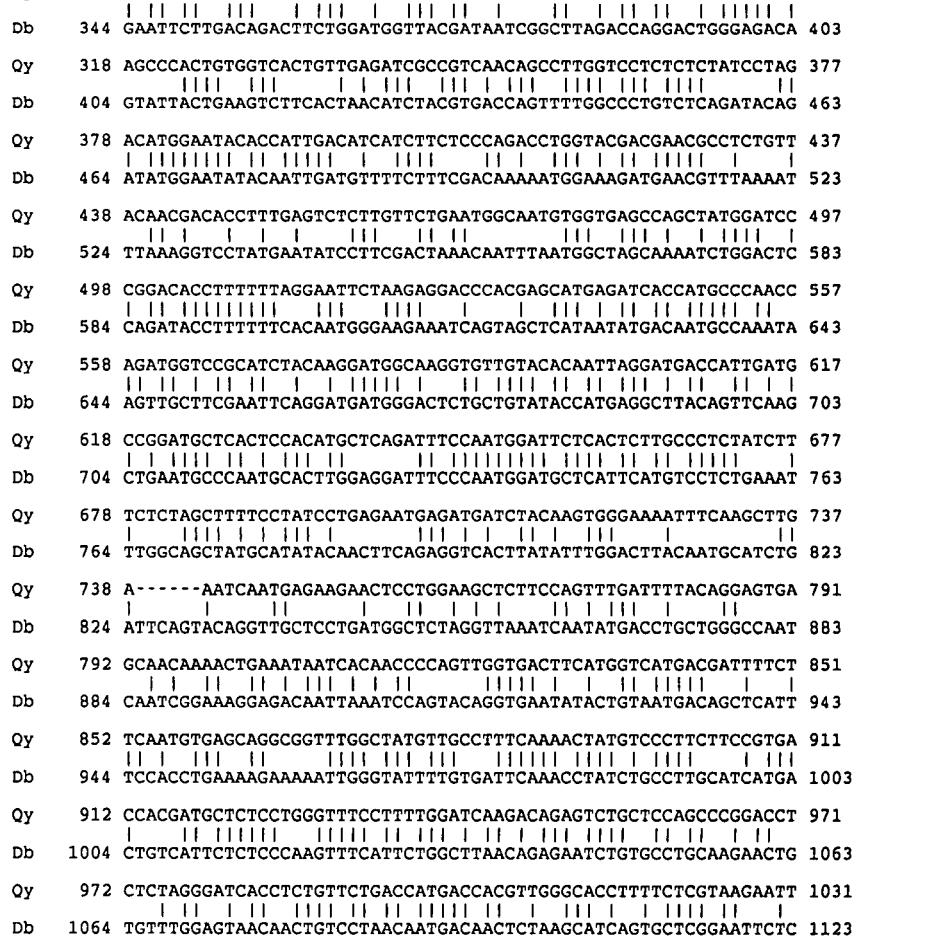
Qy     402 TCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTG 461
           | ||    ||||| ||| | || ||| | ||    |   | | | || |  ||   |||
Db     436 TTTTTCGGCAGACATGGCATGATGAAAGACTGAAATTTGATGGCCCCATGAAGATCCTTC 495

Qy     462 TTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTA 521
           |||||         |||  ||  || | ||||  ||||||||||| ||    |||   |
Db     496 CACTGAACAATCTCCTGGCTAGTAAGATCTGGACACCGGACACCTTCTTCCACAATGGCA 555
```



RESULT 13
Q33127
ID Q33127 standard; DNA; 2189 BP.
AC Q33127;
DT 10-MAY-1993 (first entry)
DE GABA-A receptor alpha-2 subunit gene.
KW Primer; human; alpha-3; subunit; gamma-amino butyric acid; GABA; -A;
KW receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW ligand; alpha; beta; gamma; delta; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 214. .1569
FT /*tag= a
PN WO9222652-A.
PD 23-DEC-1992.
PF 09-JUN-1992; G01031.
PR 11-JUN-1991; GB-012504.
PA (MERI) MERCK SHARP & DOHME LTD.
PI Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR WPI; 93-018138/02.
DR P-PSDB; R31184.
PT Stably transfected eukaryotic cell line - expresses human GABA-A
PT receptor comprising alpha, beta and gamma sub-units, useful for
PT medicament prepn.
PS Claim 5; Fig 2; 43pp; English.
CC The sequence given encodes the human alpha-2 subunit of gamma-amino
CC butyric acid (GABA)-A receptor. Bovine alpha-2 cDNA was used as a
CC probe and an alpha-2 cDNA clone was isolated from a human foetal
CC brain cDNA library. GABA-A receptor comprises a multimeric protein
CC of molecular size 230-270 kD with specific binding sites for various
CC drugs including benzodiazepines, barbiturates, and beta-carbolines,
CC in addition to the agonist ligand GABA. The receptor is composed of
CC several distinct types of subunit, which are divided into four classes
CC (alpha, beta, gamma and delta) based on sequence homology. To date
CC six types of alpha, three types of beta, two types of gamma and one
CC type of delta subunit have been identified. It has been found that
CC in addition to an alpha and a beta subunit, either gamma-1 or gamma-2
CC is also required to confer benzodiazipine sensitivity. The benzo-
CC diazepine pharmacology of the receptor is largely dependent on the
CC identity of the alpha and gamma subunits present. Receptors
CC containing a delta subunit do not appear to bind benzodiazepines.
SQ Sequence 2189 BP; 640 A; 466 C; 418 G; 665 T;

Query Match 7.1%; Score 224.4; DB 1; Length 2189;
Best Local Similarity 54.2%; Pred. No. 1e-55;
Matches 481; Conservative 0; Mismatches 401; Indels 6; Gaps 1;



```
Qy   1032 TCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCT 1091
          ||||    ||  | |||   || ||| |||| |  | ||| ||  | || |  |  ||
Db   1124 TCCCCAAAGTGGCTTATGCAACTGCCATGGACTGGTTTATTGCTGTTTGTTATGCATTTG 1183

Qy   1092 GCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACA 1139
            |||| || ||  | || |||||     | || | | | | | | |
Db   1184 TGTTCTCTGCCCTAATTGAATTTGCAACTGTTAATTACTTCACCAAAA 1231


RESULT  14
Q69139
ID   Q69139 standard; DNA; 2189 BP.
AC   Q69139;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha2 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             214. .1566
FT                   /*tag=  a
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   P-PSDB; R59862.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.2; 79pp; English.
CC   This receptor DNA may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   2189 BP;    640 A;    466 C;    418 G;    665 T;


  Query Match             7.1%;  Score 224.4;  DB 1;  Length 2189;
  Best Local Similarity   54.2%;  Pred. No. 1e-55;
  Matches  481;  Conservative    0;  Mismatches  401;  Indels    6;  Gaps    1;

Qy    258 GCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGA 317
          | || ||  |||   | |||  |  ||| ||  |    ||  | || ||  | ||||| |
Db    344 GAATTCTTGACAGACTTCTGGATGGTTACGATAATCGGCTTAGACCAGGACTGGGAGACA 403

Qy    318 AGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAG 377
            ||||  |||     | | |||  ||| | |||  |||| ||| ||||      ||
Db    404 GTATTACTGAAGTCTTCACTAACATCTACGTGACCAGTTTTGGCCCTGTCTCAGATACAG 463

Qy    378 ACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTT 437
          | |||||||| || |||||  |  ||||    || |  ||| | || |||||  |    |
Db    464 ATATGGAATATACAATTGATGTTTTCTTTCGACAAAAATGGAAAGATGAACGTTTAAAAT 523

Qy    438 ACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCC 497
          || |   |  | |    |||   || ||          |||  ||| |  | ||||  |
Db    524 TTAAAGGTCCTATGAATATCCTTCGACTAAACAATTTAATGGCTAGCAAAATCTGGACTC 583

Qy    498 CGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACC 557
          | || |||||||||   |||   ||||    |    | ||| | || || ||||| ||
Db    584 CAGATACCTTTTTTCACAATGGGAAGAAATCAGTAGCTCATAATATGACAATGCCAAATA 643

Qy    558 AGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATG 617
          || || | || ||  |  | ||||| |   || |||| || || ||| | ||  || | |
Db    644 AGTTGCTTCGAATTCAGGATGATGGGACTCTGCTGTATACCATGAGGCTTACAGTTCAAG 703

Qy    618 CCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTT 677
          | | |||| || | ||| ||      || |||||||| |||| || || |||||    |
Db    704 CTGAATGCCCAATGCACTTGGAGGATTTCCCAATGGATGCTCATTCATGTCCTCTGAAAT 763

Qy    678 TCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTG 737
          |    |||| | | ||| |       ||| | |  || |  |||     |          ||
Db    764 TTGGCAGCTATGCATATACAACTTCAGAGGTCACTTATATTTGGACTTACAATGCATCTG 823

Qy    738 A------AATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGA 791
          |      |     ||      |   ||  | | |    || | |||  |    ||
Db    824 ATTCAGTACAGGTTGCTCCTGATGGCTCTAGGTTAAATCAATATGACCTGCTGGGCCAAT 883

Qy    792 GCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCT 851
            | |  ||  || | ||| | | ||       ||||| |  |  || |||||   |  |
Db    884 CAATCGGAAAGGAGACAATTAAATCCAGTACAGGTGAATATACTGTAATGACAGCTCATT 943

Qy    852 TCAATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGA 911
          || |  |||  ||     |||| ||| |||   |||||| |||| | ||||    | |||
Db    944 TCCACCTGAAAAGAAAAATTGGGTATTTTGTGATTCAAACCTATCTGCCTTGCATCATGA 1003

Qy    912 CCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCT 971
          |    || ||||||   ||||| || ||| | || | ||| |||  || ||  | ||
Db   1004 CTGTCATTCTCTCCCAAGTTTCATTCTGGCTTAACAGAGAATCTGTGCCTGCAAGAACTG 1063

Qy    972 CTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATT 1031
            | ||  | ||  |||| || || ||||| ||  |  ||| |  | |||| ||   |
Db   1064 TGTTTGGAGTAACAACTGTCCTAACAATGACAACTCTAAGCATCAGTGCTCGGAATTCTC 1123

Qy   1032 TCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCT 1091
          |||||    ||  | |||   || ||| |||| |  | ||| ||  | || |  |  ||
Db   1124 TCCCCAAAGTGGCTTATGCAACTGCCATGGACTGGTTTATTGCTGTTTGTTATGCATTTG 1183

Qy   1092 GCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACA 1139
            |||| || ||  | || |||||     | || | | | | | | |
Db   1184 TGTTCTCTGCCCTAATTGAATTTGCAACTGTTAATTACTTCACCAAAA 1231


RESULT  15
T28989
ID   T28989 standard; cDNA; 1555 BP.
AC   T28989;
DT   06-JAN-1997  (first entry)
DE   Human GABA-A receptor delta subunit cDNA.
KW   GABA-A receptor; gamma-aminobutyric acid; delta subunit; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             47. .1405
FT                   /*tag=  a
PN   WO9610637-A1.
PD   11-APR-1996.
PF   29-SEP-1995; G02323.
PR   01-OCT-1994; GB-020010.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Le Bourdelles B,  Whiting PJ;
DR   WPI; 96-209359/21.
DR   P-PSDB; R97299.
PT   DNA encoding alpha-4 and delta subunit(s) of the human GABAa
PT   receptor  - also stably co-transfected eukaryotic cells expressing
PT   receptors contg. these subunit(s), used for screening and designing
PT   drugs
PS   Claim 10; Fig 3; 45pp; English.
CC   A cDNA clone (T28989) codes for the delta subunit (R97299) of the
CC   human GABA-A receptor.  It was isolated from human hippocampus
CC   cDNA using a probe generated from rat brain cDNA using primers (see
CC   also T28996-97) based on the rat delta sequence.  The cDNA can be
CC   incorporated into a vector and used to direct expression of the
CC   delta subunit in transfected cells, partic. rodent fibroblasts.
CC   Co-transfected host cells capable of expressing the delta, alpha-4,
CC   (see also R97298) and beta subunits can be used to screen or design
CC   drugs that act on GABA-A receptors.
SQ   Sequence   1555 BP;    289 A;    524 C;    466 G;    276 T;


  Query Match             6.2%;  Score 196.8;  DB 1;  Length 1555;
  Best Local Similarity   52.0%;  Pred. No. 1.1e-47;
  Matches  466;  Conservative    0;  Mismatches  427;  Indels    3;  Gaps    1;
```

```
Qy    257 CGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAG 316
Db    170 CCCAACCTGGACGGGCTGATAGCCGGTTACGCCCGCAACTTCCGGCCTGGCATCGGAGGC 229

Qy    317 AAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTA 376
Db    230 CCCCCCGTGAATGTGGCCCTTGCCCTGGAGGTGGCCAGCATCGACCACATCTCAGAGGCC 289

Qy    377 GACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGT 436
Db    290 AACATGGAGTACACCATGACGGTGTTCCTGCACCAGAGCTGGCGGGACAGCAGGCTCTCC 349

Qy    437 TACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATC 496
Db    350 TACAACCACACCAACGAGACCCTGGGCCTGGACAGCCGCTTCGTGGACAAGCTGTGGCTG 409

Qy    497 CCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAAC 556
Db    410 CCCGACACCTTCATCGTGAACGCCAAGTCGGCCTGGTTCCACGACGTGACGGTGGAGAAC 469

Qy    557 CAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGAT 616
Db    470 AAGCTCATCCGGCTGCAGCCCGACGGGGTGATCCTGTACAGCATCCGAATCACCTCCACT 529

Qy    617 GCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCT 676
Db    530 GTGGCCTGCGACATGGACCTGGCCAAATTCCCCATGGACGAGCAGGAGTGCATGCTGGAC 589

Qy    677 TTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTT 736
Db    590 CTGGAGAGCTACGGTTACTCATCGGAGGACATCGTCTACTACTGGTCGGAGAGCCAGGAG 649

Qy    737 GAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAAC 796
Db    650 CACATCCACGGGCTGGACAAGCTGCAGCTGGCGCAGTTCACCATCACCAGCTACCGCTTC 709

Qy    797 AAAACTGA---AATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTC 853
Db    710 ACCACGGAGCTGATGAACTTCAAGTCCGCTGGCCAGTTCCCACGGCTCAGCCTGCACTTC 769

Qy    854 AATGTGAGCAGGCGGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTTCTTCCGTGACC 913
Db    770 CACCTGCGGAGGAACCGCGGCGTGTACATCATCCAATCCTACATGCCCTCCGTCCTGCTG 829

Qy    914 ACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCT 973
Db    830 GTCGCCATGTCCTGGGTCTCCTTCTGGATCAGCCAGGCGGCGGTGCCCGCCAGGGTGTCT 889

Qy    974 CTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTC 1033
Db    890 CTAGGCATCACCACGGTGCTGACGATGACCACGCTCATGGTCAGTGCCCGCTCCTCCCTG 949

Qy   1034 CCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGC 1093
Db    950 CCACGGGCATCAGCCATCAAGGCACTGGACGTCTACTTCTGGATCTGCTATGTCTTCGTG 1009

Qy   1094 TTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAACCAGACAAA 1149
Db   1010 TTTGCCGCCCTGGTGGAGTACGCCTTTGCTCATTTCAACGCCGACTACAGGAAGAA 1065
```

Search completed: March 9, 2000, 22:45:02
Job time: 601 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2000, 02:00:13 ; Search time 3156.82 Seconds
(without alignments)
3772.291 Million cell updates/sec

Title: US-09-030-832-41
Perfect score: 3154
Sequence: 1 CGCGACCTCCGCGCAGGTGG.....AGCAAAAAGAAAAAAAAAAA 3154

Scoring table: IDENTITY_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

Number of hits that pass the threshold : 9077268

1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*
44: gb_est25:*
45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_gss1:*
80: gb_gss2:*
81: gb_gss3:*
82: gb_gss4:*
83: em_gss1:*
84: em_gss2:*
85: em_gss3:*
86: em_gss4:*
87: gb_gss5:*
88: gb_gss6:*
89: gb_gss7:*
90: gb_gss8:*
91: gb_gss9:*
92: em_gss5:*
93: em_gss6:*
94: em_gss7:*
95: em_gss8:*
96: em_gss9:*
97: em_gss10:*
98: em_gss11:*
99: gb_gss10:*
100: gb_gss11:*
101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	499.4	15.8	501	63	AI963395	AI963395 wt62f07.x
c	2	486	15.4	486	46	AI432632	AI432632 tg31g10.x
c	3	476	15.1	476	45	AI334197	AI334197 qp92d09.x
c	4	475.4	15.1	477	45	AI332325	AI332325 qp97g08.x
c	5	460	14.6	460	45	AI334196	AI334196 qp92d07.x
c	6	459	14.6	460	46	AI400573	AI400573 tg88b09.x
c	7	447	14.2	464	63	AW009693	AW009693 ws86b05.x

c	8	434	13.8	434	64	AW070871 AW070871 xa05c11.x
c	9	432	13.7	433	38	AA776409 AA776409 zj50e04.s
c	10	429.4	13.6	474	63	AW014213 AW014213 UI-H-BI0-
c	11	429	13.6	429	44	AI276837 AI276837 ql67f08.x
c	12	416.4	13.2	418	37	AA677867 AA677867 zi13e03.s
	13	398.4	12.6	404	28	C17786 C17786 C17786 Huma
	14	388.4	12.3	500	24	H63934 H63934 yr54h01.r1
c	15	375.8	11.9	403	37	AA682288 AA682288 zj85g12.s
c	16	360	11.4	371	37	AA704433 AA704433 zj22h01.s
	17	357.2	11.3	479	22	R64082 R64082 yi22g06.r1
c	18	350.4	11.1	363	41	AI040493 AI040493 ox14e03.s
c	19	348	11.0	366	20	T27014 T27014 NIBT136C07
c	20	345.4	11.0	485	24	H63532 H63532 yr54h01.s1
	21	345.2	10.9	389	24	H83086 H83086 yq46f02.r1
c	22	335.4	10.6	337	50	AI682740 AI682740 wc65f01.x
	23	334.8	10.6	387	23	R91732 R91732 yp98f02.r1
	24	317.2	10.1	386	21	T78142 T78142 yc98d07.r1
c	25	311	9.9	311	40	AA954089 AA954089 on62h10.s
c	26	308.2	9.8	450	22	R49719 R49719 yg71c11.s1
	27	301.4	9.6	303	31	AA299532 AA299532 EST12052
	28	285.2	9.0	436	26	W77939 W77939 zd71b07.r1
	29	280.4	8.9	522	22	R49718 R49718 yg71c11.r1
c	30	273	8.7	291	43	AI168466 AI168466 oo10f05.x
c	31	269.2	8.5	596	26	W72699 W72699 zd71b07.s1
c	32	255.2	8.1	260	36	AA634042 AA634042 ac74d11.s
c	33	251.2	8.0	317	21	R07883 R07883 yf16g04.s1
c	34	249.4	7.9	259	62	AI924717 AI924717 wn74g12.x
	35	246.2	7.8	465	22	R35778 R35778 yh90f03.r1
	36	245.6	7.8	623	64	AW077068 AW077068 fj04d06.y
c	37	218.6	6.9	274	23	H25140 H25140 yl43f11.s1
c	38	212	6.7	212	44	AI279924 AI279924 qx57g03.x
	39	210.4	6.7	223	20	T27015 T27015 NIBT136C07R
c	40	202	6.4	202	37	AA677292 AA677292 zj61e08.s
c	41	200.6	6.4	400	22	R35667 R35667 yh90f03.s1
	42	198	6.3	201	31	AA321214 AA321214 EST23669
c	43	198	6.3	206	32	AA368252 AA368252 EST79500
	44	183	5.8	184	27	C00867 C00867 HUMGS000316
c	45	171	5.4	177	32	AA347289 AA347289 EST53562

ALIGNMENTS

```
RESULT   1
AI963395/c
LOCUS       AI963395      501 bp    mRNA            EST       20-AUG-1999
DEFINITION  wt62f07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2512069 3',
            mRNA sequence.
ACCESSION   AI963395
VERSION     AI963395.1  GI:5756108
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 501)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Dec 20, 1995 this sequence version replaced gi:1135445.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Life Technologies catalog #: 11548-013
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco
            High quality sequence stop: 420.
FEATURES             Location/Qualifiers
     source          1. .501
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2512069"
                     /clone_lib="NCI_CGAP_Pan1"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.72 kb. Life Technologies catalog #:
                     11548-013"
BASE COUNT      141 a    113 c    114 g    133 t
ORIGIN


  Query Match             15.8%;  Score 499.4;  DB 63;  Length 501;
  Best Local Similarity   99.8%;  Pred. No. 2.4e-130;
  Matches  500;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    2650 AGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGG 2709
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     501 AGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGG 442

Qy    2710 GCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACT 2769
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     441 GCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACT 382

Qy    2770 GTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGG 2829
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     381 GTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGG 322

Qy    2830 CTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAA 2889
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     321 CTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAA 262

Qy    2890 GGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCC 2949
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     261 GGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCC 202

Qy    2950 CCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAA 3009
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     201 CCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAA 142

Qy    3010 TGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGG 3069
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     141 TGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGG 82

Qy    3070 GTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATATC 3129
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      81 GTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATATC 22

Qy    3130 AGCAAAGCAAAAAGAAAAAAA 3150
           ||||||||||||| |||||||
Db      21 AGCAAAGCAAAAAAAAAAAAA 1


RESULT   2
AI432632/c
LOCUS       AI432632      486 bp    mRNA            EST       30-MAR-1999
DEFINITION  tg31g10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2110434 3',
            mRNA sequence.
ACCESSION   AI432632
VERSION     AI432632.1  GI:4283251
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 486)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
```

```
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2949103.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Insert Length: 1551   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 462.
FEATURES             Location/Qualifiers
     source          1. .486
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2110434"
                     /clone_lib="NCI_CGAP_Pr28"
                     /sex="male"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Plasmid DNA from the
                     normalized library NCI_CGAP_Pr22 was prepared, and ss
                     circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     985608-986759, 1101192-1101959, and 1217928-1220615).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
BASE COUNT      141 a    112 c    114 g    119 t
ORIGIN


  Query Match            15.4%;  Score 486;  DB 46;  Length 486;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-126;
  Matches  486;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2652 CACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGC 2711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 CACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGC 427

Qy   2712 AGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGT 2771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 AGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGT 367

Qy   2772 GGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCT 2831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 GGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCT 307

Qy   2832 AGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGG 2891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 AGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGG 247

Qy   2892 CCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCC 2951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 CCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCC 187

Qy   2952 AAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATG 3011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 AAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATG 127

Qy   3012 CTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGT 3071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 CTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGT 67

Qy   3072 CTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATATCAG 3131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 CTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATATCAG 7

Qy   3132 CAAAGC 3137
          ||||||
Db      6 CAAAGC 1


RESULT   3
AI334197/c
LOCUS       AI334197      476 bp    mRNA            EST       13-FEB-1999
DEFINITION  qp92d09.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
            IMAGE:1930481 3', mRNA sequence.
ACCESSION   AI334197
VERSION     AI334197.1  GI:4070756
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 19, 1998 this sequence version replaced gi:2045081.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 997   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 458.
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1930481"
                     /clone_lib="Soares_fetal_lung_NbHL19W"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCAATTTTTTTTTTTTTTTTT-3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. This library was constructed
                     from the same fetus as the fetal heart library, Soares
                     fetal heart NbHH19W."
BASE COUNT      137 a    111 c    111 g    117 t
ORIGIN


  Query Match            15.1%;  Score 476;  DB 45;  Length 476;
  Best Local Similarity  100.0%;  Pred. No. 9.9e-124;
  Matches  476;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2663 AGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTAT 2722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    476 AGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTAT 417

Qy   2723 CCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTG 2782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    416 CCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTG 357

Qy   2783 GAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAG 2842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    356 GAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAG 297

Qy   2843 TTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGC 2902
```

```
Db    296 TTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGC 237

Qy   2903 GACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATC 2962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    236 GACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATC 177

Qy   2963 TCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGC 3022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    176 TCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGC 117

Qy   3023 TAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGGTGGATAGGGTGGGGTCTCCATCTACT 3082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    116 TAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGGTGGATAGGGTGGGGTCTCCATCTACT 57

Qy   3083 TTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATATCAGCAAAGCA 3138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     56 TTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATATCAGCAAAGCA 1


RESULT   4
AI332325/c
LOCUS       AI332325      477 bp    mRNA            EST       13-FEB-1999
DEFINITION  qp97g08.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
            IMAGE:1931006 3', mRNA sequence.
ACCESSION   AI332325
VERSION     AI332325.1  GI:4068884
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 477)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 14, 1998 this sequence version replaced gi:1877761.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 855   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 445.
FEATURES             Location/Qualifiers
     source          1. .477
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1931006"
                     /clone_lib="Soares_fetal_lung_NbHL19W"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCAATTTTTTTTTTTTTTTT-3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. This library was constructed
                     from the same fetus as the fetal heart library, Soares
                     fetal heart NbHH19W."
BASE COUNT      138 a    111 c    110 g    118 t
ORIGIN


  Query Match           15.1%;  Score 475.4;  DB 45;  Length 477;
  Best Local Similarity   99.8%;  Pred. No. 1.5e-123;
  Matches  476;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   2660 ACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCT 2719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    477 ACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCT 418

Qy   2720 TATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCA 2779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    417 TATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCA 358

Qy   2780 CTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCT 2839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    357 CTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCT 298

Qy   2840 CAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAAT 2899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    297 CAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAAT 238

Qy   2900 GGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAA 2959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    237 GGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAA 178

Qy   2960 ATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATA 3019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    177 ATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATA 118

Qy   3020 TGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCT 3079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    117 TGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCT 58

Qy   3080 ACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATATCAGCAAAG 3136
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     57 ACTTTTTGTCACTATCATCTGAAATGGGGAAATATGTAAATAAATATATCAGCAAAG 1


RESULT   5
AI334196/c
LOCUS       AI334196      460 bp    mRNA            EST       13-FEB-1999
DEFINITION  qp92d07.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
            IMAGE:1930477 3', mRNA sequence.
ACCESSION   AI334196
VERSION     AI334196.1  GI:4070755
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 460)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 19, 1998 this sequence version replaced gi:2045079.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1507   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 436.
FEATURES             Location/Qualifiers
     source          1. .460
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1930477"
                     /clone_lib="Soares_fetal_lung_NbHL19W"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCAATTTTTTTTTTTTTTTT-3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
```

adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHH19W."
BASE COUNT 130 a 105 c 110 g 115 t
ORIGIN

Query Match 14.6%; Score 460; DB 45; Length 460;
Best Local Similarity 100.0%; Pred. No. 3.3e-119;
Matches 460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   2679 AGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATG 2738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    460 AGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATG 401

Qy   2739 AAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGC 2798
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    400 AAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGC 341

Qy   2799 CCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCT 2858
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    340 CCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCT 281

Qy   2859 TCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTC 2918
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    280 TCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTC 221

Qy   2919 AATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTA 2978
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    220 AATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTA 161

Qy   2979 ACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGT 3038
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    160 ACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGT 101

Qy   3039 CTGTAATTTGTTGGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATC 3098
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    100 CTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATC 41

Qy   3099 TGAAATGGGGAAATATGTAAATAAATATATCAGCAAAGCA 3138
          |||||||||||||||||||||||||||||||||||||||
Db     40 TGAAATGGGGAAATATGTAAATAAATATATCAGCAAAGCA 1
```

RESULT 6
AI400573/c
LOCUS AI400573 460 bp mRNA EST 30-MAR-1999
DEFINITION tg88b09.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2115833 3', mRNA sequence.
ACCESSION AI400573
VERSION AI400573.1 GI:4243660
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 460)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3034543.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 562 Std Error: 0.00
Seq primer: -40UP from Gibco.

FEATURES Location/Qualifiers
source 1. .460
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2115833"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
BASE COUNT 129 a 106 c 110 g 114 t 1 others
ORIGIN

Query Match 14.6%; Score 459; DB 46; Length 460;
Best Local Similarity 99.8%; Pred. No. 6.4e-119;
Matches 459; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy   2678 GAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGAT 2737
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    460 GAGCTTCATGATAGCCNTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGAT 401

Qy   2738 GAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAG 2797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    400 GAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAG 341

Qy   2798 CCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTC 2857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    340 CCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTC 281

Qy   2858 TTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCT 2917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    280 TTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCT 221

Qy   2918 CAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGT 2977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    220 CAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGT 161

Qy   2978 AACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTG 3037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    160 AACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTG 101

Qy   3038 TCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCAT 3097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    100 TCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCAT 41

Qy   3098 CTGAAATGGGGAAATATGTAAATAAATATATCAGCAAAGC 3137
          |||||||||||||||||||||||||||||||||||||||
Db     40 CTGAAATGGGGAAATATGTAAATAAATATATCAGCAAAGC 1
```

RESULT 7
AW009693/c
LOCUS AW009693 464 bp mRNA EST 10-SEP-1999
DEFINITION ws86b05.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504817 3', mRNA sequence.
ACCESSION AW009693
VERSION AW009693.1 GI:5858471
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
REFERENCE   1  (bases 1 to 464)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Mar 16, 1998 this sequence version replaced gi:2961718.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
            M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arraying: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Seq primer: -40UP from Gibco
            High quality sequence stop: 366.
FEATURES             Location/Qualifiers
     source          1. .464
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2504817"
                     /clone_lib="NCI_CGAP_Co3"
                     /sex="pooled"
                     /tissue_type="colon"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from 12 pooled bulk tumor samples and primed
                     with a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector. Library went through one round of
                     normalization. "
BASE COUNT      134 a    102 c    101 g    127 t
ORIGIN


  Query Match           14.2%;  Score 447;  DB 63;  Length 464;
  Best Local Similarity  97.8%;  Pred. No. 1.6e-115;
  Matches  453;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy   2692 CCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTC 2751
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    464 CCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTC 405

Qy   2752 ACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTT 2811
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    404 ACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTT 345

Qy   2812 CTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTG 2871
          |||||||||||||||||||||||||||||||||||||||| | || |||||||| ||
Db    344 TTAGACCACATGATAGGGCTAGACAGCTCAGTTCACCATGATTTTTTTTTGTCACCTTTG 285

Qy   2872 CTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCT 2931
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    284 CTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCT 225

Qy   2932 GAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATG 2991
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    224 GAGGTGCTCAGACTGCCCCCAAGATCAAATCTTTCCTGGCTGTAGTAACCCAGTGGAATG 165

Qy   2992 AATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTG 3051
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    164 AATTTGGACATGCCCCAATGCTTTTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTG 105

Qy   3052 GGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAA 3111
          |||||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||
Db    104 GGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCCCCATCATTTGAAATGGGGAAA 45

Qy   3112 TATGTAAATAAATATATCAGCAAAGCAAAAAGAAAAAAAAAAA 3154
          |||||||||||||||||||||||||||||||| ||||||||||
Db     44 TATGTAAATAAATATATCAGCAAAGCAAAAAAAAAAAAAAAA 2


RESULT   8
AW070871/c
LOCUS       AW070871      434 bp    mRNA            EST       13-OCT-1999
DEFINITION  xa05c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:2567444 3', mRNA sequence.
ACCESSION   AW070871
VERSION     AW070871.1  GI:6025869
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 434)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jul 9, 1999 this sequence version replaced gi:5434981.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .434
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2567444"
                     /clone_lib="Soares_NFL_T_GBC_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo. "
BASE COUNT      119 a    100 c    104 g    111 t
ORIGIN


  Query Match           13.8%;  Score 434;  DB 64;  Length 434;
  Best Local Similarity  100.0%;  Pred. No. 7.4e-112;
  Matches  434;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2707 AGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGG 2766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434 AGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGG 375

Qy   2767 ACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATA 2826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 ACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATA 315

Qy   2827 GGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGG 2886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 GGGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGG 255

Qy   2887 CAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTG 2946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 CAAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTG 195

Qy   2947 CCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCC 3006
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 CCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCC 135

Qy   3007 CAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGT 3066
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 CAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGT 75

Qy   3067 GGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATAT 3126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     74 GGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATAT 15

Qy   3127 ATCAGCAAAGCAAA 3140
          ||||||||||||||
Db     14 ATCAGCAAAGCAAA 1
```

RESULT 9
AA776409/c
LOCUS AA776409 433 bp mRNA EST 05-FEB-1998
DEFINITION zj50e04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453726 3', mRNA sequence.
ACCESSION AA776409
VERSION AA776409.1 GI:2835743
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 433)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT On Jan 17, 1998 this sequence version replaced gi:2044660.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 379.
FEATURES Location/Qualifiers
source 1. .433
/organism="Homo sapiens"
/db_xref="GDB:1390082"
/db_xref="taxon:9606"
/clone="IMAGE:453726"
/clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen 1NFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 119 a 98 c 105 g 111 t
ORIGIN

Query Match 13.7%; Score 432; DB 38; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.7e-111;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   2710 GCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACT 2769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    433 GCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACT 374

Qy   2770 GTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGG 2829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    373 GTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGG 314

Qy   2830 CTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAA 2889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    313 CTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAA 254

Qy   2890 GGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCC 2949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    253 GGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCC 194

Qy   2950 CCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAA 3009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    193 CCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAA 134

Qy   3010 TGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGG 3069
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    133 TGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGG 74

Qy   3070 GTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATATC 3129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     73 GTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATATC 14

Qy   3130 AGCAAAGCAAAA 3141
          ||||||||||||
Db     13 AGCAAAGCAAAA 2
```

RESULT 10
AW014213/c
LOCUS AW014213 474 bp mRNA EST 10-SEP-1999
DEFINITION UI-H-BI0-aak-a-03-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709412 3', mRNA sequence.
ACCESSION AW014213
VERSION AW014213.1 GI:5862970
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 474)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On May 18, 1998 this sequence version replaced gi:3137517.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html The following repetitive elements were found in this cDNA sequence: 417-470, >MIR#SINE/MIR
Seq primer: M13 Forward
POLYA=No.
FEATURES Location/Qualifiers
source 1. .474
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2709412"
/clone_lib="NCI_CGAP_Sub1"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The

NCI_CGAP_Sub1 library is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10, NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1, NCI_CGAP_Lei2, NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6, NCI_CGAP_Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903, 1492104-1493255) NCI_CGAP_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439) NCI_CGAP_GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743) NCI_CGAP_Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959, 1217928-1220615) NCI_CGAP_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351) The resulting subtracted library contained 530,000 recombinants. Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.
TAG_LIB=NCI_CGAP_Co10
TAG_TISSUE=colon
TAG_SEQ=AAACG"

BASE COUNT 121 a 116 c 113 g 124 t
ORIGIN

Query Match 13.6%; Score 429.4; DB 63; Length 474;
Best Local Similarity 97.5%; Pred. No. 1.6e-110;
Matches 436; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```
Qy   2708 GGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGA 2767
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 GGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGA 406

Qy   2768 CTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAG 2827
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405 CTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAG 346

Qy   2828 GGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGC 2887
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 GGCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGC 286

Qy   2888 AAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGC 2947
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 AAGGCCCAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGC 226

Qy   2948 CCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCC 3007
          ||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 CCCCAAGATCGGATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCC 166

Qy   3008 AATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGGTGGATAGGGTG 3067
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    165 AATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGGTGGATAGGGTG 106

Qy   3068 GGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATA 3127
          |||||  ||||  ||||||  ||||||||||| |||||||||||||||||||| ||||||||
Db    105 GGGTCACCATGTACTTTCTGTCACCATCATGTGAAATGGGGAAATATGTAACTAAATATA 46

Qy   3128 TCAGCAAAGCAAAAAGAAAAAAAAAAA 3154
          || ||||||||||||||  |||| |||
Db     45 TCGGCAAAGCAAAAAGATGAAAACAAA 19
```

RESULT 11
AI276837/c
LOCUS AI276837 429 bp mRNA EST 29-JAN-1999
DEFINITION ql67f08.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1877415 3', mRNA sequence.
ACCESSION AI276837
VERSION AI276837.1 GI:3899111
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 429)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 19, 1998 this sequence version replaced gi:2286330.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 575 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 422.
FEATURES Location/Qualifiers
source 1. .429
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1877415"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT 119 a 96 c 103 g 111 t
ORIGIN

Query Match 13.6%; Score 429; DB 44; Length 429;
Best Local Similarity 100.0%; Pred. No. 1.9e-110;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   2714 GATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGG 2773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429 GATTCTTATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGG 370

Qy   2774 ATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAG 2833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 ATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAG 310

Qy   2834 ACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCC 2893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 ACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCC 250

Qy   2894 CAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAA 2953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 CAGAATGGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAA 190

Qy   2954 GATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCT 3013
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 GATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCT 130

Qy   3014 TCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCT 3073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 TCTATATGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCT 70

Qy   3074 CCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATATCAGCA 3133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 CCATCTACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATATCAGCA 10

Qy   3134 AAGCAAAAA 3142
          |||||||||
Db       9 AAGCAAAAA 1


RESULT  12
AA677867/c
LOCUS       AA677867      418 bp    mRNA            EST       19-DEC-1997
DEFINITION  zi13e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:430684 3', mRNA sequence.
ACCESSION   AA677867
VERSION     AA677867.1  GI:2658389
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 418)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     On Nov 6, 1997 this sequence version replaced gi:931632.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .418
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:430684"
                     /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.  1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      117 a     94 c    102 g    105 t
ORIGIN


  Query Match             13.2%;  Score 416.4;  DB 37;  Length 418;
  Best Local Similarity   99.8%;  Pred. No. 7e-107;
  Matches  417;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   2720 TATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCA 2779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    418 TATCCCCATTTTGCAGATGAAAACCCTGAGTCACAGATTTCTGTGGGACTGTGGATCTCA 359

Qy   2780 CTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCT 2839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    358 CTGGAAGCTATCCAAGAGCCCACTGTCACCTTCTAGACCACATGATAGGGCTAGACAGCT 299

Qy   2840 CAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTGGCAAGGCCCAGAAT 2899
          ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    298 CAGTTCACCATGATTCTCTTCTGTCACCTCTGCTGGCACACCAGTTGCAAGGCCCAGAAT 239

Qy   2900 GGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAA 2959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 GGCGACCTCTCTTTAGCTCAATTTCTGGGCCTGAGGTGCTCAGACTGCCCCCAAGATCAA 179

Qy   2960 ATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATA 3019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    178 ATCTCTCCTGGCTGTAGTAACCCAGTGGAATGAATTTGGACATGCCCCAATGCTTCTATA 119

Qy   3020 TGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCT 3079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    118 TGCTAAGTGAAATCTGTGTCTGTAATTTGTTGGGGGGTGGATAGGGTGGGGTCTCCATCT 59

Qy   3080 ACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATATCAGCAAAGC 3137
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     58 ACTTTTTGTCACCATCATCTGAAATGGGGAAATATGTAAATAAATATATCAGCAAAGC 1


RESULT  13
C17786
LOCUS       C17786        404 bp    mRNA            EST       02-OCT-1996
DEFINITION  C17786 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone
            GEN-552F09 5', mRNA sequence.
ACCESSION   C17786
VERSION     C17786.1  GI:1579389
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 404)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1404821.
            Contact: Tsutomu Fujiwara
            Otsuka GEN Research Institute
            Otsuka Pharmaceutical Co.,Ltd
            463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
            Tel: 0886-65-2888
            Fax: 0886-37-1035.
FEATURES             Location/Qualifiers
     source          1. .404
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="GEN-552F09"
                     /clone_lib="Human placenta cDNA (TFujiwara)"
                     /tissue_type="placenta"
BASE COUNT       93 a    118 c     79 g    114 t
ORIGIN


  Query Match             12.6%;  Score 398.4;  DB 28;  Length 404;
  Best Local Similarity   99.8%;  Pred. No. 8.6e-102;
  Matches  399;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   2345 CCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCC 2404
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCACCCTCTTCCTTCTCTTTGACCCCTGTGACTCTTTCTGTAACTTTCCCAGTGACTTCC 60
```

```
Qy   2405 CCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAA 2464
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCTAGCCCTGACCCAGGCACTAGGCCTTGGTGACTTCCTGGGGCCAAGAAACTAAGGAAA 120

Qy   2465 CTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCG 2524
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTCGGCTTTGCAACAGGCATTACTCGCCATTGATTGGTGCCCACCCAGGGCACACTGTCG 180

Qy   2525 GAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGC 2584
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAGTTCTATCACTTGCTTGACCCCTGGACCCATAAACCAGTCCACTGTTATACCCGGGGC 240

Qy   2585 ACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTT 2644
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACTCTAACCATCACAATCAATCAATCAAATTCCCTTAAATTTGTATGGCACTGGAACTTT 300

Qy   2645 GGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCT 2704
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGCAAAGCACTTTTGACAAGTTGTGTCTGATTGGAGCTTCATGATAGCCTTGTGACATCT 360

Qy   2705 TTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAAACC 2744
          |||||||||||||||||||||||||||||||||||| ||
Db    361 TTAGGGCAGGATTCTTATCCCCATTTTGCAGATGAAACCC 400
```

```
RESULT  14
H63934
LOCUS       H63934         500 bp    mRNA            EST       11-OCT-1995
DEFINITION  yr54h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:209137 5', mRNA sequence.
ACCESSION   H63934
VERSION     H63934.1  GI:1018735
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 500)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 877
            High quality sequence stops: 379
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 877    Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 379.
FEATURES             Location/Qualifiers
     source          1. .500
                     /organism="Homo sapiens"
                     /db_xref="GDB:3781978"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:209137"
                     /clone_lib="Soares fetal liver spleen 1NFLS"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Pac I - oligo(dT) primer
                     [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      120 a    126 c    110 g    139 t      5 others
ORIGIN
```

```
  Query Match           12.3%;  Score 388.4;  DB 24;  Length 500;
  Best Local Similarity  93.8%;  Pred. No. 6.5e-99;
  Matches  438;  Conservative    0;  Mismatches   22;  Indels    7;  Gaps    3;

Qy   2372 GTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGGCACTAGGCCT 2431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTGACTCTTTCTGTAACTTTCCCAGTGACTTCCCCTAGCCCTGACCCAGGCACTAGGCCT 60

Qy   2432 TGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGC 2491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGGTGACTTCCTGGGGCCAAGAAACTAAGGAAACTCGGCTTTGCAACAGGCATTACTCGC 120

Qy   2492 CATTGATTGGTGCCCACCCAGGGCACACTGTCGGAGTTCTATCACTTGCTTGACCCCTGG 2551
          |||||||||||||||||||| |    ||||||||||||||||||||||||||||||||
Db    121 CATTGATTGGTGCCCACCCAGGGAAGCTGGTCGGAGTTCTATCACTTGCTTGACCCCTGG 180

Qy   2552 ACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCA 2611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ACCCATAAACCAGTCCACTGTTATACCCGGGGCACTCTAACCATCACAATCAATCAATCA 240

Qy   2612 AATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTC 2671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATTCCCTTAAATTTGTATGGCACTGGAACTTTGGCAAAGCACTTTTGACAAGTTGTGTC 300

Qy   2672 TGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTT 2731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGATTGGAGCTTCATGATAGCCTTGTGACATCTTTAGGGCAGGATTCTTATCCCCATTTT 360

Qy   2732 GCAGATGAAAACCCTGAGTCACAGATT---TCTGTGGGACTGTGGATCTCACTGGAAGCT 2788
          |||||||||||||||||||||||||||   | || ||       ||||||||||||||||
Db    361 GCAGATGAAAACCCTGAGTCACAGATTTTCTGTGGGGACTGTGGGATCTCACTGGAAGCT 420

Qy   2789 A-TCCAAGAGCCCACTG---TCACCTTCTAGACCACATGATAGGGCT 2831
          | ||||||||||||||    |    |   ||||||||||||||| |
Db    421 ATTCCAAGAGCCCACTGGTCACCTTNTTAGGACCACATGATAGGGGT 467
```

```
RESULT  15
AA682288/c
LOCUS       AA682288       403 bp    mRNA            EST       19-DEC-1997
DEFINITION  zj85g12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:461734 3', mRNA sequence.
ACCESSION   AA682288
VERSION     AA682288.1  GI:2669605
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 403)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1394010.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
```

```
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 388.
FEATURES             Location/Qualifiers
     source          1. .403
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:461734"
                     /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.   1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      109 a      90 c      95 g     109 t
ORIGIN


  Query Match             11.9%;  Score 375.8;  DB 37;  Length 403;
  Best Local Similarity   99.0%;  Pred. No. 2.2e-95;
  Matches  399;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;

Qy    2751 CACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCT 2810
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     403 CACAGATTTCTGTGGGACTGTGGATCTCACTGGAAGCTATCCAAGAGCCCACTGTCACCT 344

Qy    2811 TCTAGACCACATGATAGGG-CTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTC 2869
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     343 TCTAGACCACATGATAGGGTCTAGACAGCTCAGTTCACCATGATTCTCTTCTGTCACCTC 284

Qy    2870 TGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGC-TCAATTTCTGGG 2928
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     283 TGCTGGCACACCAGTGGCAAGGCCCAGAATGGCGACCTCTCTTTAGCTTCAATTTCTGGG 224

Qy    2929 CCTGAGGTGCTCAGACTGCCCCCAAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGA 2988
           |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db     223 CCTGAGGTGCTCAGACTGCCCCCCAGATCAAATCTCTCCTGGCTGTAGTAACCCAGTGGA 164

Qy    2989 ATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTG 3048
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     163 ATGAATTTGGACATGCCCCAATGCTTCTATATGCTAAGTGAAATCTGTGTCTGTAATTTG 104

Qy    3049 TTGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGG 3108
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     103 TTGGGGGGTGGATAGGGTGGGGTCTCCATCTACTTTTTGTCACCATCATCTGAAATGGGG 44

Qy    3109 AAATATGTAAATAAATATATCAGCAAAGCAAAAAGAAAAAAAA 3151
           |||||||||||||||||||||||||||||||||| ||||||||
Db      43 AAATATGTAAATAAATATATCAGCAAAGCAAAAAAAAAAAAAA 1


Search completed: March 11, 2000, 02:00:26
Job time: 3214 sec
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 10, 2000, 09:00:09 ; Search time 3678.19 Seconds
(without alignments)
-881.399 Million cell updates/sec

Title: US-09-030-832-41_COPY_95_874
Perfect score: 780
Sequence: 1 AGGGTCGAGGGACCTCAGAC.....ATGTGAGCAGGCGGTTTGGC 780

Scoring table: IDENTITY_NUC

Searched: 4799332 seqs, -2078174120 residues

Database : Pending_Patents_NA:*

Word size : 0

Number of hits that pass the threshold : 9598654

1: /cgn2_6/ptodata/2/pna/PCTUS9_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US081A_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US081B_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US081C_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US081D_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US082A_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US082B_COMB.seq:*
10: /cgn2_6/ptodata/2/pna/US082C_COMB.seq:*
11: /cgn2_6/ptodata/2/pna/US083A_COMB.seq:*
12: /cgn2_6/ptodata/2/pna/US083B_COMB.seq:*
13: /cgn2_6/ptodata/2/pna/US084A_COMB.seq:*
14: /cgn2_6/ptodata/2/pna/US084B_COMB.seq:*
15: /cgn2_6/ptodata/2/pna/US084C_COMB.seq:*
16: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*
17: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*
18: /cgn2_6/ptodata/2/pna/US087A_COMB.seq:*
19: /cgn2_6/ptodata/2/pna/US087B_COMB.seq:*
20: /cgn2_6/ptodata/2/pna/US087C_COMB.seq:*
21: /cgn2_6/ptodata/2/pna/US088A_COMB.seq:*
22: /cgn2_6/ptodata/2/pna/US088B_COMB.seq:*
23: /cgn2_6/ptodata/2/pna/US088C_COMB.seq:*
24: /cgn2_6/ptodata/2/pna/US088D_COMB.seq:*
25: /cgn2_6/ptodata/2/pna/US089A_COMB.seq:*
26: /cgn2_6/ptodata/2/pna/US089B_COMB.seq:*
27: /cgn2_6/ptodata/2/pna/US089C_COMB.seq:*
28: /cgn2_6/ptodata/2/pna/US089D_COMB.seq:*
29: /cgn2_6/ptodata/2/pna/US089E_COMB.seq:*
30: /cgn2_6/ptodata/2/pna/US089F_COMB.seq:*
31: /cgn2_6/ptodata/2/pna/US089G_COMB.seq:*
32: /cgn2_6/ptodata/2/pna/US089H_COMB.seq:*
33: /cgn2_6/ptodata/2/pna/US089I_COMB.seq:*
34: /cgn2_6/ptodata/2/pna/US090A_COMB.seq:*
35: /cgn2_6/ptodata/2/pna/US090B_COMB.seq:*
36: /cgn2_6/ptodata/2/pna/US090C_COMB.seq:*
37: /cgn2_6/ptodata/2/pna/US090D_COMB.seq:*
38: /cgn2_6/ptodata/2/pna/US090E_COMB.seq:*
39: /cgn2_6/ptodata/2/pna/US091A_COMB.seq:*
40: /cgn2_6/ptodata/2/pna/US091B_COMB.seq:*
41: /cgn2_6/ptodata/2/pna/US091C_COMB.seq:*
42: /cgn2_6/ptodata/2/pna/US092A_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US092B_COMB.seq:*
44: /cgn2_6/ptodata/2/pna/US092C_COMB.seq:*
45: /cgn2_6/ptodata/2/pna/US092D_COMB.seq:*
46: /cgn2_6/ptodata/2/pna/US092E_COMB.seq:*
47: /cgn2_6/ptodata/2/pna/US093A_COMB.seq:*
48: /cgn2_6/ptodata/2/pna/US093B_COMB.seq:*
49: /cgn2_6/ptodata/2/pna/US093C_COMB.seq:*
50: /cgn2_6/ptodata/2/pna/US093D_COMB.seq:*
51: /cgn2_6/ptodata/2/pna/US093E_COMB.seq:*
52: /cgn2_6/ptodata/2/pna/US093F_COMB.seq:*
53: /cgn2_6/ptodata/2/pna/US094A_COMB.seq:*
54: /cgn2_6/ptodata/2/pna/US094B_COMB.seq:*
55: /cgn2_6/ptodata/2/pna/US6000_COMB.seq:*
56: /cgn2_6/ptodata/2/pna/US6001A_COMB.seq:*
57: /cgn2_6/ptodata/2/pna/US6001B_COMB.seq:*
58: /cgn2_6/ptodata/2/pna/US6002A_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6002B_COMB.seq:*
60: /cgn2_6/ptodata/2/pna/US6002C_COMB.seq:*
61: /cgn2_6/ptodata/2/pna/US6003A_COMB.seq:*
62: /cgn2_6/ptodata/2/pna/US6003B_COMB.seq:*
63: /cgn2_6/ptodata/2/pna/US6004A_COMB.seq:*
64: /cgn2_6/ptodata/2/pna/US6004B_COMB.seq:*
65: /cgn2_6/ptodata/2/pna/US6004C_COMB.seq:*
66: /cgn2_6/ptodata/2/pna/US6005_COMB.seq:*
67: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
68: /cgn2_6/ptodata/2/pna/US6007_COMB.seq:*
69: /cgn2_6/ptodata/2/pna/US6008A_COMB.seq:*
70: /cgn2_6/ptodata/2/pna/US6008B_COMB.seq:*
71: /cgn2_6/ptodata/2/pna/US6008C_COMB.seq:*
72: /cgn2_6/ptodata/2/pna/US6009A_COMB.seq:*
73: /cgn2_6/ptodata/2/pna/US6009B_COMB.seq:*
74: /cgn2_6/ptodata/2/pna/US6010A_COMB.seq:*
75: /cgn2_6/ptodata/2/pna/US6010B_COMB.seq:*
76: /cgn2_6/ptodata/2/pna/US6011A_COMB.seq:*
77: /cgn2_6/ptodata/2/pna/US6011B_COMB.seq:*
78: /cgn2_6/ptodata/2/pna/US6012A_COMB.seq:*
79: /cgn2_6/ptodata/2/pna/US6012B_COMB.seq:*
80: /cgn2_6/ptodata/2/pna/US6013A_COMB.seq:*
81: /cgn2_6/ptodata/2/pna/US6013B_COMB.seq:*
82: /cgn2_6/ptodata/2/pna/US6014A_COMB.seq:*
83: /cgn2_6/ptodata/2/pna/US6014B_COMB.seq:*
84: /cgn2_6/ptodata/2/pna/US6014C_COMB.seq:*
85: /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*
86: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:*
87: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:*
88: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
89: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
90: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
91: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
92: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	780	100.0	3154	35	US-09-030-832-41	Sequence 41, Appl
2	778.4	99.8	3268	87	US-60-172-373-15901	Sequence 15901, A
3	245.6	31.5	1565	18	US-08-716-396-7	Sequence 7, Appli
4	225.4	28.9	9631	24	US-08-888-012-5	Sequence 5, Appli
5	225.4	28.9	9631	35	US-09-030-832-5	Sequence 5, Appli
6	220.2	28.2	1097	24	US-08-888-012-4	Sequence 4, Appli
7	220.2	28.2	1097	35	US-09-030-832-4	Sequence 4, Appli
8	219.6	28.2	2434	50	US-09-354-899-7330	Sequence 7330, Ap
9	219.6	28.2	2434	51	US-09-371-168-7178	Sequence 7178, Ap
10	218	27.9	1980	54	US-09-471-275-1928	Sequence 1928, Ap
11	177.8	22.8	1707	21	US-08-809-802-7	Sequence 7, Appli
12	177.8	22.8	1679	34	US-09-016-434-1470	Sequence 1470, Ap
13	164.8	21.1	2310	2	US-07-971-767-15	Sequence 15, Appl
14	164.8	21.1	2310	12	US-08-341-610-1	Sequence 1, Appli
15	160.8	20.6	1893	87	US-60-172-373-2255	Sequence 2255, Ap
16	159.2	20.4	1408	2	US-07-971-767-17	Sequence 17, Appl
17	159.2	20.4	1408	12	US-08-341-610-3	Sequence 3, Appli
18	157.8	20.2	7479	24	US-08-888-012-6	Sequence 6, Appli
19	157.8	20.2	7479	35	US-09-030-832-6	Sequence 6, Appli
20	146.4	18.8	1638	2	US-07-971-767-13	Sequence 13, Appl

21	146.4	18.8	1638	12	US-08-341-610-9	Sequence 9, Appli
22	140.8	18.1	2189	2	US-07-971-767-11	Sequence 11, Appl
23	140.8	18.1	2189	12	US-08-341-610-7	Sequence 7, Appli
24	134.6	17.3	4310	87	US-60-172-373-2841	Sequence 2841, Ap
25	129.6	16.6	2633	86	US-60-167-245-591	Sequence 591, App
26	129.6	16.6	2633	87	US-60-173-383-17398	Sequence 17398, A
27	129.6	16.6	2633	87	US-60-173-464-13675	Sequence 13675, A
28	125.6	16.1	1555	21	US-08-809-802-11	Sequence 11, Appl
29	124.2	15.9	1253	50	US-09-354-899-7521	Sequence 7521, Ap
30	124	15.9	1985	87	US-60-172-373-2276	Sequence 2276, Ap
31	121.6	15.6	2427	86	US-60-167-216-507	Sequence 507, App
32	121.6	15.6	1723	87	US-60-173-383-19912	Sequence 19912, A
33	121.6	15.6	1723	87	US-60-173-464-15676	Sequence 15676, A
34	110.6	14.2	1834	54	US-09-471-275-2141	Sequence 2141, Ap
35	104.8	13.4	462	51	US-09-362-510-37625	Sequence 37625, A
36	100.6	12.9	1988	86	US-60-167-943-168	Sequence 168, App
37	96.6	12.4	1640	54	US-09-471-275-2757	Sequence 2757, Ap
38	96.6	12.4	1870	87	US-60-172-373-2198	Sequence 2198, Ap
39	95.4	12.2	1917	38	US-09-083-194A-7	Sequence 7, Appli
40	92.4	11.8	2193	38	US-09-083-194A-1	Sequence 1, Appli
c 41	92.4	11.8	58569	86	US-60-164-769-21735	Sequence 21735, A
42	92.4	11.8	11936	86	US-60-167-245-590	Sequence 590, App
43	92.4	11.8	11936	87	US-60-173-383-17397	Sequence 17397, A
44	92.4	11.8	6211	87	US-60-173-383-35369	Sequence 35369, A
45	92.4	11.8	11936	87	US-60-173-464-13674	Sequence 13674, A

ALIGNMENTS

```
RESULT   1
US-09-030-832-41
; Sequence 41, Application US/09030832
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/030,832
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/888,012
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950001/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3154 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  41..1558
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  41..94
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  95..1558
US-09-030-832-41


  Query Match           100.0%;  Score 780;  DB 35;  Length 3154;
  Best Local Similarity  100.0%;  Pred. No. 6.2e-233;
  Matches  780;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      95 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 154

Qy      61 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     155 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 214

Qy     121 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     215 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 274

Qy     181 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     275 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 334

Qy     241 GTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     335 GTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATT 394

Qy     301 GACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     395 GACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAG 454

Qy     361 TCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     455 TCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGG 514

Qy     421 AATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTAC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     515 AATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTAC 574

Qy     481 AAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCAC 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     575 AAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCAC 634

Qy     541 ATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTAT 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     635 ATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTAT 694

Qy     601 CCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAAC 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     695 CCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAAC 754

Qy     661 TCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACA 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     755 TCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACA 814

Qy     721 ACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     815 ACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 874


RESULT   2
US-60-172-373-15901
; Sequence 15901, Application US/60172373
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
```

```
;  APPLICANT: Lal, Preeti
;  APPLICANT: Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymorp
;  FILE REFERENCE: GX-0006 P
;  CURRENT APPLICATION NUMBER: US/60/172,373
;  CURRENT FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: 25,772
;  SOFTWARE: PERL Program
; SEQ ID NO 15901
;   LENGTH: 3268
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 331742.2
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 3257, 3265
;   OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-15901


  Query Match             99.8%;  Score 778.4;  DB 87;  Length 3268;
  Best Local Similarity   99.9%;  Pred. No. 2e-232;
  Matches  779;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     190 agggtcgagggacctcagactgaatcaaagaatgaagcctcttcccgtgatgttgtctat 249

Qy      61 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     250 ggcccccagccccagcctctggaaaatcagctcctctctgaggaaacaaagtcaactgag 309

Qy     121 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     310 actgagactgggagcagagttggcaaactgccagaagcctctcgcatcctgaacactatc 369

Qy     181 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     370 ctgagtaattatgaccacaaactgcgccctggcattggagagaagcccactgtggtcact 429

Qy     241 GTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATT 300
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     430 gttgagatctccgtcaacagccttggtcctctctctatcctagacatggaatacaccatt 489

Qy     301 GACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     490 gacatcatcttctcccagacctggtacgacgaacgcctctgttacaacgacacctttgag 549

Qy     361 TCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     550 tctcttgttctgaatggcaatgtggtgagccagctatggatcccggacacctttttagg 609

Qy     421 AATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTAC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     610 aattctaagaggacccacgagcatgagatcaccatgcccaaccagatggtccgcatctac 669

Qy     481 AAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     670 aaggatggcaaggtgttgtacacaattaggatgaccattgatgccggatgctcactccac 729

Qy     541 ATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTAT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     730 atgctcagatttccaatggattctcactcttgccctctatctttctctagcttttcctat 789

Qy     601 CCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     790 cctgagaatgagatgatctacaagtgggaaaatttcaagcttgaaatcaatgagaagaac 849

Qy     661 TCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     850 tcctggaagctcttccagtttgattttacaggagtgagcaacaaaactgaaataatcaca 909

Qy     721 ACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     910 accccagttggtgacttcatggtcatgacgattttcttcaatgtgagcaggcggtttggc 969


RESULT   3
US-08-716-396-7
; Sequence 7, Application US/08716396
;  GENERAL INFORMATION:
;    APPLICANT:  Whiting, Paul J.
;    TITLE OF INVENTION:  HUMAN GAMMA 3 GABA-A- RECEPTOR SUBUNIT
;    TITLE OF INVENTION:  AND STABLY CO-TRANSFECTED CELL LINES
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. Mark Hand - Merck & Co., Inc.
;      STREET:  126 E. Lincoln Avenue - P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/716,396
;      FILING DATE:  20-SEP-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hand, J. Mark
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1271
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-3905
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1565 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  33..1436
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1436
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  33..1436
US-08-716-396-7


  Query Match             31.5%;  Score 245.6;  DB 18;  Length 1565;
  Best Local Similarity   61.9%;  Pred. No. 9.5e-66;
  Matches  389;  Conservative    0;  Mismatches  239;  Indels    0;  Gaps    0;

Qy     152 CAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTG 211
           | || |   |||  || || ||||   | || ||  | |||||  | || ||| | || |
Db     166 CCGACGTGACTCTTATTCTCAACAAGTTGCTAAGAGAGTATGATAAAAAGCTGAGGCCAG 225

Qy     212 GCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTC 271
           ||||||   || || || ||  |    ||||| ||    || |||||| ||||||||
Db     226 ATATTGGAATAAAACCGACCGTAATTGACGTTGACATTTATGTTAACAGCATTGGTCCTG 285

Qy     272 TCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACG 331
           | ||     || ||||||||||   ||||||||  | ||  | |||||||||   ||
Db     286 TGTCATCAATAAACATGGAATACCAAATTGACATATTTTTTGCTCAGACCTGGACAGATA 345
```

```
Qy     332 AACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCC 391
           |||||  | | ||||  |||  |  |  ||||  ||||||  ||||  ||||| |
Db     346 GTCGCCTTCGATTCAACAGCACAATGAAAATTCTTACTCTGAACAGCAACATGGTGGGGT 405

Qy     392 AGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCA 451
           | ||||||||| |||||| | ||  | ||||||||  |   |  | |  ||   |||||
Db     406 TAATCTGGATCCCAGACACCATCTTCCGCAATTCTAAAACCGCAGAGGCTCACTGGATCA 465

Qy     452 CCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGA 511
           |||  ||||| ||| |  |||| || |  || || || ||  |  | |||||  | |||
Db     466 CCACACCCAATCAGCTCCTCCGGATTTGGAATGACGGGAAAATCCTTTACACTTTGAGGC 525

Qy     512 TGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTT 571
           | |||||  |||| |  |||   || ||  ||| ||  || || |||||    ||||| |
Db     526 TCACCATCAATGCTGAGTGCCAGCTGCAGCTGCACAACTTCCCCATGGACGAACACTCCT 585

Qy     572 GCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAA 631
           ||||  ||   |||||| |||| |  ||||||  |  | || ||||| || |  |||  ||
Db     586 GCCCGCTGATTTTCTCCAGCTATGGCTATCCCAAAGAAGAAATGATTTATAGATGGAGAA 645

Qy     632 ATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAG 691
           |       | ||      |||  |||| || |||  ||| |  |||||||| || |  |
Db     646 AAAATTCAGTGGAGGCAGCTGACCAGAAATCATGGCGGCTTTATCAGTTTGACTTCATGG 705

Qy     692 GAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGA 751
           |  | || ||||  || |||||  | |||||  | |  |||||  |   | ||||||| |
Db     706 GCCTCAGAAACACCACAGAAATCGTGACAACGTCTGCAGGTGATTATGTTGTCATGACTA 765

Qy     752 TTTTCTTCAATGTGAGCAGGCGGTTTGG 779
           | |  ||  |  |||| ||  |  | ||
Db     766 TATATTTTGAATTGAGTAGAAGAATGGG 793
```

RESULT 4
US-08-888-012-5
; Sequence 5, Application US/08888012
; GENERAL INFORMATION:
; APPLICANT: Hanna, Michael C.
; APPLICANT: Kirkness, Ewen F.
; TITLE OF INVENTION: ET2: An Alternative Transcript of the GABA-A
; TITLE OF INVENTION: Receptor n Subunit
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Avenue, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,012
; FILING DATE: Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0950000/EKS/SGW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9631 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-888-012-5

Query Match 28.9%; Score 225.4; DB 24; Length 9631;
Best Local Similarity 91.9%; Pred. No. 6.1e-59;
Matches 238; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```
Qy     252 CGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTT 311
           | ||  ||    ||  | | ||| |       ||  ||||||||||||||||||||||
Db     264 CATCCCCAAGTATGTGCTTTTCTGTCCTTCCCACCAGGAATACACCATTGACATCATCTT 323

Qy     312 CTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCT 371
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     324 CTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCT 383

Qy     372 GAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAG 431
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     384 GAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAG 443

Qy     432 GACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAA 491
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     444 GACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAA 503

Qy     492 GGTGTTGTACACAATTAGG 510
           |||||||||||||||||||
Db     504 GGTGTTGTACACAATTAGG 522
```

RESULT 5
US-09-030-832-5
; Sequence 5, Application US/09030832
; GENERAL INFORMATION:
; APPLICANT: Hanna, Michael C.
; APPLICANT: Kirkness, Ewen F.
; TITLE OF INVENTION: GABAA Receptor Epsilon Subunit
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,832
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/888,012
; FILING DATE: 03-JUL-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0950001/EKS/SGW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9631 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-030-832-5

Query Match 28.9%; Score 225.4; DB 35; Length 9631;

```
  Best Local Similarity   91.9%;  Pred. No. 6.1e-59;
  Matches  238;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy    252 CGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTT 311
          | ||  ||    ||  | | ||| |        ||  ||||||||||||||||||||||
Db    264 CATCCCCAAGTATGTGCTTTTCTGTCCTTCCCACCAGGAATACACCATTGACATCATCTT 323

Qy    312 CTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCT 371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 CTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCT 383

Qy    372 GAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAG 431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 GAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAG 443

Qy    432 GACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAA 491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 GACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAA 503

Qy    492 GGTGTTGTACACAATTAGG 510
          ||||||||||||||||||
Db    504 GGTGTTGTACACAATTAGG 522


RESULT   6
US-08-888-012-4
; Sequence 4, Application US/08888012
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  ET2: An Alternative Transcript of the GABA-A
;    TITLE OF INVENTION:  Receptor n Subunit
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,012
;      FILING DATE:  Herewith
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950000/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1097 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-888-012-4


  Query Match             28.2%;  Score 220.2;  DB 24;  Length 1097;
  Best Local Similarity   98.7%;  Pred. No. 6.9e-58;
  Matches  222;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 121

Qy     61 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 181

Qy    121 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 241

Qy    181 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAG 225
          |||||||||||||||||||||||||||||||||||||||||||||
Db    242 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGGTGAG 286


RESULT   7
US-09-030-832-4
; Sequence 4, Application US/09030832
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/030,832
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/888,012
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950001/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1097 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-030-832-4


  Query Match             28.2%;  Score 220.2;  DB 35;  Length 1097;
  Best Local Similarity   98.7%;  Pred. No. 6.9e-58;
  Matches  222;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 121

Qy     61 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 181

Qy    121 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    182 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 241

Qy    181 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAG 225
          |||||||||||||||||||||||||||||||||||||||||||   ||
Db    242 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGGTGAG 286


RESULT   8
US-09-354-899-7330
; Sequence 7330, Application US/09354899
; GENERAL INFORMATION:
;  APPLICANT: Glucksmann, M. Alexandra
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
;  TITLE OF INVENTION: HUMAN BRAIN LIBRARY
;  FILE REFERENCE: MLN98-35pA
;  CURRENT APPLICATION NUMBER: US/09/354,899
;  CURRENT FILING DATE: 1999-07-09
;  EARLIER APPLICATION NUMBER: 60/092,406
;  EARLIER FILING DATE: 1998-07-10
;  NUMBER OF SEQ ID NOS: 8631
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7330
;   LENGTH: 2434
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(2434)
;   OTHER INFORMATION: n = A,T,C or G
US-09-354-899-7330


  Query Match             28.2%;  Score 219.6;  DB 50;  Length 2434;
  Best Local Similarity   59.4%;  Pred. No. 1.7e-57;
  Matches  372;  Conservative    0;  Mismatches  254;  Indels    0;  Gaps    0;

Qy    154 GAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGC 213
          || | | ||  |||| | ||||   | |||      |||||| | ||||| || ||||
Db    181 gatgtcactgtcatcttaaacaacctgctggaaggatatgacaataaacttcggcctgat 240

Qy    214 ATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTC 273
          || |||| |||||| ||  |  |       || ||    || || ||| |||||||  |
Db    241 ataggagtgaagccaacgttaattcacacagacatgtatgtgaatagcattggtccagtg 300

Qy    274 TCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAA 333
              | | ||||||||||| ||||| ||  | ||  | || || ||||| |||  |
Db    301 aacgctatcaatatggaatacactattgatatatttttgcgcaaacgtggtatgacaga 360

Qy    334 CGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAG 393
          ||  |    |  |||  |||| || |    ||     ||||  ||||  |||||  |  |
Db    361 cgtttgaaatttaacagcaccattaaagtcctccgattgaacagcaacatggtggggaaa 420

Qy    394 CTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACC 453
          | ||||| || ||||| || || || ||||| || |    |  | |  ||   |||||||
Db    421 atctggattccagacactttcttcagaaattccaaaaaagctgatgcacactggatcacc 480

Qy    454 ATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATG 513
          |  ||||||  |||| |  | || |  || |||||    ||| | |||||  | ||| ||
Db    481 acccccaacaggatgctgagaatttggaatgatggtcgagtgctctacaccctaaggttg 540

Qy    514 ACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGC 573
          || |||||||| |  |||  | | ||  ||| ||  ||||||||||||   ||||| |||
Db    541 acaattgatgctgagtgccaattacaattgcacaactttccaatggatgaacactcctgc 600

Qy    574 CCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAAT 633
          ||  |    ||||| || | |  ||||||      | || ||  | ||  | ||| |
Db    601 cccttggagttctccagttatggctatccacgtgaagaaattgtttatcaatggaagcga 660

Qy    634 TTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGA 693
            |    ||||| |    || | |  ||||||| ||| |  || ||    |||   ||
Db    661 agctctgttgaagtgggcgacacaagatcctggaggctttatcaattctcatttgttggt 720

Qy    694 GTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATT 753
          | || || |  || ||| || | |  ||  |    || || |   |||||||| |  |
Db    721 ctaagaaataccaccgaagtagtgaagacaacttccggagattatgtggtcatgtctgtc 780

Qy    754 TTCTTCAATGTGAGCAGGCGGTTTGG 779
          | |||  || |||||||  |  | ||
Db    781 tactttgatctgagcagaagaatggg 806


RESULT   9
US-09-371-168-7178
; Sequence 7178, Application US/09371168
; GENERAL INFORMATION:
;  APPLICANT: Glucksmann, M. Alexandra
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
;  TITLE OF INVENTION: HUMAN BRAIN LIBRARY
;  FILE REFERENCE: MLN98-37pA
;  CURRENT APPLICATION NUMBER: US/09/371,168
;  CURRENT FILING DATE: 1999-08-10
;  EARLIER APPLICATION NUMBER: 60/095,907
;  EARLIER FILING DATE: 1998-08-10
;  EARLIER APPLICATION NUMBER: 60/103,145
;  EARLIER FILING DATE: 1998-10-05
;  NUMBER OF SEQ ID NOS: 8285
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7178
;   LENGTH: 2434
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(2434)
;   OTHER INFORMATION: n = A,T,C or G
US-09-371-168-7178


  Query Match             28.2%;  Score 219.6;  DB 51;  Length 2434;
  Best Local Similarity   59.4%;  Pred. No. 1.7e-57;
  Matches  372;  Conservative    0;  Mismatches  254;  Indels    0;  Gaps    0;

Qy    154 GAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGC 213
          || | | ||  |||| | ||||   | |||      |||||| | ||||| || ||||
Db    181 gatgtcactgtcatcttaaacaacctgctggaaggatatgacaataaacttcggcctgat 240

Qy    214 ATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTC 273
          || |||| |||||| ||  |  |       || ||    || || ||| |||||||  |
Db    241 ataggagtgaagccaacgttaattcacacagacatgtatgtgaatagcattggtccagtg 300

Qy    274 TCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAA 333
              | | ||||||||||| ||||| ||  | ||  | || || ||||| |||  |
Db    301 aacgctatcaatatggaatacactattgatatatttttgcgcaaacgtggtatgacaga 360

Qy    334 CGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAG 393
          ||  |    |  |||  |||| || |    ||     ||||  ||||  |||||  |  |
Db    361 cgtttgaaatttaacagcaccattaaagtcctccgattgaacagcaacatggtggggaaa 420

Qy    394 CTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACC 453
          | ||||| || ||||| || || || ||||| || |    |  | |  ||   |||||||
Db    421 atctggattccagacactttcttcagaaattccaaaaaagctgatgcacactggatcacc 480

Qy    454 ATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATG 513
          |  ||||||  |||| |  | || |  || |||||    ||| | |||||  | ||| ||
Db    481 acccccaacaggatgctgagaatttggaatgatggtcgagtgctctacaccctaaggttg 540

Qy    514 ACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGC 573
          || |||||||| |  |||  | | ||  ||| ||  ||||||||||||   ||||| |||
Db    541 acaattgatgctgagtgccaattacaattgcacaactttccaatggatgaacactcctgc 600

Qy    574 CCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAAT 633
          ||  |    ||||| || | |  ||||||      | || ||  | ||  | ||| |
Db    601 cccttggagttctccagttatggctatccacgtgaagaaattgtttatcaatggaagcga 660

Qy    634 TTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGA 693
            |    ||||| |    || | |  ||||||| ||| |  || ||    |||   ||
```

```
Db    661 agctctgttgaagtgggcgacacaagatcctggaggctttatcaattctcatttgttggt 720

Qy    694 GTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATT 753
          | || || |  || ||| || | |  ||  |    || || |  |||||||| | |
Db    721 ctaagaaataccaccgaagtagtgaagacaacttccggagattatgtggtcatgtctgtc 780

Qy    754 TTCTTCAATGTGAGCAGGCGGTTTGG 779
          | |||  || |||||||  |  | ||
Db    781 tactttgatctgagcagaagaatggg 806


RESULT 10
US-09-471-275-1928
; Sequence 1928, Application US/09471275
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: Novel Contigs Obtained
;  TITLE OF INVENTION: From Various Libraries
;  FILE REFERENCE: 782
;  CURRENT APPLICATION NUMBER: US/09/471,275
;  CURRENT FILING DATE: 1999-12-23
;  EARLIER APPLICATION NUMBER: US 09/235,076
;  EARLIER FILING DATE: 1999-01-20
;  EARLIER APPLICATION NUMBER: US 09/234,611
;  EARLIER FILING DATE: 1999-01-22
;  EARLIER APPLICATION NUMBER: US 09/240,371
;  EARLIER FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: US 09/277,227
;  EARLIER FILING DATE: 1999-03-25
;  EARLIER APPLICATION NUMBER: US 09/271,490
;  EARLIER FILING DATE: 1999-03-18
;  EARLIER APPLICATION NUMBER: US 09/293,972
;  EARLIER FILING DATE: 1999-04-15
;  EARLIER APPLICATION NUMBER: US 09/274,861
;  EARLIER FILING DATE: 1999-03-23
;  EARLIER APPLICATION NUMBER: US 60/125,453
;  EARLIER FILING DATE: 1999-03-19
;  EARLIER APPLICATION NUMBER: US 60/126,605
;  EARLIER FILING DATE: 1999-03-26
;  EARLIER APPLICATION NUMBER: US 09/306,350
;  EARLIER FILING DATE: 1999-05-07
;  EARLIER APPLICATION NUMBER: US 09/399,720
;  EARLIER FILING DATE: 1999-09-21
;  EARLIER APPLICATION NUMBER: US 09/404,284
;  EARLIER FILING DATE: 1999-09-21
;  EARLIER APPLICATION NUMBER:
;  EARLIER FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: 10451
;  SOFTWARE: pt_CT_genes Version 1.0
; SEQ ID NO 1928
;  LENGTH: 1980
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (461)...(1866)
;  OTHER INFORMATION: similar to gi5738138 in the genepept database release 114,
;  OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
US-09-471-275-1928


  Query Match             27.9%;  Score 218;  DB 54;  Length 1980;
  Best Local Similarity   59.3%;  Pred. No. 4.8e-57;
  Matches  371;  Conservative    0;  Mismatches  255;  Indels    0;  Gaps    0;

Qy    154 GAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGC 213
          || | | ||  |||| | ||||   | |||      |||||| | ||||| || ||||
Db    653 gatgtcactgtcatcttaaacaacctgctggaaggatatgacaataaacttcggcctgat 712

Qy    214 ATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTC 273
          || |||| |||||| ||  |  |       || ||    || || ||| |||||||  |
Db    713 ataggagtgaagccaacgttaattcacacagacatgtatgtgaatagcattggtccagtg 772

Qy    274 TCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAA 333
            |    |  | ||||||||||| ||||| ||  | ||  | || || ||||| |||  |
Db    773 aatgctatcaatatggaatacactattgatatatttttgcgcaaacgtggtatgacaga 832

Qy    334 CGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAG 393
          ||  |    |  |||  |||| || |    ||     ||||  ||||  ||||| |  |
Db    833 cgtttgaaatttaacagcaccattaaagtcctccgattgaacagcaacatggtggggaaa 892

Qy    394 CTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACC 453
          | ||||| || ||||| || || || ||||| || |   |  | |  ||  |||||||
Db    893 atctggattccagacactttcttcagaaattccaaaaaagctgatgcacactggatcacc 952

Qy    454 ATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATG 513
          |  ||||||  |||| |  | || |  || |||||    ||| | ||| |  | ||| ||
Db    953 acccccaacaggatgctgagaatttggaatgatggtcgagtgctctactccctaaggttg 1012

Qy    514 ACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGC 573
          || |||||||| |  |||  | | ||  ||| ||  |||||||||||||   ||||| |||
Db   1013 acaattgatgctgagtgccaattacaattgcacaattttccaatggatgaacactcctgc 1072

Qy    574 CCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAAT 633
          ||  |    ||||| || | |  ||||||     | || ||  | ||  | ||| |
Db   1073 cccttggagttctccagttatggctatccacgtgaagaaattgtttatcaatggaagcga 1132

Qy    634 TTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGA 693
                |||||  |    || |  |  ||||||| ||| |  || ||    |||   ||
Db   1133 agttctgttgaagtgggcgacacaagatcctggaggctttatcaattctcatttgttggt 1192

Qy    694 GTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATT 753
          | || || |  || ||| || | |  ||  |    || || |  |||||||| | |
Db   1193 ctaagaaataccaccgaagtagtgaagacaacttccggagattatgtggtcatgtctgtc 1252

Qy    754 TTCTTCAATGTGAGCAGGCGGTTTGG 779
          | |||  || |||||||  |  | ||
Db   1253 tactttgatctgagcagaagaatggg 1278


RESULT 11
US-08-809-802-7
; Sequence 7, Application US/08809802
;  GENERAL INFORMATION:
;    APPLICANT:  Le Bourdelles, Beatrice
;    APPLICANT:  Whiting, Paul John
;    TITLE OF INVENTION:  HUMAN ALPHA 4 RECEPTOR SUBUNIT
;    TITLE OF INVENTION:  OF THE GABA-A RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merck & Co., Inc.
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/809,802
;      FILING DATE:  19-JUN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/02323
;      FILING DATE:  29-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Yablonsky, Michael D
;      REGISTRATION NUMBER:  40,407
;      REFERENCE/DOCKET NUMBER:  T1292
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  732-594-4678
;      TELEFAX:  732-594-4720
;      TELEX:
```

```
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1707 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  39...1700
;      OTHER INFORMATION:
US-08-809-802-7

  Query Match             22.8%;  Score 177.8;  DB 21;  Length 1707;
  Best Local Similarity   56.5%;  Pred. No. 1.7e-44;
  Matches  354;  Conservative    0;  Mismatches  267;  Indels    6;  Gaps    1;

Qy    159 CTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGG 218
          | | |||||||||| ||| | | ||   |  ||||||| |||  |||| |||||  |||| 
Db    182 CACCCGCATCCTGGACAGTTTGCTCGATGGTTATGACAACAGGCTGCGTCCTGGATTTGG 241

Qy    219 AGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTAT 278
            |       || |  || |    ||| ||    |||| |||| |||| ||| | |||
Db    242 GGGTCCTGTTACAGAAGTGAAAACTGACATATATGTCACCAGCTTTGGACCTGTTTCTGA 301

Qy    279 CCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCT 338
            | ||  |||||||||| || ||  |  |||||   ||||| |||   ||| || |  |
Db    302 TGTTGAAGTGGAATACACAATGGATGTGTTCTTCAGGCAGACATGGATTGACAAAAGATT 361

Qy    339 CTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATG 398
            ||  ||| | || ||||   | |    ||||  |   |||| |   |  | ||
Db    362 AAAATATGACGGCCCCATTGAAATTTTGAGATTGAACAATATGATGGTAACGAAAGTGTG 421

Qy    399 GATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCC 458
          || ||| || || || || ||||||   ||||   |   |  ||| | || ||    ||
Db    422 GACCCCTGATACTTTCTTCAGGAATGGAAAGAAATCTGTCTCACATAATATGACAGCTCC 481

Qy    459 CAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCAT 518
            ||  || |  |  | ||    |  |||| |   | || |||||||| ||  | |||||
Db    482 AAATAAGCTTTTTAGAATTATGAGAAATGGTACTATTTTATACACAATGAGACTCACCAT 541

Qy    519 TGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCT 578
            ||| |  ||  |  |    || |   ||||| ||||||  |||  | ||||||  |
Db    542 AAGTGCGGAGTGTCCCATGAGATTGGTGGATTTTCCCATGGATGGTCATGCATGCCCTGT 601

Qy    579 ATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA------ 633
            |||   || | | |||||||  ||| ||||||||||||  |  |||  |||
Db    602 GAAATTCGGGAGTTATGCCTATCCAAAGAGTGAGATGATCTATACCTGGACAAAAGGTCC 661

Qy    633 TTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGG 692
            |   ||    |       |  |||| | || |   |  | || | ||||||  |  ||
Db    662 TGAGAAATCAGTTGAAGTTCCGAAGGAGTCTTCCAGCTTAGTTCAATATGATTTGATTGG 721

Qy    693 AGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGAT 752
            | |     || |||||  |||| | |       |||| |  || || |||||| |  |
Db    722 GCAAACCGTATCAAGTGAAACCATCAAATCAATTACGGGTGAATATATTGTTATGACGGT 781

Qy    753 TTTCTTCAATGTGAGCAGGCGGTTTGG 779
          || |||| |  | ||  ||  | | ||
Db    782 TTACTTCCACCTCAGACGGAAGATGGG 808


RESULT  12
US-09-016-434-1470
; Sequence 1470, Application US/09016434
;  GENERAL INFORMATION:
;    APPLICANT:  Janice Au-Young
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;    TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;    NUMBER OF SEQUENCES:  1490
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1470:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g905392
US-09-016-434-1470

  Query Match             22.8%;  Score 177.8;  DB 34;  Length 1679;
  Best Local Similarity   56.5%;  Pred. No. 1.7e-44;
  Matches  354;  Conservative    0;  Mismatches  267;  Indels    6;  Gaps    1;

Qy    159 CTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGG 218
          | | |||||||||| ||| | | ||   |  ||||||| |||  |||| |||||  |||| 
Db    158 CACCCGCATCCTGGACAGTTTGCTCGATGGTTATGACAACAGGCTGCGTCCTGGATTTGG 217

Qy    219 AGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTAT 278
            |       || |  || |    ||| ||    |||| |||| |||| ||| | |||
Db    218 GGGTCCTGTTACAGAAGTGAAAACTGACATATATGTCACCAGCTTTGGACCTGTTTCTGA 277

Qy    279 CCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCT 338
            | ||  |||||||||| || ||  |  |||||   ||||| |||   ||| || |  |
Db    278 TGTTGAAATGGAATACACAATGGATGTGTTCTTCAGGCAGACATGGATTGACAAAAGATT 337

Qy    339 CTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATG 398
            ||  ||| | || ||||   | |    ||||  |   |||| |   |  | ||
Db    338 AAAATATGACGGCCCCATTGAAATTTTGAGATTGAACAATATGATGGTAACGAAAGTGTG 397

Qy    399 GATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCC 458
          || ||| || || || || ||||||   ||||   |   |  ||| | || ||    ||
Db    398 GACCCCTGATACTTTCTTCAGGAATGGAAAGAAATCTGTCTCACATAATATGACAGCTCC 457

Qy    459 CAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCAT 518
            ||  || |  |  | ||    |  |||| |   | || |||||||| ||  | |||||
Db    458 AAATAAGCTTTTTAGAATTATGAGAAATGGTACTATTTTATACACAATGAGACTCACCAT 517

Qy    519 TGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCT 578
            ||| |  ||  |  |    || |   ||||| ||||||  |||  | ||||||  |
Db    518 AAGTGCGGAGTGTCCCATGAGATTGGTGGATTTTCCCATGGATGGTCATGCATGCCCTTT 577

Qy    579 ATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA------ 633
            |||   || | | |||||||  ||| ||||||||||||  |  |||  |||
Db    578 GAAATTCGGGAGTTATGCCTATCCAAAGAGTGAGATGATCTATACCTGGACAAAAGGTCC 637
```

```
Qy    633 TTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGG 692
Db    638 TGAGAAATCAGTTGAAGTTCCGAAGGAGTCTTCCAGCTTAGTTCAATATGATTTGATTGG 697

Qy    693 AGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGAT 752
Db    698 GCAAACCGTATCAAGTGAAACCATCAAATCAATTACGGGCGAATATATTGTTATGACGGT 757

Qy    753 TTTCTTCAATGTGAGCAGGCGGTTTGG 779
Db    758 TTACTTCCACCTCAGACGGAAGATGGG 784


RESULT 13
US-07-971-767-15
; Sequence 15, Application US/07971767
;  GENERAL INFORMATION:
;    APPLICANT:  Hadingham, Karen L.
;    APPLICANT:  Le Bourdelles, Beatrice
;    APPLICANT:  Whiting, Paul J.
;    APPLICANT:  Wingrove, Peter B.
;    TITLE OF INVENTION:  GABA-A RECEPTOR SUBUNITS (ALPHA-2,
;    TITLE OF INVENTION:  ALPHA-3, ALPHA-5, ALPHA-6, BETA-2) AND TRANSFECTED CELLS
;    TITLE OF INVENTION:  EXPRESSING THEM
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robert J. North
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,767
;      FILING DATE:  19930202
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  North, Robert J.
;      REGISTRATION NUMBER:  27,366
;      REFERENCE/DOCKET NUMBER:  T-1109
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908 594-7262
;      TELEFAX:  908 594-4720
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2310 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-971-767-15


  Query Match             21.1%;  Score 164.8;  DB 2;  Length 2310;
  Best Local Similarity   53.8%;  Pred. No. 2.4e-40;
  Matches  365;  Conservative    0;  Mismatches  307;  Indels    6;  Gaps    1;

Qy    109 AAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATC 168
Db    394 ATGCCAACCAGTTCAGTGAAAGATGAGACCAATGACAACATCACGATATTTACCAGGATC 453

Qy    169 CTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCC 228
Db    454 TTGGATGGGCTCTTGGATGGCTACGACAACAGACTTCGGCCCGGGCTGGGAGAGCGCATC 513

Qy    229 ACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATG 288
Db    514 ACTCAGGTGAGGACCGACATCTACGTCACCAGCTTCGGCCCGGTGTCCGACACGGAAATG 573

Qy    289 GAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAAC 348
Db    574 GAGTACACCATAGACGTGTTTTTCCGACAAAGCTGGAAAGATGAAAGGCTTCGGTTTAAG 633

Qy    349 GACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGAC 408
Db    634 GGGCCCATGCAGCGCCTCCCTCTCAACAACCTCCTTGCCAGCAAGATCTGGACCCCAGAC 693

Qy    409 ACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATG 468
Db    694 ACGTTCTTCCACAACGGGAAGAAGTCCATCGCTCACAACATGACCACGCCCAACAAGCTG 753

Qy    469 GTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGA 528
Db    754 CTGCGGCTGGAGGACGACGGCACCCTGCTCTACACCATGCGCTTGACCATCTCTGCAGAG 813

Qy    529 TGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCT 588
Db    814 TGCCCCATGCAGCTTGAGGACTTCCCGATGGATGCGCACGCTTGCCCTCTGAAATTTGGC 873

Qy    589 AGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA------TTTCAAGCTT 642
Db    874 AGCTATGCGTACCCTAATTCTGAAGTCGTTTACGTCTGGACCAACGGCTCCACCAAGTCG 933

Qy    643 GAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAAC 702
Db    934 GTGGTGGTGGCGGAAGATGGCTCCAGACTGAACCAGTACCACCTGATGGGGCAGACGGTG 993

Qy    703 AAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAAT 762
Db    994 GGCACTGAGAACATCAGCACCAGCACAGGCGAATACACAATCATGACAGCTCACTTCCAC 1053

Qy    763 GTGAGCAGGCGGTTTGGC 780
Db   1054 CTGAAAAGGAAGATTGGC 1071


RESULT 14
US-08-341-610-1
; Sequence 1, Application US/08341610
;  GENERAL INFORMATION:
;    APPLICANT:  Karen Hadingham
;    APPLICANT:  Paul John Whiting
;    TITLE OF INVENTION:  Stably transfected cell lines expressing GABA-A receptors
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jack L. Tribble
;      STREET:  126 E. Lincoln Avenue, P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/341,610
;      FILING DATE:  17-NOV-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tribble, Jack L.
;      REGISTRATION NUMBER:  32,633
;      REFERENCE/DOCKET NUMBER:  T-1220Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)594-5321
;      TELEFAX:  (908)594-4720
;  INFORMATION FOR SEQ ID NO:  1:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2310 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  298..1683
US-08-341-610-1


  Query Match             21.1%;  Score 164.8;  DB 12;  Length 2310;
  Best Local Similarity   53.8%;  Pred. No. 2.4e-40;
  Matches  365;  Conservative    0;  Mismatches  307;  Indels    6;  Gaps    1;

Qy    109 AAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATC 168
Db    394 ATGCCAACCAGTTCAGTGAAAGATGAGACCAATGACAACATCACGATATTTACCAGGATC 453

Qy    169 CTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCC 228
Db    454 TTGGATGGGCTCTTGGATGGCTACGACAACAGACTTCGGCCCGGGCTGGGAGAGCGCATC 513

Qy    229 ACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATG 288
Db    514 ACTCAGGTGAGGACCGACATCTACGTCACCAGCTTCGGCCCGGTGTCCGACACGGAAATG 573

Qy    289 GAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAAC 348
Db    574 GAGTACACCATAGACGTGTTTTTCCGACAAAGCTGGAAAGATGAAAGGCTTCGGTTTAAG 633

Qy    349 GACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGAC 408
Db    634 GGGCCCATGCAGCGCCTCCCTCTCAACAACCTCCTTGCCAGCAAGATCTGGACCCCAGAC 693

Qy    409 ACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATG 468
Db    694 ACGTTCTTCCACAACGGGAAGAAGTCCATCGCTCACAACATGACCACGCCCAACAAGCTG 753

Qy    469 GTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGA 528
Db    754 CTGCGGCTGGAGGACGACGGCACCCTGCTCTACACCATGCGCTTGACCATCTCTGCAGAG 813

Qy    529 TGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCT 588
Db    814 TGCCCCATGCAGCTTGAGGACTTCCCGATGGATGCGCACGCTTGCCCTCTGAAATTTGGC 873

Qy    589 AGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA------TTTCAAGCTT 642
Db    874 AGCTATGCGTACCCTAATTCTGAAGTCGTTTACGTCTGGACCAACGGCTCCACCAAGTCG 933

Qy    643 GAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAAC 702
Db    934 GTGGTGGTGGCGGAAGATGGCTCCAGACTGAACCAGTACCACCTGATGGGGCAGACGGTG 993

Qy    703 AAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAAT 762
Db    994 GGCACTGAGAACATCAGCACCAGCACAGGCGAATACACAATCATGACAGCTCACTTCCAC 1053

Qy    763 GTGAGCAGGCGGTTTGGC 780
Db   1054 CTGAAAAGGAAGATTGGC 1071


RESULT  15
US-60-172-373-2255
; Sequence 2255, Application US/60172373
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT: Lal, Preeti
;  APPLICANT: Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polym
;  FILE REFERENCE: GX-0006 P
;  CURRENT APPLICATION NUMBER: US/60/172,373
;  CURRENT FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: 25,772
;  SOFTWARE: PERL Program
; SEQ ID NO 2255
;   LENGTH: 1893
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 481863.1
US-60-172-373-2255


  Query Match             20.6%;  Score 160.8;  DB 87;  Length 1893;
  Best Local Similarity   54.6%;  Pred. No. 3.9e-39;
  Matches  346;  Conservative    0;  Mismatches  282;  Indels    6;  Gaps    1;

Qy    153 AGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGG 212
Db    250 aaacgtcagtcggatcctggacaacttgcttgaaggctatgacaatcggctgcggccggg 309

Qy    213 CATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCT 272
Db    310 atttggaggtgctgtcactgaagtcaaaacagacatttatgtgaccagttttgggcccgt 369

Qy    273 CTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGA 332
Db    370 gtcagatgtggagatggagtatacgatggatgttttttccgccagacctggactgatga 429

Qy    333 ACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCA 392
Db    430 gaggttgaagtttgggggccaactgagattctgagtctgaataatttgatggtcagtaa 489

Qy    393 GCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCAC 452
Db    490 aatctggacgcctgacacctttttcagaaatggtaaaaagtccattgctcacaacatgac 549

Qy    453 CATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGAT 512
Db    550 aactcctaataaactcttcagaataatgcagaatggaaccattttatacaccatgaggct 609

Qy    513 GACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTG 572
Db    610 taccatcaatgctgactgtcccatgaggctggttaactttcctatggatgggcatgcttg 669

Qy    573 CCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA 632
Db    670 tccactcaagtttgggagctatgcttatcccaaaagtgaaatcatatatacgtggaaaaa 729

Qy    633 TTTCAAGCTTGAAATCAATGA------GAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 686
Db    730 aggaccactttactcagtagaagtcccagaagaatcttcaagccttctccagtatgatct 789

Qy    687 TACAGGAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCAT 746
Db    790 gattggacaaacagtatctagtgagacaattaaatctaacacaggtgaatacgttataat 849

Qy    747 GACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 780
Db    850 gacagtttacttccacttgcaaaggaagatgggc 883


Search completed: March 10, 2000, 09:00:30
Job time: 9108 sec
```

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2000, 01:34:52 ; Search time 4946.18 Seconds
(without alignments)
-478.830 Million cell updates/sec

Title: US-09-030-832-41_COPY_95_874
Perfect score: 780
Sequence: 1 AGGGTCGAGGGACCTCAGAC.....ATGTGAGCAGGCGGTTTGGC 780

Scoring table: IDENTITY_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl:*

Word size : 0

Number of hits that pass the threshold : 1642386

1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pr1:*
10: gb_pr2:*
11: gb_pr3:*
12: gb_ro:*
13: gb_sts:*
14: gb_sy:*
15: gb_un:*
16: gb_vi:*
17: em_fun:*
18: em_hum1:*
19: em_hum2:*
20: em_in:*
21: em_om:*
22: em_or:*
23: em_ov:*
24: em_pat:*
25: em_ph:*
26: em_pl:*
27: em_ro:*
28: em_sts:*
29: em_sy:*
30: em_un:*
31: em_vi:*
32: gb_htg1:*
33: gb_htg2:*
34: gb_in1:*
35: gb_in2:*
36: em_ba1:*
37: em_ba2:*
38: em_hum3:*
39: em_hum4:*
40: gb_pr4:*
41: gb_htg3:*
42: gb_htg4:*
43: gb_htg5:*
44: gb_htg6:*
45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	780	100.0	3154	10	HSU66661	U66661 Human GABA-
2	778.4	99.8	3150	10	HSY09765	Y09765 Homo sapien
3	764	97.9	3153	9	HSGABACHL	Y07637 H.sapiens m
4	301	38.6	10897	10	HSY09764	Y09764 Homo sapien
5	290.8	37.3	1572	4	GGGABAA	X73533 G.domesticu
6	285.8	36.6	714	11	HUMZD71B07	AF086385 Homo sapi
c 7	269.2	34.5	596	13	G60680	G60680 SHGC-57595
8	255.2	32.7	1598	12	MMGSGABA	X59300 Mouse mRNA
9	252	32.3	1930	12	RNGABAG3	X63324 R.norvegicu
10	250.4	32.1	1654	12	RATGABAA	M81142 Rat GABA-A
11	245.6	31.5	1565	5	A46959	A46959 Sequence 7
12	245.6	31.5	1536	10	S82769	S82769 GABAA recep
13	238.2	30.5	2206	4	GDGABAAR	X54944 Chicken mRN
14	238.2	30.5	2231	12	MUSGABAAG2	M62374 Mus musculu
15	237	30.4	2036	12	MUSGABAAR	M86572 Mouse gamma
16	231.2	29.6	1739	12	RNGABA	X57514 R.norvegicu
17	230.8	29.6	1838	12	RATGABAAI	L08497 Rattus ratt
18	227	29.1	1428	3	BOVGABAARG	M55563 Bovine gamm
19	225.4	28.9	9631	11	HSGABRE3	U92283 Human GABA-
c 20	225.4	28.9	158898	11	U82696	U82696 Homo sapien
21	221.6	28.4	1995	12	MMGABAG1	X55272 Mouse mRNA
22	220.2	28.2	1097	11	HSGABRE2	U92282 Human GABA-
23	219.6	28.2	1336	4	GLGABABRA	Z25467 Gallus dome
24	214.8	27.5	1745	9	HSGABAAS	X15376 Human mRNA
25	182.2	23.4	1345	4	CAGABANTS	X94342 C.auratus m
26	177.8	22.8	1707	5	A50024	A50024 Sequence 7
27	177.8	22.8	1679	10	HSU30461	U30461 Human GABAA
28	173.6	22.3	1843	12	RATGABAAE	L08493 Rattus ratt
29	173.6	22.3	1843	12	S55933	S55933 GABAA recep
30	166.4	21.3	346	12	AF090376	AF090376 Mus muscu
31	164.8	21.1	2310	5	A28104	A28104 Human GABAa
32	164.8	21.1	2310	5	A39276	A39276 Sequence 1
33	164.8	21.1	2310	5	I88879	I88879 Sequence 15
34	164.8	21.1	2318	9	HUMGABRA5Y	L08485 Human GABA-
35	164.6	21.1	1908	3	BTGABAA	X61456 Bovine GABA
36	161.8	20.7	1439	4	GGGABAA6S	X94343 G.gallus mR
37	160.8	20.6	2111	12	RATGABAAG	L08495 Rattus ratt
38	160.8	20.6	1805	12	RNGABAA6A	X55742 R.norvegicu
39	159.2	20.4	1408	5	A28106	A28106 Human GABAa
40	159.2	20.4	1408	5	A39278	A39278 Sequence 3
41	159.2	20.4	1732	5	I88880	I88880 Sequence 17
42	159.2	20.4	1732	10	S81944	S81944 gamma-amino
43	157.8	20.2	7479	12	RNU92284	U92284 Rattus norv
44	152	19.5	2591	12	RNGABAA5	X51992 R.norvegicu
45	150.4	19.3	1874	12	RATGABAAF	L08494 Rattus ratt

ALIGNMENTS

RESULT 1
HSU66661
LOCUS HSU66661 3154 bp mRNA PRI 11-MAR-1997
DEFINITION Human GABA-A receptor epsilon subunit mRNA, complete cds.
ACCESSION U66661
VERSION U66661.1 GI:1857125
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3154)

```
  AUTHORS   Davies,P.A., Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Insensitivity to anaesthetic agents conferred by a class of GABA(A)
            receptor subunit
  JOURNAL   Nature 385 (6619), 820-823 (1997)
  MEDLINE   97192095
REFERENCE   2  (bases 1 to 3154)
  AUTHORS   Davies,P.A., Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-1996) Department of Cellular and Molecular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .3154
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             41. .1561
                     /codon_start=1
                     /product="GABA-A receptor epsilon subunit"
                     /protein_id="AAB49284.1"
                     /db_xref="GI:1857126"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIA
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRR
                     FGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV
                     SYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRA
                     RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWC
                     KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
BASE COUNT      725 a    886 c    686 g    857 t
ORIGIN
```

```
  Query Match           100.0%;  Score 780;  DB 10;  Length 3154;
  Best Local Similarity  100.0%;  Pred. No. 5.4e-214;
  Matches  780;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      95 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 154

Qy      61 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     155 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 214

Qy     121 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     215 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 274

Qy     181 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     275 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 334

Qy     241 GTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     335 GTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATT 394

Qy     301 GACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     395 GACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAG 454

Qy     361 TCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     455 TCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGG 514

Qy     421 AATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTAC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     515 AATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTAC 574

Qy     481 AAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     575 AAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCAC 634

Qy     541 ATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTAT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     635 ATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTAT 694

Qy     601 CCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     695 CCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAAC 754

Qy     661 TCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     755 TCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACA 814

Qy     721 ACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     815 ACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 874
```

```
RESULT   2
HSY09765
LOCUS       HSY09765     3150 bp    mRNA            PRI       31-OCT-1997
DEFINITION  Homo sapiens mRNA for putative GABA receptor epsilon subunit.
ACCESSION   Y09765
VERSION     Y09765.1  GI:2285960
KEYWORDS    GABA receptor; GABRE gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3150)
  AUTHORS   Wilke,K., Gaul,R., Klauck,S.M. and Poustka,A.
  TITLE     A gene in human chromosome band Xq28 (GABRE) defines a putative new
            subunit class of the GABAA neurotransmitter receptor
  JOURNAL   Genomics 45 (1), 1-10 (1997)
  MEDLINE   97480709
REFERENCE   2  (bases 1 to 3150)
  AUTHORS   Wilke,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1996) K. Wilke, Deutsches Krebsforschungszentrum,
            Abteilung Molekulare Genomanalyse (840), Im Neuenheimer Feld 280,
            D-69120 Heidelberg, FRG
FEATURES             Location/Qualifiers
     source          1. .3150
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /map="q28"
     CDS             55. .1575
                     /note="putative"
                     /codon_start=1
                     /product="GABA receptor epsilon subunit"
                     /protein_id="CAA70904.1"
                     /db_xref="GI:2285961"
                     /db_xref="SPTREMBL:O15346"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIS
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRR
                     FGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV
                     SYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRA
                     RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWC
                     KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
BASE COUNT      712 a    889 c    690 g    859 t
ORIGIN
```

```
  Query Match           99.8%;  Score 778.4;  DB 10;  Length 3150;
  Best Local Similarity  99.9%;  Pred. No. 1.6e-213;
  Matches  779;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 60
```

```
Db    109 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 168

Qy     61 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 120

Db    169 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 228

Qy    121 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 180

Db    229 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 288

Qy    181 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 240

Db    289 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 348

Qy    241 GTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATT 300

Db    349 GTTGAGATCTCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATT 408

Qy    301 GACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAG 360

Db    409 GACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAG 468

Qy    361 TCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGG 420

Db    469 TCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGG 528

Qy    421 AATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTAC 480

Db    529 AATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTAC 588

Qy    481 AAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCAC 540

Db    589 AAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCAC 648

Qy    541 ATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTAT 600

Db    649 ATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTAT 708

Qy    601 CCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAAC 660

Db    709 CCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAAC 768

Qy    661 TCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACA 720

Db    769 TCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACA 828

Qy    721 ACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 780

Db    829 ACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 888
```

```
RESULT   3
HSGABACHL
LOCUS       HSGABACHL    3153 bp    mRNA            PRI       03-MAR-1997
DEFINITION  H.sapiens mRNA for putative GABA-gated chloride channel.
ACCESSION   Y07637
VERSION     Y07637.1  GI:1747370
KEYWORDS    GABA-gated chloride channel.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3153)
  AUTHORS   Garret,M., Bascles,L., Boue-Grabot,E., Sartor,P., Charron,G.,
            Bloch,B. and Margolskee,R.F.
  TITLE     An mRNA encoding a putative GABA-gated chloride channel is
            expressed in the human cardiac conduction system
  JOURNAL   J. Neurochem. 68 (4), 1382-1389 (1997)
  MEDLINE   97238072
REFERENCE   2  (bases 1 to 3153)
  AUTHORS   Garret,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-AUG-1996) M. Garret, CNRS UMR5543, Laboratoire de
            Neurophysiologie, Universite de Bordeaux2, 146 rue Leo Saignat,
            33076 Bordeaux Cedex, FRANCE
FEATURES             Location/Qualifiers
     source          1. .3153
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             51. .1568
                     /function="expressed in cardiac conduction system"
                     /codon_start=1
                     /product="putative GABA-gated chloride channel"
                     /protein_id="CAA68914.1"
                     /db_xref="GI:1747371"
                     /db_xref="SPTREMBL:Q99520"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIA
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPGDFMVMTIFFNVSRRF
                     GYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVS
                     YITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRAR
                     SRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCK
                     RFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
     polyA_signal    3118. .3123
BASE COUNT      726 a    885 c    687 g    855 t
ORIGIN
```

```
  Query Match             97.9%;  Score 764;  DB 9;  Length 3153;
  Best Local Similarity   99.6%;  Pred. No. 2.2e-209;
  Matches  777;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    1;

Qy      1 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 60

Db    105 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 164

Qy     61 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 120

Db    165 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 224

Qy    121 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 180

Db    225 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 284

Qy    181 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 240

Db    285 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 344

Qy    241 GTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATT 300

Db    345 GTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATT 404

Qy    301 GACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAG 360

Db    405 GACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAG 464

Qy    361 TCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGG 420

Db    465 TCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGG 524

Qy    421 AATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTAC 480

Db    525 AATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTAC 584

Qy    481 AAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCAC 540

Db    585 AAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCAC 644

Qy    541 ATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTAT 600

Db    645 ATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTAT 704

Qy    601 CCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAAC 660
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705 CCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAAC 764

Qy    661 TCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    765 TCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACA 824

Qy    721 ACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 780
          ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    825 ACCCCA---GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 881


RESULT   4
HSY09764
LOCUS       HSY09764    10897 bp    DNA             PRI       31-OCT-1997
DEFINITION  Homo sapiens GABRE gene, exon 2-8.
ACCESSION   Y09764
VERSION     Y09764.1  GI:2285959
KEYWORDS    GABA receptor; GABRE gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10897)
  AUTHORS   Wilke,K.; Gaul,R., Klauck,S.M. and Poustka,A.
  TITLE     A gene in human chromosome band Xq28 (GABRE) defines a putative new
            subunit class of the GABAA neurotransmitter receptor
  JOURNAL   Genomics 45 (1), 1-10 (1997)
  MEDLINE   97480709
REFERENCE   2  (bases 1 to 10897)
  AUTHORS   Wilke,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1996) K. Wilke, Deutsches Krebsforschungszentrum,
            Abteilung Molekulare Genomanalyse (840), Im Neuenheimer Feld 280,
            D-69120 Heidelberg, FRG
FEATURES             Location/Qualifiers
     source          1. .10897
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="q28"
                     /clone="cosmid Qc11C8"
     gene            1334. .10897
                     /gene="GABRE"
     exon            1334. .1551
                     /gene="GABRE"
                     /number=2
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            2000. .2288
                     /gene="GABRE"
                     /number=3
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            3346. .3428
                     /gene="GABRE"
                     /number=4
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            4736. .4873
                     /gene="GABRE"
                     /number=5
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            8163. .8315
                     /gene="GABRE"
                     /number=6
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            8456. .8655
                     /gene="GABRE"
                     /number=7
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            8939. .10897
                     /gene="GABRE"
                     /number=8
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
BASE COUNT     2630 a    2703 c    2465 g    3099 t
ORIGIN


  Query Match             38.6%;  Score 301;  DB 10;  Length 10897;
  Best Local Similarity   98.4%;  Pred. No. 5.1e-76;
  Matches  304;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy     202 CTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGC 261
           | || ||||| |||| ||||||||||||||||||||||||||||||||| ||||||||||
Db    1981 CCGCCCCCTGCCATTAGAGAGAAGCCCACTGTGGTCACTGTTGAGATCTCCGTCAACAGC 2040

Qy     262 CTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACC 321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 CTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACC 2100

Qy     322 TGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAAT 381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 TGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAAT 2160

Qy     382 GTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAG 441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 GTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAG 2220

Qy     442 CATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTAC 501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221 CATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTAC 2280

Qy     502 ACAATTAGG 510
           |||||||||
Db    2281 ACAATTAGG 2289


RESULT   5
GGGABAA
LOCUS       GGGABAA      1572 bp    mRNA            VRT       26-SEP-1994
DEFINITION  G.domesticus mRNA for GABA-A receptor gamma-4 subunit.
ACCESSION   X73533
VERSION     X73533.1  GI:414021
KEYWORDS    GABA-A receptor; GABA-A receptor gamma-4 subunit; glycoprotein;
            ligand gated ion channel; membrane spanning; multigene family;
            neurotransmitter receptor.
SOURCE      chicken.
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
            Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1572)
  AUTHORS   Harvey,R.J., Kim,H.C. and Darlison,M.G.
  TITLE     Molecular cloning reveals the existence of a fourth gamma subunit
            of the vertebrate brain GABAA receptor
  JOURNAL   FEBS Lett. 331 (3), 211-216 (1993)
  MEDLINE   93387470
REFERENCE   2  (bases 1 to 1572)
  AUTHORS   Darlison,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUN-1993) M. Darlison, Inst. fuer Zellbiochemie und
            Klinische Neurobiologie, Universitaet-Krankenhaus Eppendorf, Univ.
            Hamburg, 2000 Hamburg 20, FRG
FEATURES             Location/Qualifiers
     source          1. .1572
                     /organism="Gallus gallus"
                     /strain="Commercial Rhode Island cross"
                     /db_xref="taxon:9031"
                     /dev_stage="embryonic"
                     /tissue_type="whole brain"
                     /clone_lib="lambda gt10 cDNA library"
                     /clone="pcGR lambda4.1"
```

```
     CDS             88. .1461
                     /note="gamma-4 subunit"
                     /codon_start=1
                     /product="GABA-A receptor"
                     /protein_id="CAA51939.1"
                     /db_xref="GI:414022"
                     /db_xref="SWISS-PROT:P34904"
                     /translation="MPAMVLLLCLALGPALRSARCESTEEYDYDYLSINKTWVLTPKA
                     QETDATQILNSLLKNYDNKLRPDIGIKPTFIDVDIYVNSIGPVSVIQMEYTIDIFFAQ
                     TWYDRRLRFNSTLKALTLNTNMVSRIWIPDTFFRNSKRADSHWITTPNQLLRIWNDGK
                     VLYTLRLTIEAECLLQLQNFPMDTHSCPLVFSSYGYPREEIVYRWRRYSIEVSDQRTW
                     RLYQFDFTGLRNTSEVLRTGAGEYMVMTVSFDLSRRMGYFAIQTYIPCILTVVLSWVS
                     FWIKRDSTPARTSLGITTVLTMTTLSTISRKHLPRVSYITAMDLFVSVCFIFVFAALM
                     EYATLNYLVGNKKPLEHSSRKARLPPAGAQVMPSFTAININININMHWPPEIEEDEDD
                     DPGSPCLEGKECERFFCCIEDCQTGMWREGRVRIHISRLDSYSRVFFPTAFLLFNIVY
                     WIAYLYL"
     sig_peptide     88. .150
     mat_peptide     151. .1458
                     /product="GABA A receptor"
     misc_feature    151. .858
                     /note="large extracellular domain; putative"
     misc_feature    190. .198
                     /note="N-linked glycosylation site; putative"
     misc_feature    421. .429
                     /note="N-linked glycosylation site; putative"
     misc_feature    604. .648
                     /note="dicysteine loop; putative"
     misc_feature    775. .783
                     /note="N-linked glycosylation site; putative"
     misc_feature    859. .924
                     /note="membrane spanning domain; putative"
     misc_feature    937. .1002
                     /note="membrane spanning domain; putative"
     misc_feature    1036. .1104
                     /note="membrane spanning domain; putative"
     misc_feature    1105. .1386
                     /note="large intracellular loop; putative"
     misc_feature    1135. .1146
                     /note="casein kinase I phosphorylation site; putative"
     misc_feature    1141. .1149
                     /note="protein C kinase phosphorylation site; putative"
     misc_feature    1144. .1152
                     /note="protein C kinase phosphorylation site; putative"
     misc_feature    1375. .1386
                     /note="multifunctional calmodulin-dependent protein kinase
                     II phosphorylation site; putative"
     misc_feature    1387. .1458
                     /note="membrane spanning domain; putative"
BASE COUNT      356 a    443 c    385 g    388 t
ORIGIN


  Query Match             37.3%;  Score 290.8;  DB 4;  Length 1572;
  Best Local Similarity   66.3%;  Pred. No. 3.6e-73;
  Matches  418;  Conservative    0;  Mismatches  212;  Indels    0;  Gaps    0;

Qy    150 GCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCC 209
          | | || ||| | |  ||||| ||| |  | ||||  || || ||| |||||||| | ||
Db    225 GACGGATGCCACGCAGATCCTCAACTCGCTACTGAAGAACTACGACAACAAACTGAGGCC 284

Qy    210 TGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCC 269
          || |||||    |||||||| |  ||  ||| || |||  ||| ||||| |||| ||
Db    285 TGACATTGGCATCAAGCCCACGTTTATCGATGTGGATATCTACGTGAACAGCATTGGGCC 344

Qy    270 TCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGA 329
            | ||| || |  | ||||| |||||||||||| ||| ||||  | ||||| ||||||||
Db    345 CGTGTCTGTCATCCAAATGGAGTACACCATTGATATCTTCTTTGCTCAGACATGGTACGA 404

Qy    330 CGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAG 389
          |   || ||  ||| |||| ||||||  || | ||    |||||    ||| |||||||
Db    405 CCGGCGTCTTCGTTTCAACAGCACCTTGAAGGCCCTCACACTGAACACTAATATGGTGAG 464

Qy    390 CCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGAT 449
          ||   | |||||||| || |||||||||||||| || |||||| |  |    ||   |||
Db    465 CCGCATCTGGATCCCAGATACCTTTTTTAGGAACTCCAAGAGGGCTGATTCCCACTGGAT 524

Qy    450 CACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAG 509
           ||||  || || ||| |  ||||||| |  || ||||| || ||| | |||||| | ||
Db    525 AACCACTCCAAATCAGCTCCTCCGCATTTGGAATGATGGAAAAGTGCTCTACACACTCAG 584

Qy    510 GATGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTC 569
          | |||| || || || | |||    |||||  |||  |  || ||||||||  |||||||
Db    585 GCTGACGATCGAGGCTGAATGTCTGCTCCAGCTGCAGAATTTCCCAATGGACACTCACTC 644

Qy    570 TTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGA 629
          ||||||  |   ||| ||||| | |  ||| ||     | |||||  ||||    |||
Db    645 CTGCCCTTTGGTTTTTTCTAGTTATGGCTACCCACGTGAGGAGATTGTCTATCGATGGAG 704

Qy    630 AAATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTAC 689
          |  |      ||||  ||  |||  ||  | ||||||  ||| | |||  |||||  || ||
Db    705 ACGCTATTCCATTGAGGTCTCTGACCAGCGCACCTGGAGGCTTTACCAATTTGACTTCAC 764

Qy    690 AGGAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGAC 749
           ||  |||| ||||   | ||| |  |||  ||   ||  || || | ||||| |||||
Db    765 GGGGCTGAGGAACACCTCGGAAGTCCTCAGGACTGGAGCAGGGGAGTACATGGTGATGAC 824

Qy    750 GATTTTCTTCAATGTGAGCAGGCGGTTTGG 779
          | ||| |||  |  | || || ||  | ||
Db    825 GGTTTCCTTTGACTTAAGTAGACGTATGGG 854


RESULT   6
HUMZD71B07
LOCUS       HUMZD71B07    714 bp    mRNA            PRI       29-AUG-1998
DEFINITION  Homo sapiens full length insert cDNA clone ZD71B07.
ACCESSION   AF086385
VERSION     AF086385.1  GI:3483730
KEYWORDS    FLI_CDNA.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 714)
  AUTHORS   Woessner,J., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J.,
            Marth,G., Bowles,L., Wylie,T., Bowers,Y., Steptoe,M., Theising,B.,
            Geisel,S., Allen,M., Underwood,K., Chappell,J., Person,B.,
            Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R.,
            Schurk,R., Ritter,E., Kohn,S., Swaller,T., Behymer,K., Hillier,L.,
            Wilson,R. and Waterston,R.
  TITLE     Full Clone Sequencing of the Longest Available Member from Each
            Unigene Cluster
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 714)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-AUG-1998) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     SUBMITTED BY:
            Genome Sequencing Center
            Department of Genetics
            Washington University
            St. Louis MO 63108, USA
            http://genome.wustl.edu/gsc
            mailto:est@watson.wustl.edu

            NOTICE:  This sequence represents the full insert of this cDNA.  No
            attempt has been made to verify whether this corresponds to the
            full-length of the original mRNA from which it was derived.  We
            have tried to obtain double-stranded, or double chemistry sequence
            across the entire clone, but potentially, there are areas in the
            sequence where this level of coverage was not achieved.
            Nevertheless, we are confident of the accuracy of this sequence as
            all regions of low quality, as defined by PHRAP (P. Green, in
            preparation), were visually inspected and edited accordingly.  The
            consensus quality values for this sequence have been submitted
            separately.
```

```
            SIMILARITY INFORMATION:
            similar to Homo sapiens protein Y09763 (PID:g2285958) GABRE

            The location of this clone is unknown.
FEATURES             Location/Qualifiers
     source          1. .714
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Soares_fetal_heart_NbHH19W"
                     /clone="IMAGE:346069"
     misc_feature    146. .514
                     /note="similar to Homo sapiens protein Y09763
                     (PID:g2285958)"
     misc_feature    146. .514
                     /note="similar to Homo sapiens protein Y07637
                     (PID:g1747371)"
     misc_feature    146. .514
                     /note="similar to Homo sapiens protein U66661
                     (PID:g1857126)"
     misc_feature    146. .514
                     /note="similar to Homo sapiens protein U92283
                     (PID:g2285961)"
     misc_feature    302. .445
                     /note="similar to Gallus gallus protein P34904
                     (PID:g462150)"
BASE COUNT      195 a    163 c    151 g    205 t
ORIGIN


  Query Match             36.6%;  Score 285.8;  DB 11;  Length 714;
  Best Local Similarity   99.3%;  Pred. No. 9.3e-72;
  Matches  287;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    149 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 208

Qy     61 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    209 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 268

Qy    121 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 180
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db    269 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCTTGAACACTATC 328

Qy    181 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    329 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 388

Qy    241 GTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGG 289
          |||||||| ||||||||||||||||||||||||||||||||||||||||
Db    389 GTTGAGATCTCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGG 437


RESULT   7
G60680/c
LOCUS       G60680        596 bp    DNA             STS       26-OCT-1999
DEFINITION  SHGC-57595 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION   G60680
VERSION     G60680.1  GI:6125849
KEYWORDS    STS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 596)
  AUTHORS   Myers,R.M.
  TITLE     Human STSs (1999)
  JOURNAL   Unpublished (1999)
COMMENT
            Contact: Richard M. Myers
            Stanford Human Genome Center (SHGC)
            Stanford University School of Medicine
            Department of Genetics, M-344, Stanford, CA 94305, USA
            Tel: 4157259687
            Fax: 4157259689
            Email: myers@shgc.stanford.edu
            Primer A: AGAGGCTTCTGGCAGTTTGC
            Primer B: CCCAGCCTCTGGAAAATCAG
            STS size: 92
            PCR Profile:
                    Initial incubation: 95 degrees C for 10 minutes
                    Denaturation:       94 degrees C for 30 seconds
                    Annealing:          60 degrees C for 30 seconds
                    Polymerization:     72 degrees C for 23 seconds
                    PCR Cycles:         30
                    Thermal Cycler:     Perkin Elmer 9700
            Protocol:
                    Template:                   25 ng
                    Primer:                     each 1 uM
                    dNTPs:                      each 200 uM
                    AmpliTaq Gold Polymerase: 0.07 units/ul
                    Total Vol:                  5 ul

            Buffer:
                    MgCl2:          2.5 mM
                    KCl:            50 mM
                    Tris-HCl:       10 mM
                    pH:             8.3

            Prepared with primer pairs derived from W72699 -- Unigene.
FEATURES             Location/Qualifiers
     source          1. .596
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="X"
                     /clone_lib="Human"
     STS             399. .490
     primer_bind     399. .418
     primer_bind     complement(471. .490)
BASE COUNT      163 a    133 c    138 g    158 t      4 others
ORIGIN


  Query Match             34.5%;  Score 269.2;  DB 13;  Length 596;
  Best Local Similarity   97.6%;  Pred. No. 5.5e-67;
  Matches  282;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy      2 GGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTATG 61
          |||||||||||||||||||| |||| || |||||| ||||||||||||||||||||||
Db    559 GGGTCGAGGGACCTCAGACTGANTCAAGGANTGAAGCNTCTTCCCGTGATGTTGTCTATG 500

Qy     62 GCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAGA 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 GCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAGA 440

Qy    122 CTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATCC 181
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    439 CTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCTTGAACACTATCC 380

Qy    182 TGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTC-ACT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||| |
Db    379 TGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCAACT 320

Qy    241 GTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGG 289
          |||||||| ||||||||||||||||||||||||||||||||||||||||
Db    319 GTTGAGATCTCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGG 271


RESULT   8
MMGSGABA
LOCUS       MMGSGABA     1598 bp    mRNA            ROD       28-OCT-1991
DEFINITION  Mouse mRNA for gamma subunit of the GABA-alpha receptor.
ACCESSION   X59300
VERSION     X59300.1  GI:51121
```

```
KEYWORDS    GABA-Alpha receptor; gamma subunit.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1598)
  AUTHORS   Wilson-Shaw,D., Robinson,M., Alaljev,B., Siegel,R.E. and
            Sikela,J.M.
  TITLE     A novel gamma subunit of the GABA-alpha receptor identified using
            the polymerase chain reaction
  JOURNAL   FEBS Lett. In press
REFERENCE   2  (bases 1 to 1598)
  AUTHORS   Sikela,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAY-1991) Sikela J.M., University of Colorado Helth
            Sciences Centre, Pharmacology Department, 4200 East 9th Ave,
            Denver, Colorado 80262, USA
REFERENCE   3  (bases 1 to 1598)
  AUTHORS   Wilson-Shaw,D., Robinson,M., Gambarana,C., Siegel,R.E. and
            Sikela,J.M.
  TITLE     A novel gamma subunit of the GABAA receptor identified using the
            polymerase chain reaction
  JOURNAL   FEBS Lett. 284 (2), 211-215 (1991)
  MEDLINE   91285135
FEATURES             Location/Qualifiers
     source          1. .1598
                     /organism="Mus musculus"
                     /strain="C57"
                     /db_xref="taxon:10090"
                     /dev_stage="adult"
                     /tissue_type="brain"
     mRNA            1. .1598
     CDS             29. .1432
                     /codon_start=1
                     /product="gamma subunit of GABA-alpha receptor"
                     /protein_id="CAA41988.1"
                     /db_xref="GI:51122"
                     /db_xref="MGD:MGI:95624"
                     /db_xref="SWISS-PROT:P27681"
                     /translation="MAAKLLLLLCLFSGLHARSRRVEEDENEDSPSNQKWVLAPKPQD
                     TDATLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSINMEYQIDIFFAQTW
                     TDSRLRFNSTMKTLTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQLLRIWNDGKIL
                     YTLRLTINAECQLQLHNFPMDAHACPLTFSSYGYPKEEMIYRWRKNSVEAADQKSWRL
                     YQFDFMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFW
                     IKKDATPARTTLGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEY
                     ATLNYYSSCRKPTIRKKKTSLLHPDSTRWIPDRISLQAPSNYSLLDMRPPPPVMITLN
                     NSMYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSWRRGRIHIDVSELDSYSRVFFP
                     TSFLLFNLVYWVGYLYL"
     misc_feature    92. .94
                     /note="glycosylation site"
     misc_feature    209. .214
                     /note="glycosylation site"
BASE COUNT      442 a    392 c    351 g    413 t
ORIGIN
```

```
  Query Match             32.7%;  Score 255.2;  DB 12;  Length 1598;
  Best Local Similarity   62.9%;  Pred. No. 6.5e-63;
  Matches  395;  Conservative    0;  Mismatches  233;  Indels    0;  Gaps    0;

Qy    152 CAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTG 211
          | || ||  | |  || || ||||   |  ||||  | |||||| | || ||| | || |
Db    162 CCGATGCAACGCTGATTCTCAACAAATTGTTGAGAGAATATGACAAAAAGCTGAGACCGG 221

Qy    212 GCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTC 271
           |||||||   || || |||||| ||  ||| || ||    || |||||| ||||||||
Db    222 ACATTGGAATAAAACCAACTGTGATCGATGTGGACATTTATGTTAACAGCATTGGTCCTG 281

Qy    272 TCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACG 331
          | ||   | || ||||||||||||   ||||| ||  | ||  | || ||||||   |||
Db    282 TGTCATCCATAAACATGGAATACCAAATTGATATATTTTTTGCTCAAACCTGGACAGACA 341

Qy    332 AACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCC 391
          |||||  | | ||||  |||  |  |  | ||   |||||| ||||  ||||| ||
Db    342 GTCGCCTTCGATTCAACAGCACAATGAAAACACTAACTCTGAACAGCAACATGGTGGGCT 401

Qy    392 AGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCA 451
           | ||||||| || |||||| | ||| | |||||||| |    |  | |  ||   |||||
Db    402 TGATATGGATTCCAGACACCATCTTTCGAAATTCTAAAACAGCGGAGGCTCACTGGATCA 461

Qy    452 CCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGA 511
          |||  |||||||||| |  || | ||||  || ||||| ||  |  | |||||| | |||
Db    462 CCACACCCAACCAGCTCCTCAGAATCTGGAATGATGGGAAAATCCTTTACACATTAAGGC 521

Qy    512 TGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTT 571
          | || ||  |||| |  |||   || ||  |||  |  || || |||||| | ||  | |
Db    522 TCACTATCAATGCAGAGTGCCAGCTGCAACTGCATAACTTCCCTATGGATGCGCATGCCT 581

Qy    572 GCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAA 631
          ||||  |  | ||||||||||| |  ||| ||  |  | || ||||| ||    |||   |
Db    582 GCCCCTTGACCTTCTCTAGCTATGGCTACCCCAAAGAAGAAATGATTTATCGTTGGAGGA 641

Qy    632 ATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAG 691
          |        ||||      |||  |||| || |||  |||||  |||||||| || |  |
Db    642 AAAATTCAGTTGAGGCAGCTGATCAGAAATCATGGCGGCTCTATCAGTTTGACTTCATGG 701

Qy    692 GAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGA 751
          |  | || ||||  || |||||  | |||||  | |  |||||  |   | ||||||| |
Db    702 GCCTCAGAAACACTACAGAAATCGTGACAACATCTGCAGGTGATTATGTTGTCATGACTA 761

Qy    752 TTTTCTTCAATGTGAGCAGGCGGTTTGG 779
          | |  ||  |  ||||  |  |  | ||
Db    762 TCTATTTTGAACTGAGTCGAAGAATGGG 789
```

```
RESULT   9
RNGABAG3
LOCUS       RNGABAG3     1930 bp    mRNA            ROD       18-AUG-1992
DEFINITION  R.norvegicus mRNA for GABA-receptor gamma 3 subunit sequence.
ACCESSION   X63324
VERSION     X63324.1  GI:56181
KEYWORDS    GABA-A receptor gamma-3 subunit.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 1930)
  AUTHORS   Knoflach,F., Rhyner,T., Villa,M., Kellenberger,S., Drescher,U.,
            Malherbe,P., Sigel,E. and Mohler,H.
  TITLE     The gamma 3-subunit of the GABAA-receptor confers sensitivity to
            benzodiazepine receptor ligands
  JOURNAL   FEBS Lett. 293 (1-2), 191-194 (1991)
  MEDLINE   92070559
REFERENCE   2  (bases 1 to 1930)
  AUTHORS   Villa,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-AUG-1992) M. Villa, Parmacology, ETH and Univ of
            Zurich, Gloriastrasse 32, CH-8006 Zurich, SWITZERLAND
FEATURES             Location/Qualifiers
     source          1. .1930
                     /organism="Rattus norvegicus"
                     /strain="Zur-Siv"
                     /db_xref="taxon:10116"
                     /dev_stage="newborn"
                     /tissue_type="brain"
     CDS             177. .1580
                     /codon_start=1
                     /product="GABA-A receptor gamma-3 subunit"
                     /protein_id="CAA44930.1"
                     /db_xref="GI:56182"
                     /db_xref="SWISS-PROT:P28473"
                     /translation="MAAKLLLLLCLFSGLHARSRRVEEDDSEDSPSNQKWVLAPKSQD
                     TDVTLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSINMEYQIDIFFAQTW
                     TDSRLRFNSTMKILTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQLLRIWNDGKIL
                     YTLRLTINAECQLQLHNFPMDAHACPLTFSSYGYPKEEMIYRWRKNSVEAADQKSWRL
                     YQFDFMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFW
```

```
                     IKKDATPARTTLGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEY
                     ATLNYYSSCRKPTIRKKKTSLLHPDSTRWIPDRISLQAPSNYSLLDMRPPPPVMITLN
                     NSMYWQEFEDTCVYECLDGKDCQTFFCCYEECKSGSWRRGRIHIDVSELDSYSRVFFP
                     TSFLLFNLVYWVGYLYL"
BASE COUNT      554 a    520 c    398 g    458 t
ORIGIN


  Query Match           32.3%;  Score 252;  DB 12;  Length 1930;
  Best Local Similarity   62.6%;  Pred. No. 5.5e-62;
  Matches  393;  Conservative    0;  Mismatches  235;  Indels    0;  Gaps    0;

Qy     152 CAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTG 211
           | || |   | |  || || ||||   | ||| |  | |||||| | ||  || | || |
Db     310 CCGATGTGACACTGATTCTCAACAAATTGCTGCGAGAATATGACAAAAAGTTGAGACCAG 369

Qy     212 GCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTC 271
           |||||||   || || |||||| ||  ||| || ||    || |||||| ||||||||
Db     370 ACATTGGAATAAAACCAACTGTGATCGATGTGGACATTTATGTTAACAGCATTGGTCCTG 429

Qy     272 TCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACG 331
           | ||   | || ||||||||||   ||||| ||  | ||  | || ||||||   |||
Db     430 TGTCATCCATAAACATGGAATACCAAATTGATATATTTTTTGCTCAAACCTGGACAGACA 489

Qy     332 AACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCC 391
           |||||  | | ||||  |||  |  |    |||  ||||||  ||||  ||||| |
Db     490 GTCGCCTTCGATTCAACAGCACAATGAAAATACTTACTCTGAACAGCAACATGGTGGGTT 549

Qy     392 AGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCA 451
           | ||||||| || |||||| | ||| | || ||||| |    |  | |  ||   |||||
Db     550 TGATATGGATACCAGACACCATCTTTCGAAACTCTAAAACAGCAGAGGCTCACTGGATCA 609

Qy     452 CCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGA 511
           |||  |||||||| |  |  | ||||  || ||||| ||  |  | |||||| | |||
Db     610 CCACACCCAACCAGCTCCTTAGAATCTGGAATGATGGGAAAATCCTTTACACATTAAGGC 669

Qy     512 TGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTT 571
           | |||||  |||| |  |||   || ||  |||  |  || || |||||| | ||  | |
Db     670 TTACCATCAATGCAGAGTGCCAGCTGCAACTGCATAACTTCCCCATGGATGCGCATGCCT 729

Qy     572 GCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAA 631
           ||||| |  | |||||||||| |  ||| ||  |  | || ||||| ||    |||  |
Db     730 GCCCTTTGACCTTCTCTAGCTATGGCTACCCCAAAGAAGAAATGATTTATCGTTGGAGGA 789

Qy     632 ATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAG 691
           |       ||||      |||  |||| || |||  |||||  |||||||| || |  |
Db     790 AAAATTCAGTTGAGGCAGCTGATCAGAAATCATGGCGGCTCTATCAGTTTGACTTCATGG 849

Qy     692 GAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGA 751
           |  | || ||||  || |||||  | |||||  | |  ||||| |   | ||||||| |
Db     850 GCCTCAGAAACACTACAGAAATCGTGACAACATCTGCAGGTGATTATGTTGTCATGACTA 909

Qy     752 TTTTCTTCAATGTGAGCAGGCGGTTTGG 779
           | | |||  |  ||||  |  |  | ||
Db     910 TCTACTTTGAACTGAGTCGAAGAATGGG 937


RESULT  10
RATGABAA
LOCUS       RATGABAA     1654 bp    mRNA            ROD       27-APR-1993
DEFINITION  Rat GABA-A receptor gamma-3 subunit mRNA, complete cds.
ACCESSION   M81142
VERSION     M81142.1  GI:204199
KEYWORDS    GABA-alpha receptor gamma-3 subunit.
SOURCE      Rattus rattus unknown adult fore brain cDNA to mRNA.
  ORGANISM  Rattus rattus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 1654)
  AUTHORS   Herb,A., Wisden,W., Lueddens,H., Puia,G., Vicini,S. and
            Seeburg,P.H.
  TITLE     The third gamma subunit of the gamma-aminobutyric acid type A
            receptor family
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89, 1433-1437 (1992)
  MEDLINE   92159063
FEATURES             Location/Qualifiers
     source          1. .1654
                     /organism="Rattus rattus"
                     /db_xref="taxon:10117"
                     /dev_stage="adult"
                     /sex="unknown"
                     /tissue_type="fore brain"
     sig_peptide     103. .153
                     /gene="GABA-alpha receptor gamma-3 subunit"
     CDS             103. .1506
                     /gene="GABA-alpha receptor gamma-3 subunit"
                     /codon_start=1
                     /product="GABA-alpha receptor gamma-3 subunit"
                     /protein_id="AAA41181.1"
                     /db_xref="GI:204200"
                     /translation="MAAKLLLLLCLFSGLHARSRRVEEDDSEDSPSNQKWVLAPKSQD
                     TDVTLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSINMEYQIDIFFAQTW
                     TDSRLRFNSTMKILTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQLLRIWNDGKIL
                     YTLRLTINAECQLQLHNFPMDAHACPLTFSSYGYPKEEMIYRWRKNSVEAADQKSWRL
                     YQFDFMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFW
                     IKKDATPARTTLGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEY
                     ATLNYYSSCRKPTIRKKKTSLLHPDSTRWIPDRISLQAPSNYSLLDMRPPPPVMITLN
                     NSMYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSWRRGRIHIDVSELDSYSRVFFP
                     TSFLLFNLVYWVGYLYL"
     gene            103. .1506
                     /gene="GABA-alpha receptor gamma-3 subunit"
     mat_peptide     154. .1503
                     /gene="GABA-alpha receptor gamma-3 subunit"
                     /product="GABA-alpha receptor gamma-3 subunit"
BASE COUNT      449 a    414 c    374 g    417 t
ORIGIN


  Query Match           32.1%;  Score 250.4;  DB 12;  Length 1654;
  Best Local Similarity   62.4%;  Pred. No. 1.6e-61;
  Matches  392;  Conservative    0;  Mismatches  236;  Indels    0;  Gaps    0;

Qy     152 CAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTG 211
           | || |   | |  || || ||||   | ||| |  | |||||| | ||  || | || |
Db     236 CCGATGTGACACTGATTCTCAACAAATTGCTGCGAGAATATGACAAAAAGTTGAGACCAG 295

Qy     212 GCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTC 271
           |||||||   || || |||||| ||  ||| || ||    || |||||| ||||||||
Db     296 ACATTGGAATAAAACCAACTGTGATCGATGTGGACATTTATGTTAACAGCATTGGTCCTG 355

Qy     272 TCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACG 331
           | ||   | || ||||||||||   ||||| ||  | ||  | || ||||||   |||
Db     356 TGTCATCCATAAACATGGAATACCAAATTGATATATTTTTTGCTCAAACCTGGACAGACA 415

Qy     332 AACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCC 391
           |||||  | | ||||  |||  |  |    |||  ||||||  ||||  ||||| |
Db     416 GTCGCCTTCGATTCAACAGCACAATGAAAATACTTACTCTGAACAGCAACATGGTGGGTT 475

Qy     392 AGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCA 451
           | ||||||| || |||||| | ||| | || ||||| |    |  | |  ||   |||||
Db     476 TGATATGGATACCAGACACCATCTTTCGAAACTCTAAAACAGCAGAGGCTCACTGGATCA 535

Qy     452 CCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGA 511
           |||  |||||||| |  |  | ||||  || ||||| ||  |  | |||||| | |||
Db     536 CCACACCCAACCAGCTCCTTAGAATCTGGAATGATGGGAAAATCCTTTACACATTAAGGC 595

Qy     512 TGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTT 571
           | |||||  |||| |  |||   || ||  |||  |  || || |||||| | ||  | |
Db     596 TTACCATCAATGCAGAGTGCCAGCTGCAACTGCATAACTTCCCCATGGATGCGCATGCCT 655

Qy     572 GCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAA 631
           ||||| |  | |||||||||| |  ||| ||  |  | || ||||| ||    |||  |
Db     656 GCCCTTTGACCTTCTCTAGCTATGGCTACCCCAAAGAAGAAATGATTTATCGTTGGAGGA 715

Qy     632 ATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAG 691
           |       ||||      |||  |||| || |||  |||||  |||||||| || |  |
```

```
Db    716 AAAATTCAGTTGAGGCAGCTGATCAGAAATCATGGCGGCTCTATCAGTTTGACTTCATGG 775

Qy    692 GAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGA 751
          |  | || |||| || ||||| | || ||  | |  ||||| |   | ||||||| |
Db    776 GCCTCAGAAACACTACAGAAATCGTGACTACATCTGCAGGTGATTATGTTGTCATGACTA 835

Qy    752 TTTTCTTCAATGTGAGCAGGCGGTTTGG 779
          | | |||  |  |||| |  |  | ||
Db    836 TCTACTTTGAACTGAGTCGAAGAATGGG 863


RESULT  11
A46959
LOCUS       A46959       1565 bp    DNA             PAT       07-MAR-1997
DEFINITION  Sequence 7 from Patent WO9529234.
ACCESSION   A46959
VERSION     A46959.1  GI:2300979
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1565)
  AUTHORS   Whiting,P.J.
  TITLE     HUMAN GAMMA 3 GABA-A RECEPTOR SUBUNIT AND STABLY CO-TRANSFECTED
            CELL LINES
  JOURNAL   Patent: WO 9529234-A 7 02-NOV-1995;
            MERCK SHARP & DOHME (GB)
FEATURES             Location/Qualifiers
     source          1. .1565
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     CDS             33. .1436
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAA02960.1"
                     /db_xref="GI:2300980"
                     /translation="MAPKLLLLLCLFSGLHARSRKVEEDEYEDSSSNQKWVLAPKSQD
                     TDVTLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSINMEYQIDIFFAQTW
                     TDSRLRFNSTMKILTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQLLRIWNDGKIL
                     YTLRLTINAECQLQLHNFPMDEHSCPLIFSSYGYPKEEMIYRWRKNSVEAADQKSWRL
                     YQFDFMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFW
                     IKKDATPARTALGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEY
                     ATLNYYSSCRKPTTTKKTTSLLHPDSSRWIPERISLQAPSNYSLLDMRPPPPAMITLN
                     NSVYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSWRKGRIHIDILELDSYSRVFFP
                     TSFLLFNLVYWVGYLYL"
BASE COUNT      430 a    393 c    343 g    399 t
ORIGIN


  Query Match           31.5%;  Score 245.6;  DB 5;  Length 1565;
  Best Local Similarity  61.9%;  Pred. No. 3.8e-60;
  Matches  389;  Conservative    0;  Mismatches  239;  Indels    0;  Gaps    0;

Qy    152 CAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTG 211
          | || |   |||  || || ||||   | || ||  | |||||  | || ||| | || |
Db    166 CCGACGTGACTCTTATTCTCAACAAGTTGCTAAGAGAGTATGATAAAAAGCTGAGGCCAG 225

Qy    212 GCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTC 271
            ||||||   || || ||  |    ||||| ||     || |||||| ||||||||
Db    226 ATATTGGAATAAAACCGACCGTAATTGACGTTGACATTTATGTTAACAGCATTGGTCCTG 285

Qy    272 TCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACG 331
          | ||     || ||||||||||||   ||||||||  | ||  | |||||||||   ||
Db    286 TGTCATCAATAAACATGGAATACCAAATTGACATATTTTTTGCTCAGACCTGGACAGATA 345

Qy    332 AACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCC 391
            |||||  | | ||||  |||  |  |   |||| ||||||  ||||  ||||| |
Db    346 GTCGCCTTCGATTCAACAGCACAATGAAAATTCTTACTCTGAACAGCAACATGGTGGGGT 405

Qy    392 AGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCA 451
            | |||||||| |||||| | ||  | |||||||| |   |  | |  ||   |||||
Db    406 TAATCTGGATCCCAGACACCATCTTCCGCAATTCTAAAACCGCAGAGGCTCACTGGATCA 465

Qy    452 CCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGA 511
          |||  ||||| ||| |  |||| || |  || || || ||  |  | |||||  | |||
Db    466 CCACACCCAATCAGCTCCTCCGGATTTGGAATGACGGGAAAATCCTTTACACTTTGAGGC 525

Qy    512 TGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTT 571
          | |||||  |||| |  |||   || ||  ||| ||  || || |||||    ||||| |
Db    526 TCACCATCAATGCTGAGTGCCAGCTGCAGCTGCACAACTTCCCCATGGACGAACACTCCT 585

Qy    572 GCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAA 631
          |||| ||   |||||| |||| |  ||||||  |  | || ||||| || |  |||  ||
Db    586 GCCCGCTGATTTTCTCCAGCTATGGCTATCCCAAAGAAGAAATGATTTATAGATGGAGAA 645

Qy    632 ATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAG 691
          |       | ||      |||  |||| || |||  ||| |  |||||||| || |  |
Db    646 AAAATTCAGTGGAGGCAGCTGACCAGAAATCATGGCGGCTTTATCAGTTTGACTTCATGG 705

Qy    692 GAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGA 751
          |  | || |||| || |||||  | |||||  | |  |||||  |   | ||||||| |
Db    706 GCCTCAGAAACACCACAGAAATCGTGACAACGTCTGCAGGTGATTATGTTGTCATGACTA 765

Qy    752 TTTTCTTCAATGTGAGCAGGCGGTTTGG 779
          | |  ||  |  |||| ||  |  | ||
Db    766 TATATTTTGAATTGAGTAGAAGAATGGG 793


RESULT  12
S82769
LOCUS       S82769       1536 bp    mRNA            PRI       28-DEC-1996
DEFINITION  GABAA receptor gamma 3 subunit [human, fetal brain, mRNA Partial,
            1536 nt].
ACCESSION   S82769
VERSION     S82769.1  GI:1754748
KEYWORDS    .
SOURCE      human fetal brain.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1536)
  AUTHORS   Hadingham,K.L., Wafford,K.A., Thompson,S.A., Palmer,K.J. and
            Whiting,P.J.
  TITLE     Expression and pharmacology of human GABAA receptors containing
            gamma 3 subunits
  JOURNAL   Eur. J. Pharmacol. 291 (3), 301-309 (1995)
  MEDLINE   96360042
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 179067] from the original journal article.
            This sequence comes from Fig. 1.
FEATURES             Location/Qualifiers
     source          1. .1536
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     gene            33. .1436
                     /gene="GABAA receptor gamma 3 subunit"
     CDS             33. .1436
                     /gene="GABAA receptor gamma 3 subunit"
                     /note="This sequence comes from Fig. 1."
                     /codon_start=1
                     /product="GABAA receptor gamma 3 subunit"
                     /protein_id="AAB39369.1"
                     /db_xref="GI:1754749"
                     /translation="MAPKLLLLLCLFSGLHARSRKVEEDEYEDSSSNQKWVLAPKSQD
                     TDVTLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSINMEYQIDIFFAQTW
                     TDSRLRFNSTMKILTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQLLRIWNDGKIL
                     YTLRLTINAECQLQLHNFPMDEHSCPLIFSSYGYPKEEMIYRWRKNSVEAADQKSWRL
                     YQFDFMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFW
                     IKKDATPARTALGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEY
                     ATLNYYSSCRKPTTTKKTTSLLHPDSSRWIPERISLQAPSNYSLLDMRPPPPAMITLN
                     NSVYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSWRKGRIHIDILELDSYSRVFFP
                     TSFLLFNLVYWVGYLYL"
BASE COUNT      423 a    387 c    337 g    389 t
ORIGIN
```

```
  Query Match           31.5%;  Score 245.6;  DB 10;  Length 1536;
  Best Local Similarity  61.9%;  Pred. No. 3.8e-60;
  Matches  389;  Conservative    0;  Mismatches  239;  Indels    0;  Gaps    0;

Qy    152 CAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTG 211
Db    166 CCGACGTGACTCTTATTCTCAACAAGTTGCTAAGAGAGTATGATAAAAAGCTGAGGCCAG 225

Qy    212 GCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTC 271
Db    226 ATATTGGAATAAAACCGACCGTAATTGACGTTGACATTTATGTTAACAGCATTGGTCCTG 285

Qy    272 TCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACG 331
Db    286 TGTCATCAATAAACATGGAATACCAAATTGACATATTTTTTGCTCAGACCTGGACAGATA 345

Qy    332 AACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCC 391
Db    346 GTCGCCTTCGATTCAACAGCACAATGAAAATTCTTACTCTGAACAGCAACATGGTGGGGT 405

Qy    392 AGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCA 451
Db    406 TAATCTGGATCCCAGACACCATCTTCCGCAATTCTAAAACCGCAGAGGCTCACTGGATCA 465

Qy    452 CCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGA 511
Db    466 CCACACCCAATCAGCTCCTCCGGATTTGGAATGACGGGAAAATCCTTTACACTTTGAGGC 525

Qy    512 TGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTT 571
Db    526 TCACCATCAATGCTGAGTGCCAGCTGCAGCTGCACAACTTCCCCATGGACGAACACTCCT 585

Qy    572 GCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAA 631
Db    586 GCCCGCTGATTTTCTCCAGCTATGGCTATCCCAAAGAAGAAATGATTTATAGATGGAGAA 645

Qy    632 ATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAG 691
Db    646 AAAATTCAGTGGAGGCAGCTGACCAGAAATCATGGCGGCTTTATCAGTTTGACTTCATGG 705

Qy    692 GAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGA 751
Db    706 GCCTCAGAAACACCACAGAAATCGTGACAACGTCTGCAGGTGATTATGTTGTCATGACTA 765

Qy    752 TTTTCTTCAATGTGAGCAGGCGGTTTGG 779
Db    766 TATATTTTGAATTGAGTAGAAGAATGGG 793


RESULT  13
GDGABAAR
LOCUS       GDGABAAR     2206 bp    mRNA            VRT      15-JUL-1991
DEFINITION  Chicken mRNA for GABA-A receptor gamma-2 subunit.
ACCESSION   X54944
VERSION     X54944.1  GI:62896
KEYWORDS    GABA-A receptor.
SOURCE      chicken.
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
            Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 2206)
  AUTHORS   Glencorse,T.A. and Bateson,A.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-OCT-1990) Glencorse T.A., Bateson A.N., Molecular
            Neurobiology Unit, MRC Centre, Hills Road, Cambridge CB2 2QH,
            United Kingdom
REFERENCE   2  (bases 1 to 2206)
  AUTHORS   Glencorse,T.A., Bateson,A.N. and Darlison,M.G.
  TITLE     Sequence of the chicken GABAA receptor gamma 2-subunit cDNA
  JOURNAL   Nucleic Acids Res. 18 (23), 7157 (1990)
  MEDLINE   91088318
FEATURES             Location/Qualifiers
     source          1. .2206
                     /organism="Gallus gallus"
                     /strain="Commercial Rhode Island Cross"
                     /db_xref="taxon:9031"
                     /dev_stage="embryo"
                     /tissue_type="whole brain"
                     /clone_lib="lambda gt10"
                     /clone="pcGRgamma2"
     mRNA            <671. .>2095
     sig_peptide     671. .784
                     /product="putative"
     CDS             671. .2095
                     /codon_start=1
                     /product="GABA-A receptor gamma-2 subunit"
                     /protein_id="CAA38704.1"
                     /db_xref="GI:62897"
                     /db_xref="SWISS-PROT:P21548"
                     /translation="MTPSNPTRLGSTALLNPAFSLKMMVWALVFLSLIQCSTQKGDDD
                     YEDYTSNKTWVLTPKVHESDVTLILNGLLEGYDNKLRPDIGVKPTVIHTDMYVNSIGP
                     VNAINMEYTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAH
                     WITTPNRMLRIWNDGRVLYTLRLTIDAECQLQLHNFPMDAHSCPLEFSSYGYPREEII
                     YQWKRSSVEVGDTRSWRLYQFSFTGLRNTTEVVKTTSGDYVVMSVYFNLSRRMGYFTI
                     QTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAM
                     DLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPLLRMFSFKAPTIDIRPR
                     SATIQMNNATHLQERDEEYGYECLDGKDCASFFCCFEDCRTGAWRHGRIHIRIAKMDS
                     YARIFFPTAFCLFNLVYWVSYLYL"
     mat_peptide     785. .2092
                     /product="GABA-A receptor gamma-2 subunit"
     misc_feature    1796. .1819
                     /note="insertion relative to the human gamma-2  sequence
                     which is proposed to be caused by  alternative splicing"
BASE COUNT      600 a    468 c    479 g    659 t
ORIGIN


  Query Match           30.5%;  Score 238.2;  DB 4;  Length 2206;
  Best Local Similarity  59.3%;  Pred. No. 5.3e-58;
  Matches  405;  Conservative    0;  Mismatches  278;  Indels    0;  Gaps    0;

Qy     97 TCTGAGGAAACAAAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAA 156
Db    803 TATGAAGATTACACTTCAAATAAGACTTGGGTTTTGACTCCCAAAGTTCATGAGAGTGAT 862

Qy    157 GCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATT 216
Db    863 GTCACTCTTATTTTAAATGGCTTGCTGGAAGGATATGACAACAAGTTACGACCTGATATA 922

Qy    217 GGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCT 276
Db    923 GGAGTTAAGCCGACAGTAATTCATACTGATATGTATGTGAACAGCATTGGGCCAGTGAAT 982

Qy    277 ATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGC 336
Db    983 GCTATCAATATGGAATATACAATTGATATATTTTTCGCCCAAACGTGGTATGACAGACGT 1042

Qy    337 CTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTA 396
Db   1043 CTGAAGTTCAACAGCACTATAAAAGTGCTCAGATTAAACAGCAACATGGTTGGGAAGATC 1102

Qy    397 TGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATG 456
Db   1103 TGGATACCTGATACATTTTTCCGAAATTCCAAGAAAGCTGATGCTCATTGGATAACAACT 1162

Qy    457 CCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACC 516
Db   1163 CCTAATAGGATGCTCAGGATCTGGAATGATGGCAGAGTGTTGTACACACTGAGACTGACG 1222

Qy    517 ATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCT 576
Db   1223 ATTGATGCTGAGTGTCAGCTACAGTTACACAACTTCCCAATGGATGCCCATTCCTGCCCC 1282

Qy    577 CTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTTC 636
Db   1283 CTGGAATTTTCAAGCTATGGTTACCCAAGGGAAGAGATCATTTACCAATGGAAGCGCAGC 1342
```

```
Qy     637 AAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTG 696
           | ||  |    || |  | ||||||| ||||| ||||||    ||||| ||| |
Db    1343 TCAGTGGAGGTGGGAGATACCAGGTCCTGGAGGCTCTACCAGTTCTCCTTTACGGGATTA 1402

Qy     697 AGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTC 756
           || || | |||||  |  | |  ||  ||   || ||||   | |||||| |  ||| |
Db    1403 AGAAATACAACTGAGGTGGTGAAGACTACATCAGGAGACTATGTAGTCATGTCCGTTTAC 1462

Qy     757 TTCAATGTGAGCAGGCGGTTTGG 779
           || ||  |||||||| |  | ||
Db    1463 TTTAACCTGAGCAGGAGAATGGG 1485


RESULT 14
MUSGABAAG2
LOCUS       MUSGABAAG2   2231 bp    mRNA            ROD       27-APR-1993
DEFINITION  Mus musculus GABA-A receptor gamma-2 subunit mRNA, complete cds.
ACCESSION   M62374
VERSION     M62374.1  GI:193403
KEYWORDS    GABA-alpha receptor gamma-2 subunit.
SOURCE      Mouse, cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2231)
  AUTHORS   Sikela,J.M., Shaw,W.D., Khan,A.S., Lin,L.-H., Leidenheimer,G. and
            Siegel,R.E.
  TITLE     A novel form of the gamma2 subunit of the GABA-A receptor:
            Functional, expresison and localization
  JOURNAL   Unpublished (1991)
FEATURES             Location/Qualifiers
     source          1. .2231
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
     CDS             348. .1772
                     /codon_start=1
                     /product="GABA-alpha receptor gamma-2 subunit"
                     /protein_id="AAA37653.1"
                     /db_xref="GI:193404"
                     /translation="MSSPNTWSIGSSVYSPVFSQKMTLWILLLLSLYPGFTSQKSDDD
                     YEDYASNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGP
                     VNAINMEYTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAH
                     WITTPNRMLRIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIV
                     YQWKRSSVEVGDTRSWRLYQFSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTI
                     QTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAM
                     DLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPLLRMFSFKAPTIDIRPR
                     SATIQMNNATHLQERDEEYGYECLDGKDCASFFCCFEDCRTGAWRHGRIHIRIAKMDS
                     YARIFFPTAFCLFNLVYWVSYLYL"
BASE COUNT      626 a    476 c    485 g    644 t
ORIGIN


  Query Match           30.5%;  Score 238.2;  DB 12;  Length 2231;
  Best Local Similarity  61.2%;  Pred. No. 5.3e-58;
  Matches  384;  Conservative    0;  Mismatches  243;  Indels    0;  Gaps    0;

Qy     154 GAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGC 213
           || | | ||  |||| | ||||   | |||      |||||| ||||||| || |||| |
Db     537 GATGTCACTGTCATCTTAAACAACCTGCTGGAAGGGTATGACAACAAACTTCGACCTGAC 596

Qy     214 ATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTC 273
           || |||| ||| || ||  |  |   |   || ||    || |||||| |||||||  |
Db     597 ATCGGAGTGAAACCAACATTAATTCATACAGATATGTATGTGAACAGCATTGGTCCAGTG 656

Qy     274 TCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAA 333
             |   |  | |||||||| || ||||| ||  | ||  |||| |||||||| |||  |
Db     657 AATGCTATCAATATGGAATATACAATTGATATTTTTTTTGCCCAAACCTGGTATGACAGA 716

Qy     334 CGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAG 393
           ||  |    |  |||   ||| || |   |||     ||||| ||||| ||||| |  |
Db     717 CGTTTGAAATTTAACAGTACCATTAAAGTTCTCCGGTTGAATAGCAATATGGTGGGGAAA 776

Qy     394 CTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACC 453
           | ||||| || ||||| || || ||||| || || | | |  | |  ||   |||||||
Db     777 ATCTGGATTCCAGACACTTTCTTCAGGAACTCCAAAAAGGCTGATGCTCACTGGATCACC 836

Qy     454 ATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATG 513
           |  ||||||  |||| |  | || |  || |||||    ||  | |||||  | ||| |
Db     837 ACTCCCAACAGGATGCTGAGAATTTGGAATGATGGTCGAGTTCTCTACACCTTAAGGCTA 896

Qy     514 ACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGC 573
           || |||||||| |  |||    | ||  | | ||  || |||||||||   ||||| |||
Db     897 ACAATTGATGCTGAGTGCCAGTTGCAATTACACAACTTCCCAATGGATGAACACTCCTGC 956

Qy     574 CCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAAT 633
           || ||    ||||| || | |   ||||||    | || ||  | ||  | ||| |
Db     957 CCCCTGGAGTTCTCCAGTTATGGATATCCTCGTGAAGAAATTGTTTATCAATGGAAGCGC 1016

Qy     634 TTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGA 693
           |||||  |   ||| |  |  || |||| ||| |  || |||   |||   |||
Db    1017 AGTTCTGTTGAAGTGGGTGACACAAGATCATGGAGGCTGTATCAATTTTCCTTTGTTGGA 1076

Qy     694 GTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATT 753
           |||| || | ||||||| || | |  ||  |   |||||||   |||| ||| |  |
Db    1077 TTGAGGAATACAACTGAAGTAGTGAAGACAACTTCTGGTGACTATGTGGTGATGTCTGTG 1136

Qy     754 TTCTTCAATGTGAGCAGGCGGTTTGGC 780
           | |||| || |||||||  |  | |||
Db    1137 TACTTCGATCTGAGCAGAAGAATGGGC 1163


RESULT 15
MUSGABAAR
LOCUS       MUSGABAAR    2036 bp    mRNA            ROD       08-NOV-1993
DEFINITION  Mouse gamma-aminobutyric acid A receptor gamma-2 subunit mRNA,
            complete cds.
ACCESSION   M86572 M57522
VERSION     M86572.1  GI:193405
KEYWORDS    GABA-alpha receptor gamma-2 subunit; gamma-aminobutyric acid-A
            receptor.
SOURCE      Mus musculus (strain DBA/2J) adult brain cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2036)
  AUTHORS   Kofuji,P., Wang,J.B., Moss,S.J., Huganir,R.L. and Burt,D.R.
  TITLE     Generation of two forms of the gamma-aminobutyric acid A receptor
            gamma-2 subunit in mice by alternative splicing
  JOURNAL   J. Neurochem. 56, 713-715 (1991)
  MEDLINE   91108470
FEATURES             Location/Qualifiers
     source          1. .2036
                     /organism="Mus musculus"
                     /strain="DBA/2J"
                     /db_xref="taxon:10090"
                     /dev_stage="adult"
                     /tissue_type="brain"
     gene            177. .1577
                     /gene="GABA-A receptor gamma-2 subunit"
     sig_peptide     177. .290
                     /gene="GABA-A receptor gamma-2 subunit"
     CDS             177. .1577
                     /gene="GABA-A receptor gamma-2 subunit"
                     /codon_start=1
                     /product="gamma-aminobutyric acid A receptor gamma-2
                     subunit"
                     /protein_id="AAB59635.1"
                     /db_xref="GI:193406"
                     /translation="MSSPNTWSIGSSVYSPVFSQKMTLWILLLLSLYPGFTSQKSDDD
                     YEDYTSNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGP
                     VNAINMEYTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAH
                     WITTPNRMLRIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIV
                     YQWKRSSVEVGDTRSWRLYQFSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTI
                     QTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAM
                     DLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPAPTIDIRPRSATIQMNN
```

```
                     ATHLQERDEEYGYQCLDGKDCASFFCCFEDCRTGAWRHGRIHMRIAKMDSYARIFFPT
                     AFCLFNLVYWVSYLYL"
     mat_peptide     291. .1574
                     /gene="GABA-A receptor gamma-2 subunit"
                     /product="gamma-aminobutyric acid A receptor gamma-2
                     subunit"
     allele          321
                     /gene="GABA-A receptor gamma-2 subunit"
                     /note="found in strains DBA/2J and C57BL/6J polymorphism"
                     /replace="g"
     variation       1302^1303
                     /gene="GABA-A receptor gamma-2 subunit"
                     /replace="cttcttcggatgttttccttcaag"
BASE COUNT      597 a    422 c    443 g    574 t
ORIGIN


  Query Match             30.4%;  Score 237;  DB 12;  Length 2036;
  Best Local Similarity   59.1%;  Pred. No. 1.2e-57;
  Matches  405;  Conservative    0;  Mismatches  280;  Indels    0;  Gaps    0;

Qy      96 CTCTGAGGAAACAAAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGA 155
           || ||| ||    |  || | | | ||   |     ||    |   |    |  |   ||
Db     308 CTATGAAGATTACACTTCTAATAAAACATGGGTGTTGACTCCAAAAGTTCCAGAGGGTGA 367

Qy     156 AGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCAT 215
            | | ||  |||| | ||||   | |||      |||||| ||||||| || |||| |||
Db     368 TGTCACTGTCATCTTAAACAACCTGCTGGAAGGCTATGACAACAAACTTCGACCTGACAT 427

Qy     216 TGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTC 275
           |||| ||| || ||  |  |   |   || ||    || |||||| |||||||  |
Db     428 CGGAGTGAAACCAACATTAATTCATACAGATATGTATGTGAACAGCATTGGTCCAGTGAA 487

Qy     276 TATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACG 335
           |    |  | |||||||| || ||||| ||  | ||  |||| |||||||| |||  |||
Db     488 TGCTATCAATATGGAATATACAATTGATATTTTTTTTGCCCAAACCTGGTATGACAGACG 547

Qy     336 CCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCT 395
           |    |  |||   ||| || |   |||     ||||| ||||| ||||| |  |  |
Db     548 TTTGAAATTTAACAGTACCATTAAAGTTCTCCGGTTGAATAGCAATATGGTGGGGAAAAT 607

Qy     396 ATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCAT 455
           |||||  || ||||| || ||  ||||| || || | | |  | |  ||   ||||||||
Db     608 CTGGATTCCAGACACTTTCTTCAGGAACTCCAAAAAGGCTGATGCTCACTGGATCACCAC 667

Qy     456 GCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGAC 515
           ||||||  |||| |  | || |  || |||||    ||  | |||||  | ||| | ||
Db     668 TCCCAACAGGATGCTGAGAATTTGGAATGATGGTCGAGTTCTCTACACCTTAAGGCTAAC 727

Qy     516 CATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCC 575
           ||||||||  |  |||    | ||  | | ||  || |||||||||   ||||| |||||
Db     728 AATTGATGCTGAGTGCCAGTTGCAATTACACAACTTCCCAATGGATGAACACTCCTGCCC 787

Qy     576 TCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTT 635
           ||    ||||| || | |   ||||||    | || ||  | ||  | ||| |
Db     788 CCTGGAGTTCTCCAGTTATGGATATCCTCGTGAAGAAATTGTTTATCAATGGAAGCGCAG 847

Qy     636 CAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGT 695
                |||||  |   ||| |  |  || |||| ||| |' || |||   |||   ||| |
Db     848 TTCTGTTGAAGTGGGTGACACAAGATCATGGAGGCTGTATCAATTTTCCTTTGTTGGATT 907

Qy     696 GAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTT 755
           ||| || | ||| ||| || | |  ||  |   |||||||   |||| ||| |  | |
Db     908 GAGGAATACAACGGAAGTAGTGAAGACAACTTCTGGTGACTATGTGGTGATGTCTGTGTA 967

Qy     756 CTTCAATGTGAGCAGGCGGTTTGGC 780
           |||| || |||||||  |  | |||
Db     968 CTTCGATCTGAGCAGAAGAATGGGC 992


Search completed: March  9, 2000, 01:35:15
Job time: 7098 sec
```

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2000, 13:39:48 ; Search time 147.28 Seconds
(without alignments)
634.054 Million cell updates/sec

Title: US-09-030-832-41_COPY_95_874
Perfect score: 780
Sequence: 1 AGGGTCGAGGGACCTCAGAC.....ATGTGAGCAGGCGGTTTGGC 780

Scoring table: IDENTITY_NUC

Searched: 214294 seqs, 59861208 residues

Database : Issued_Patents_NA:*

Word size : 0

Number of hits that pass the threshold : 428588
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	164.8	21.1	2310	2	US-08-417-330A-15	Sequence 15, Appl
	2	159.2	20.4	1732	2	US-08-417-330A-17	Sequence 17, Appl
	3	146.4	18.8	1638	2	US-08-417-330A-13	Sequence 13, Appl
	4	140.8	18.1	2191	2	US-08-417-330A-11	Sequence 11, Appl
	5	129.6	16.6	2635	3	US-08-768-301-3	Sequence 3, Appli
	6	86.8	11.1	1866	2	US-08-417-330A-19	Sequence 19, Appl
	7	72.6	9.3	1542	1	US-08-249-112-1	Sequence 1, Appli
	8	72.6	9.3	1542	6	PCT-US95-06556-1	Sequence 1, Appli
	9	70.4	9.0	1650	1	US-08-459-100A-1	Sequence 1, Appli
	10	70.4	9.0	1650	6	PCT-US94-09589-1	Sequence 1, Appli
	11	70	9.0	3958	2	US-08-435-933-5	Sequence 5, Appli
	12	70	9.0	3958	6	PCT-US96-06035-5	Sequence 5, Appli
	13	61.4	7.9	1657	2	US-08-554-659-1	Sequence 1, Appli
	14	61.4	7.9	1657	2	US-08-554-659-3	Sequence 3, Appli
	15	50.4	6.5	1479	1	US-08-249-112-2	Sequence 2, Appli
	16	50.4	6.5	1479	6	PCT-US95-06556-2	Sequence 2, Appli
	17	47.6	6.1	1491	1	US-08-137-614A-3	Sequence 3, Appli
	18	47.6	6.1	1491	3	US-08-768-301-1	Sequence 1, Appli
	19	36.6	4.7	1345	2	US-08-525-654A-134	Sequence 134, App
	20	34.8	4.5	7218	1	US-08-232-463-14	Sequence 14, Appl
c	21	34.2	4.4	300	7	5218100-5	Patent No. 5218100
c	22	32.6	4.2	2313	1	US-08-133-248-7	Sequence 7, Appli
c	23	32.6	4.2	2085	1	US-08-371-930-9	Sequence 9, Appli
c	24	32.6	4.2	3353	1	US-08-123-702-1	Sequence 1, Appli
c	25	32.6	4.2	3148	1	US-08-123-702-3	Sequence 3, Appli
c	26	32.6	4.2	8591	1	US-08-462-859A-6	Sequence 6, Appli
c	27	32.6	4.2	8591	1	US-08-462-859A-8	Sequence 8, Appli
c	28	32.6	4.2	8591	1	US-08-123-659A-6	Sequence 6, Appli
c	29	32.6	4.2	8591	1	US-08-123-659A-8	Sequence 8, Appli
c	30	32.6	4.2	3353	1	US-08-456-420-12	Sequence 12, Appl
c	31	32.6	4.2	8591	2	US-08-464-247A-6	Sequence 6, Appli
c	32	32.6	4.2	8591	2	US-08-464-247A-8	Sequence 8, Appli
c	33	32.6	4.2	8591	2	US-08-464-248A-6	Sequence 6, Appli
c	34	32.6	4.2	8591	2	US-08-464-248A-8	Sequence 8, Appli
c	35	32.6	4.2	2088	3	US-08-104-165-4	Sequence 4, Appli
c	36	32.6	4.2	2265	3	US-08-104-165-5	Sequence 5, Appli
c	37	32.6	4.2	2256	4	US-08-422-333-1	Sequence 1, Appli
c	38	32.6	4.2	3520	4	US-08-422-333-20	Sequence 20, Appl
c	39	32.6	4.2	2085	6	PCT-US94-01712-9	Sequence 9, Appli
c	40	32.6	4.2	2256	7	5187153-1	Patent No. 5187153
c	41	32.6	4.2	3353	7	5218100-1	Patent No. 5218100
c	42	32.6	4.2	2088	7	5218100-4	Patent No. 5218100
c	43	32.6	4.2	2256	7	5220013-1	Patent No. 5220013
c	44	32.6	4.2	2256	7	5223482-1	Patent No. 5223482
	45	32.4	4.2	3200	1	US-08-444-405-1	Sequence 1, Appli

ALIGNMENTS

```
RESULT   1
US-08-417-330A-15
; Sequence 15, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2310 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  298...1683
;      OTHER INFORMATION:
US-08-417-330A-15


  Query Match             21.1%;  Score 164.8;  DB 2;  Length 2310;
```

```
  Best Local Similarity   53.8%;  Pred. No. 2.2e-42;
  Matches  365;  Conservative    0;  Mismatches  307;  Indels    6;  Gaps    1;

Qy    109 AAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATC 168
Db    394 ATGCCAACCAGTTCAGTGAAAGATGAGACCAATGACAACATCACGATATTTACCAGGATC 453

Qy    169 CTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCC 228
Db    454 TTGGATGGGCTCTTGGATGGCTACGACAACAGACTTCGGCCCGGGCTGGGAGAGCGCATC 513

Qy    229 ACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATG 288
Db    514 ACTCAGGTGAGGACCGACATCTACGTCACCAGCTTCGGCCCGGTGTCCGACACGGAAATG 573

Qy    289 GAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAAC 348
Db    574 GAGTACACCATAGACGTGTTTTTCCGACAAAGCTGGAAAGATGAAAGGCTTCGGTTTAAG 633

Qy    349 GACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGAC 408
Db    634 GGGCCCATGCAGCGCCTCCCTCTCAACAACCTCCTTGCCAGCAAGATCTGGACCCCAGAC 693

Qy    409 ACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATG 468
Db    694 ACGTTCTTCCACAACGGGAAGAAGTCCATCGCTCACAACATGACCACGCCCAACAAGCTG 753

Qy    469 GTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGA 528
Db    754 CTGCGGCTGGAGGACGACGGCACCCTGCTCTACACCATGCGCTTGACCATCTCTGCAGAG 813

Qy    529 TGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCT 588
Db    814 TGCCCCATGCAGCTTGAGGACTTCCCGATGGATGCGCACGCTTGCCCTCTGAAATTTGGC 873

Qy    589 AGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA------TTTCAAGCTT 642
Db    874 AGCTATGCGTACCCTAATTCTGAAGTCGTTTACGTCTGGACCAACGGCTCCACCAAGTCG 933

Qy    643 GAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAAC 702
Db    934 GTGGTGGTGGCGGAAGATGGCTCCAGACTGAACCAGTACCACCTGATGGGGCAGACGGTG 993

Qy    703 AAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAAT 762
Db    994 GGCACTGAGAACATCAGCACCAGCACAGGCGAATACACAATCATGACAGCTCACTTCCAC 1053

Qy    763 GTGAGCAGGCGGTTTGGC 780
Db   1054 CTGAAAAGGAAGATTGGC 1071


RESULT   2
US-08-417-330A-17
; Sequence 17, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1732 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  27...1385
;      OTHER INFORMATION:
US-08-417-330A-17


  Query Match             20.4%;  Score 159.2;  DB 2;  Length 1732;
  Best Local Similarity   54.4%;  Pred. No. 1.1e-40;
  Matches  345;  Conservative    0;  Mismatches  283;  Indels    6;  Gaps    1;

Qy    153 AGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGG 212
Db    116 AAACGTCAGTCGGATCCTGGACAACTTGCTTGAAGGCTATGACAATCGGCTGCGGCCGGG 175

Qy    213 CATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCT 272
Db    176 ATTTGGAGGTGCTGTCACTGAAGTCAAAACAGACATTTATGTGACCAGTTTTGGGCCCGT 235

Qy    273 CTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGA 332
Db    236 GTCAGATGTGGAGATGGAGTATACGATGGATGTTTTTTTTCGCCAGACCTGGACTGATGA 295

Qy    333 ACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCA 392
Db    296 GAGGTTGAAGTTTGGGGGGCCAACTGAGATTCTGAGTCTGAATAATTTGATGGTCAGTAA 355

Qy    393 GCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCAC 452
Db    356 AATCTGGACGCCTGACACCTTTTTCAGAAATGGTAAAAAGTCCATTGCTCACAACATGAC 415

Qy    453 CATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGAT 512
Db    416 AACTCCTAATAAACTCTTCAGAATAATGCAGAATGGAACCATTTTATACACCATGAGGCT 475

Qy    513 GACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTG 572
Db    476 TACCATCAATGCTGACTGTCCCATGAGGCTGGTTAACTTTCCTATGGATGGGCATGCTTG 535

Qy    573 CCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA 632
Db    536 TCCACTCAAGTTTGGGAGCTATGCTTATCCCAAAAGTGAAATCATATATACGTGGAAAAA 595

Qy    633 TTTCAAGCTTGAAATCAATGA------GAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 686
Db    596 AGGACCACTTTACTCAGTAGAAGTCCCAGAAGAATCTTCAAGCCTTCTCCAGTATGATCT 655
```

```
Qy    687 TACAGGAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCAT 746
Db    656 GATTGGACAAACAGTATCTAGTGAGACAATTAAATCTAACACAGGTGAATACGTTATAAT 715

Qy    747 GACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 780
Db    716 GACAGTTTACTTCCACTTGCAAAGGAAGATGGGC 749


RESULT   3
US-08-417-330A-13
; Sequence 13, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1638 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  87...1562
;      OTHER INFORMATION:
US-08-417-330A-13


  Query Match           18.8%;  Score 146.4;  DB 2;  Length 1638;
  Best Local Similarity  55.8%;  Pred. No. 1.2e-36;
  Matches  279;  Conservative    0;  Mismatches  221;  Indels    0;  Gaps    0;

Qy    128 CTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTA 187
Db    256 CTGATGACAGCACTGACAACATCACTATCTTCACCAGAATCTTGGATCGTCTTCTGGACG 315

Qy    188 ATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGA 247
Db    316 GCTATGACAACCGGCTGCGACCTGGGCTTGGAGATGCAGTGACTGAAGTGAAGACTGACA 375

Qy    248 TCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCA 307
Db    376 TCTACGTGACCAGTTTTGGCCCTGTGTCAGACACTGACATGGAGTACACTATTGATGTAT 435

Qy    308 TCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTG 367
Db    436 TTTTTCGGCAGACATGGCATGATGAAAGACTGAAATTTGATGGCCCCATGAAGATCCTTC 495

Qy    368 TTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTA 427
Db    496 CACTGAACAATCTCCTGGCTAGTAAGATCTGGACACCGGACACCTTCTTCCACAATGGCA 555

Qy    428 AGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATG 487
Db    556 AGAAATCAGTGGCTCATAACATGACCACGCCCAACAAGCTGCTCAGATTGGTGGACAACG 615

Qy    488 GCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCA 547
Db    616 GAACCCTCCTCTATACAATGAGGTTAACAATTCATGCTGAGTGTCCCATGCATTTGGAAG 675

Qy    548 GATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGA 607
Db    676 ATTTTCCCATGGATGTGCATGCCTGCCCACTGAAGTTTGGAAGCTATGCCTATACAACAG 735

Qy    608 ATGAGATGATCTACAAGTGG 627
Db    736 CTGAAGTGGTTTATTCTTGG 755


RESULT   4
US-08-417-330A-11
; Sequence 11, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
```

```
;      LENGTH:  2191 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  214...1566
;      OTHER INFORMATION:
US-08-417-330A-11


  Query Match             18.1%;  Score 140.8;  DB 2;  Length 2191;
  Best Local Similarity   56.5%;  Pred. No. 8.3e-35;
  Matches  262;  Conservative    0;  Mismatches  202;  Indels    0;  Gaps    0;

Qy    164 GCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGA 223
          | || ||  |||   | |||  |  ||| ||  |    ||  | || ||  | ||||| |
Db    344 GAATTCTTGACAGACTTCTGGATGGTTACGATAATCGGCTTAGACCAGGACTGGGAGACA 403

Qy    224 AGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAG 283
              ||||  |||     | | |||  ||| | |||  |||| ||| ||||      ||
Db    404 GTATTACTGAAGTCTTCACTAACATCTACGTGACCAGTTTTGGCCCTGTCTCAGATACAG 463

Qy    284 ACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTT 343
          | ||||||||  || |||||  |  ||||    || |  ||| | || |||||  |    |
Db    464 ATATGGAATATACAATTGATGTTTTCTTTCGACAAAAATGGAAAGATGAACGTTTAAAAT 523

Qy    344 ACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCC 403
            || |   |  |  |    |||   || ||        |||  ||| |  | ||||  |
Db    524 TTAAAGGTCCTATGAATATCCTTCGACTAAACAATTTAATGGCTAGCAAAATCTGGACTC 583

Qy    404 CGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACC 463
          | || |||||||||   |||   ||||   |    |  ||| | || || ||||| ||
Db    584 CAGATACCTTTTTTCACAATGGGAAGAAATCAGTAGCTCATAATATGACAATGCCAAATA 643

Qy    464 AGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATG 523
          || || | || ||  |  | ||||| |   || |||| || || ||| | ||  || | |
Db    644 AGTTGCTTCGAATTCAGGATGATGGGACTCTGCTGTATACCATGAGGCTTACAGTTCAAG 703

Qy    524 CCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTT 583
          | | |||| || | ||| ||      || |||||||| |||| || || |||||    |
Db    704 CTGAATGCCCAATGCACTTGGAGGATTTCCCAATGGATGCTCATTCATGTCCTCTGAAAT 763

Qy    584 TCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGG 627
          |    |||| | | ||| |       ||| | |  || |  |||
Db    764 TTGGCAGCTATGCATATACAACTTCAGAGGTCACTTATATTTGG 807


RESULT   5
US-08-768-301-3
; Sequence 3, Application US/08768301
; Patent No. 5854002
;  GENERAL INFORMATION:
;    APPLICANT:  Tomalski, Michael D.
;    APPLICANT:  Gant, Daniel B.
;    TITLE OF INVENTION:  METHOD OF IDENTIFYING COMPOUNDS THAT BIND
;    TITLE OF INVENTION:  TO THE INSECT GABA RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brumbaugh, Graves, Donohue & Raymond
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  10112-0228
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/768,301
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacLeod, Janet M
;      REGISTRATION NUMBER:  35,263
;      REFERENCE/DOCKET NUMBER:  A30693
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-408-2500
;      TELEFAX:  212-765-2519
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2635 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
US-08-768-301-3


  Query Match             16.6%;  Score 129.6;  DB 3;  Length 2635;
  Best Local Similarity   53.1%;  Pred. No. 3.2e-31;
  Matches  276;  Conservative    0;  Mismatches  244;  Indels    0;  Gaps    0;

Qy    167 TCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGC 226
          | ||| ||| | | ||| |    ||||||  | |   | || || |   | || |     |
Db    693 TACTGGACAATCTGCTGCGCGGCTATGACAATAGCATACGTCCGGATTTCGGTGGACCTC 752

Qy    227 CCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACA 286
          | |      |    || || ||    ||   |||| | || ||  | ||     | || |
Db    753 CAGCCACTATTGAAGTGGATATAATGGTTCGCAGCATGGGCCCAATATCAGAGGTCGATA 812

Qy    287 TGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACA 346
          ||   ||| | || |||      |||  |||  |||||   ||  |||| |||   | |
Db    813 TGACCTACTCGATGGACTGTTATTTCCGCCAATCCTGGGTGGATAAACGTCTCGCATTCG 872

Qy    347 ACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGG 406
          | | | ||   ||  | || |  |||  | |    || ||   | | | ||||  ||||
Db    873 AGGGCGCCCAGGACACGCTGGCACTGAGCGTCTCGATGTTGGCACGGATTTGGAAGCCGG 932

Qy    407 ACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGA 466
          | || |  |||  ||    |||  || | |  |||   ||| |||| ||| ||  ||
Db    933 ATACGTACTTTTACAACGGCAAGCAGAGCTATTTGCACACGATTACCACGCCAAATAAGT 992

Qy    467 TGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCG 526
          | ||  | |||||  || | ||    ||| ||||| | |   || |||| ||| | ||||
Db    993 TTGTGAGGATCTATCAGAACGGACGCGTGCTGTACTCCAGCCGGCTGACAATTAAAGCCG 1052

Qy    527 GATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCT 586
          | ||| |  |  |  ||  |   ||||||||||||   ||    || |||||    |||
Db   1053 GCTGCCCCATGAATCTGGCCGATTTTCCAATGGATATACAAAAGTGTCCTCTGAAATTCG 1112

Qy    587 CTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAA 646
            |   |||  |||  |   |   ||  | ||||||   ||| | ||    |  |
Db   1113 GTTCATTTGGCTACACAACGTCGGATGTCATCTACCGTTGGAACAAAGAAAGACCACCCG 1172

Qy    647 TCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 686
          ||           |   |  |||||| | ||| || |||||
Db   1173 TCGCCATTGCCGAGGACATGAAGCTGTCCCAATTCGATTT 1212


RESULT   6
US-08-417-330A-19
; Sequence 19, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1866 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  225...1646
;      OTHER INFORMATION:
US-08-417-330A-19


  Query Match             11.1%;  Score 86.8;  DB 2;  Length 1866;
  Best Local Similarity   49.3%;  Pred. No. 8.7e-18;
  Matches  226;  Conservative    0;  Mismatches  232;  Indels    0;  Gaps    0;

Qy    170 TGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCA 229
          || | |   ||||||     ||||||      ||| | || |   ||||||     |||
Db    343 TGGATAGACTCCTGAAAGGCTATGACATTCGTCTGAGACCAGATTTTGGAGGTCCCCCCG 402

Qy    230 CTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGG 289
            ||      |  | || | | |   |||| | | |    | |||    |  | ||||
Db    403 TGGCTGTGGGGATGAACATTGACATTGCCAGCATCGATATGGTTTCTGAAGTCAATATGG 462

Qy    290 AATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACG 349
          | || ||| |    ||   |||    ||  |||||   ||  |  | || |  || || |
Db    463 ATTATACCTTGACAATGTACTTTCAACAAGCCTGGAGAGATAAGAGGCTGTCCTATAATG 522

Qy    350 ACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACA 409
            |    |       |   |||| |   ||  ||||    |||||| ||| | || || |
Db    523 TAATACCTTTAAACTTGACTCTGGACAACAGAGTGGCAGACCAGCTCTGGGTGCCTGATA 582

Qy    410 CCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGG 469
          ||| |||   |||   ||||| | |    | ||| |   | ||  |    ||||  |||
Db    583 CCTATTTCCTGAACGATAAGAAGTCATTTGTGCACGGAGTGACTGTTAAGAACCGCATGA 642

Qy    470 TCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGAT 529
          | ||| |  |    |||||||  ||  | ||   | | || || || |     || | |
Db    643 TTCGCCTGCATCCTGATGGCACCGTCCTTTATGGACTCAGAATCACAACCACAGCTGCCT 702

Qy    530 GCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTA 589
          ||    |  || |    || |  ||| |||||   ||    ||| | |     |   |
Db    703 GCATGATGGACCTAAGGAGGTACCCACTGGATGAACAAAACTGCACCTTGGAAATTGAGA 762

Qy    590 GCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGG 627
          ||| |   ||  |     |||| ||    |   | |||
Db    763 GCTATGGATACACAACTGATGACATTGAGTTTTACTGG 800


RESULT   7
US-08-249-112-1
; Sequence 1, Application US/08249112
; Patent No. 5527703
;  GENERAL INFORMATION:
;    APPLICANT:  Cully, Doris F.
;    APPLICANT:  Arena, Joseph P.
;    APPLICANT:  Liu, Ken K.
;    APPLICANT:  Vassilatis, Demetrios
;    TITLE OF INVENTION:  DNA ENCODING GLUTAMATE GATED CHLORIDE
;    TITLE OF INVENTION:  CHANNELS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wallen, John W.
;      STREET:  126 E. Lincoln Ave., P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/249,112
;      FILING DATE:  25-MAY-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wallen, John W.
;      REGISTRATION NUMBER:  35,403
;      REFERENCE/DOCKET NUMBER:  19194
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-3905
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1542 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-249-112-1


  Query Match             9.3%;  Score 72.6;  DB 1;  Length 1542;
  Best Local Similarity   50.4%;  Pred. No. 2.4e-13;
  Matches  208;  Conservative    0;  Mismatches  199;  Indels    6;  Gaps    1;

Qy    226 CCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGAC 285
          ||   ||||||  | ||| | ||   | |    |   ||        |  | | | | |
Db    312 CCAGTTGTGGTTTCAGTTAACATGCTCCTTCGAACTATTTCAAAGATAGATGTTGTGAAT 371

Qy    286 ATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTAC 345
          ||||| || |    | | | | ||     |||  |||   ||| | | ||| | |||
Db    372 ATGGAGTATAGTGCTCAATTGACATTGCGAGAGAGTTGGATTGACAAGAGACTCAGCTAC 431

Qy    346 ------AACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGG 399
                ||  |       | || |   | || ||| |  || ||| |     ||  | |||
Db    432 GGAGTAAAAGGAGATGGTCAGCCAGATTTTGTGATTCTCACTGTTGGACATCAAATTTGG 491
```

```
Qy    400 ATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCC 459
          || || ||||| |||||   ||||   ||     |  || |||||  |||    | |||
Db    492 ATGCCCGACACGTTTTTCCCGAATGAGAAACAAGCTTACAAGCATACGATTGATAAGCCG 551

Qy    460 AACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATT 519
          ||     || | || ||  |||| |||||  |  || ||||||  |  || | ||  |  |
Db    552 AATGTATTGATTCGAATACACAATGATGGTACAGTATTGTACTCTGTTCGTATTTCACTA 611

Qy    520 GATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTA 579
          |    |   ||| || |  |  | |      | ||||||||||  |||    ||  |  |
Db    612 GTCCTCTCTTGCCCAATGTATCTACAGTACTATCCAATGGATGTTCAACAGTGTTCCATT 671

Qy    580 TCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA 632
            |  |    | | ||||  ||   || || ||    ||   |||| || |
Db    672 GATCTTGCATCGTATGCCTACACTACAAAAGATATCGAATATTTGTGGAAAGA 724
```

RESULT 8
PCT-US95-06556-1
; Sequence 1, Application PC/TUS9506556
; GENERAL INFORMATION:
; APPLICANT: Cully, Doris F.
; APPLICANT: Arena, Joseph P.
; APPLICANT: Liu, Ken K.
; APPLICANT: Vassilatis, Demetrios
; TITLE OF INVENTION: DNA ENCODING GLUTAMATE GATED CHLORIDE
; TITLE OF INVENTION: CHANNELS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wallen, John W.
; STREET: 126 E. Lincoln Ave., P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06556
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/249,112
; FILING DATE: 25-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 19194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US95-06556-1

Query Match 9.3%; Score 72.6; DB 6; Length 1542;
Best Local Similarity 50.4%; Pred. No. 2.4e-13;
Matches 208; Conservative 0; Mismatches 199; Indels 6; Gaps 1;

```
Qy    226 CCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGAC 285
          ||   ||||||  | ||| | ||   | |    |   ||       |   | |  |  |
Db    312 CCAGTTGTGGTTTCAGTTAACATGCTCCTTCGAACTATTTCAAAGATAGATGTTGTGAAT 371
```

```
Qy    286 ATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTAC 345
          ||||| || |    | |  | |  ||     |||  |||   ||| |  | ||| | |||
Db    372 ATGGAGTATAGTGCTCAATTGACATTGCGAGAGAGTTGGATTGACAAGAGACTCAGCTAC 431

Qy    346 ------AACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGG 399
                ||  |      | ||  |   | ||  ||| |  ||  ||| |     ||  | |||
Db    432 GGAGTAAAAGGAGATGGTCAGCCAGATTTTGTGATTCTCACTGTTGGACATCAAATTTGG 491

Qy    400 ATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCC 459
          || || ||||| |||||   ||||   ||     |  || |||||  |||    | |||
Db    492 ATGCCCGACACGTTTTTCCCGAATGAGAAACAAGCTTACAAGCATACGATTGATAAGCCG 551

Qy    460 AACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATT 519
          ||     || | || ||  |||| |||||  |  || ||||||  |  || | ||  |  |
Db    552 AATGTATTGATTCGAATACACAATGATGGTACAGTATTGTACTCTGTTCGTATTTCACTA 611

Qy    520 GATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTA 579
          |    |   ||| || |  |  | |      | ||||||||||  |||    ||  |  |
Db    612 GTCCTCTCTTGCCCAATGTATCTACAGTACTATCCAATGGATGTTCAACAGTGTTCCATT 671

Qy    580 TCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA 632
            |  |    | | ||||  ||   || || ||    ||   |||| || |
Db    672 GATCTTGCATCGTATGCCTACACTACAAAAGATATCGAATATTTGTGGAAAGA 724
```

RESULT 9
US-08-459-100A-1
; Sequence 1, Application US/08459100A
; Patent No. 5654172
; GENERAL INFORMATION:
; APPLICANT: Li, ET AL.
; TITLE OF INVENTION: GABAA Receptor Epsilon Subunit
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,100A
; FILING DATE: June 2, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09589
; FILING DATE: 26 AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-325
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1650 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
US-08-459-100A-1

Query Match 9.0%; Score 70.4; DB 1; Length 1650;
Best Local Similarity 52.3%; Pred. No. 1.2e-12;
Matches 180; Conservative 0; Mismatches 161; Indels 3; Gaps 1;

```
Qy    284 ACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTT 343
          ||||||| |||||      |||   | ||   |||  ||||   ||| | || ||    |
Db    392 ACATGGACTACACAGCCACCATATACCTCCGACAGCGCTGGATGGACCAGCGGCTGGTGT 451

Qy    344 ACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCC 403
          | | || |    ||    |   |||| ||| |    | |||      || ||| | |
Db    452 TTGAAGGCAAC---AAGAGCTTCACTCTGGATGCCCGCCTCGTGGAGTTCCTCTGGGTGC 508

Qy    404 CGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACC 463
          | || || |   ||  | | || |||| | ||  |   ||||  ||||  ||   |||
Db    509 CAGATACTTACATTGTGGAGTCCAAGAAGTCCTTCCTCCATGAAGTCACTGTGGGAAACA 568

Qy    464 AGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATG 523
          | |  ||||| ||| |    |||||| |||  ||||  |  | || || || |    ||
Db    569 GGCTCATCCGCCTCTTCTCCAATGGCACGGTCCTGTATGCCCTCAGAATCACGACAACTG 628

Qy    524 CCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTT 583
          | |||     |  | ||   | ||  || |||||  | ||  | |||     |
Db    629 TTGCATGTAACATGGATCTGTCTAAATACCCCATGGACACACAGACATGCAAGTTGCAGC 688

Qy    584 TCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGG 627
          |    ||||    ||||  ||  |||||  ||   | ||  |||
Db    689 TGGAAAGCTGGGGCTATGATGGAAATGATGTGGAGTTCACCTGG 732
```

RESULT 10
PCT-US94-09589-1
; Sequence 1, Application PC/TUS9409589
; GENERAL INFORMATION:
; APPLICANT: KIRKNESS, ET AL.
; TITLE OF INVENTION: GABAA Receptor Epsilon Subunit
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09589
; FILING DATE: Submitted herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-188
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1650 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
PCT-US94-09589-1

Query Match 9.0%; Score 70.4; DB 6; Length 1650;
Best Local Similarity 52.3%; Pred. No. 1.2e-12;
Matches 180; Conservative 0; Mismatches 161; Indels 3; Gaps 1;

```
Qy    284 ACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTT 343
          ||||||| |||||      |||   | ||   |||  ||||   ||| | || ||    |
Db    392 ACATGGACTACACAGCCACCATATACCTCCGACAGCGCTGGATGGACCAGCGGCTGGTGT 451

Qy    344 ACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCC 403
          | | || |    ||    |   |||| ||| |    | |||      || ||| | |
Db    452 TTGAAGGCAAC---AAGAGCTTCACTCTGGATGCCCGCCTCGTGGAGTTCCTCTGGGTGC 508

Qy    404 CGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACC 463
          | || || |   ||  | | || |||| | ||  |   ||||  ||||  ||   |||
Db    509 CAGATACTTACATTGTGGAGTCCAAGAAGTCCTTCCTCCATGAAGTCACTGTGGGAAACA 568

Qy    464 AGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATG 523
          | |  ||||| ||| |    |||||| |||  ||||  |  | || || || |    ||
Db    569 GGCTCATCCGCCTCTTCTCCAATGGCACGGTCCTGTATGCCCTCAGAATCACGACAACTG 628

Qy    524 CCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTT 583
          | |||     |  | ||   | ||  || |||||  | ||  | |||     |
Db    629 TTGCATGTAACATGGATCTGTCTAAATACCCCATGGACACACAGACATGCAAGTTGCAGC 688

Qy    584 TCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGG 627
          |    ||||    ||||  ||  |||||  ||   | ||  |||
Db    689 TGGAAAGCTGGGGCTATGATGGAAATGATGTGGAGTTCACCTGG 732
```

RESULT 11
US-08-435-933-5
; Sequence 5, Application US/08435933
; Patent No. 5693492
; GENERAL INFORMATION:
; APPLICANT: Cully, Doris F.
; APPLICANT: Arena, Joseph P.
; APPLICANT: Paress, Philip S.
; APPLICANT: Liu, Ken K.
; TITLE OF INVENTION: DNA ENCODING GLUTAMATE GATED CHLORIDE
; TITLE OF INVENTION: CHANNELS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John W. Wallen III
; STREET: 126 East Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,933
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, III John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 19264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-435-933-5

Query Match 9.0%; Score 70; DB 2; Length 3958;
Best Local Similarity 48.9%; Pred. No. 2.7e-12;

```
  Matches  218;  Conservative    0;  Mismatches  225;  Indels    3;  Gaps    1;

Qy     219 AGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTAT 278
           |||    ||| |  | ||||   |  |  |  |||  |||  ||    |  |  |
Db     578 AGATGGTCCCGCCATAGTCAGAATCAATCTATTCGTTCGCAGTATTATGACGATTAGTGA 637

Qy     279 CCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCT 338
             |  | ||||| ||||   |  |  | | ||||    |    |||   || ||||||||
Db     638 TATTAAAATGGAGTACAGTGTGCAGTTAACCTTCCGTGAACAGTGGACGGATGAACGCCT 697

Qy     339 CTGTTACAACGACACCTTTGAGTCTCT---TGTTCTGAATGGCAATGTGGTGAGCCAGCT 395
           |   | | |||| | |    |      ||       |||||     |  | || || ||   |
Db     698 CAAGTTCGACGATATCCAGGGTCGCCTAAAGTATCTGACCCTGACGGAGGCGAACCGCGT 757

Qy     396 ATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCAT 455
           |||||| || ||    || ||   |||    |||  |   |||   ||  | |||| |||
Db     758 GTGGATGCCCGATCTTTTCTTCTCGAACGAGAAGGAGGGACACTTCCACAACATCATCAT 817

Qy     456 GCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGAC 515
           ||||||   |    | |||||||  |    | ||    ||| | || |  ||  | ||  |
Db     818 GCCCAATGTGTATATTCGCATCTTCCCCAACGGATCTGTGCTATATAGTATACGTATCTC 877

Qy     516 CATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCC 575
           |       |  ||| || |  || |      | |||  ||||   ||    ||| |
Db     878 GCTGACATTGGCCTGCCCAATGAACCTAAAGCTGTATCCGCTGGATAGACAGATCTGCTC 937

Qy     576 TCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTT 635
           |||    |  | |||| |  ||   |    || ||  || ||| |  |||| |  |
Db     938 ACTACGGATGGCCAGCTATGGCTGGACCACCAACGACTTGGTCTTCCTGTGGAAGGAGGG 997

Qy     636 CAAGCTTGAAATCAATGAGAAGAACT 661
           | | |  | |      |  |||||||
Db     998 CGATCCCGTACAGGTGGTAAAGAACT 1023


RESULT  12
PCT-US96-06035-5
; Sequence 5, Application PC/TUS9606035
;  GENERAL INFORMATION:
;    APPLICANT:  Cully, Doris F.
;    APPLICANT:  Arena, Joseph P.
;    APPLICANT:  Paress, Philip S.
;    APPLICANT:  Liu, Ken K.
;    TITLE OF INVENTION:  DNA ENCODING GLUTAMATE GATED CHLORIDE
;    TITLE OF INVENTION:  CHANNELS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jody M. Giesser
;      STREET:  126 East Lincoln Avenue - P.O. BOX 2000-0907
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  US
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/06035
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Giesser, Jody M.
;      REGISTRATION NUMBER:  32,838
;      REFERENCE/DOCKET NUMBER:  19264 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-3046
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3958 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US96-06035-5


  Query Match             9.0%;  Score 70;  DB 6;  Length 3958;
  Best Local Similarity   48.9%;  Pred. No. 2.7e-12;
  Matches  218;  Conservative    0;  Mismatches  225;  Indels    3;  Gaps    1;

Qy     219 AGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTAT 278
           |||    ||| |  | ||||   |  |  |  |||  |||  ||    |  |  |
Db     578 AGATGGTCCCGCCATAGTCAGAATCAATCTATTCGTTCGCAGTATTATGACGATTAGTGA 637

Qy     279 CCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCT 338
             |  | ||||| ||||   |  |  | | ||||    |    |||   || ||||||||
Db     638 TATTAAAATGGAGTACAGTGTGCAGTTAACCTTCCGTGAACAGTGGACGGATGAACGCCT 697

Qy     339 CTGTTACAACGACACCTTTGAGTCTCT---TGTTCTGAATGGCAATGTGGTGAGCCAGCT 395
           |   | | |||| | |    |      ||       |||||     |  | || || ||   |
Db     698 CAAGTTCGACGATATCCAGGGTCGCCTAAAGTATCTGACCCTGACGGAGGCGAACCGCGT 757

Qy     396 ATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCAT 455
           |||||| || ||    || ||   |||    |||  |   |||   ||  | |||| |||
Db     758 GTGGATGCCCGATCTTTTCTTCTCGAACGAGAAGGAGGGACACTTCCACAACATCATCAT 817

Qy     456 GCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGAC 515
           ||||||   |    | |||||||  |    | ||    ||| | || |  ||  | ||  |
Db     818 GCCCAATGTGTATATTCGCATCTTCCCCAACGGATCTGTGCTATATAGTATACGTATCTC 877

Qy     516 CATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCC 575
           |       |  ||| || |  || |      | |||  ||||   ||    ||| |
Db     878 GCTGACATTGGCCTGCCCAATGAACCTAAAGCTGTATCCGCTGGATAGACAGATCTGCTC 937

Qy     576 TCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTT 635
           |||    |  | |||| |  ||   |    || ||  || ||| |  |||| |  |
Db     938 ACTACGGATGGCCAGCTATGGCTGGACCACCAACGACTTGGTCTTCCTGTGGAAGGAGGG 997

Qy     636 CAAGCTTGAAATCAATGAGAAGAACT 661
           | | |  | |      |  |||||||
Db     998 CGATCCCGTACAGGTGGTAAAGAACT 1023


RESULT  13
US-08-554-659-1
; Sequence 1, Application US/08554659
; Patent No. 5767261
;  GENERAL INFORMATION:
;    APPLICANT:  Wingate, Vincent
;    APPLICANT:  Wolff, Mark
;    TITLE OF INVENTION:  LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
;    TITLE OF INVENTION:  AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/554,659
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9732
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1657 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  115..1581
US-08-554-659-1


  Query Match             7.9%;  Score 61.4;  DB 2;  Length 1657;
  Best Local Similarity   47.2%;  Pred. No. 8.6e-10;
  Matches  225;  Conservative    0;  Mismatches  246;  Indels    6;  Gaps    1;

Qy    159 CTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGG 218
          |||   |||  || |  |  |       |  || ||| | | | || | ||   |  |||
Db    243 CTCAGCCATTTTGGATTCGCTAAGTGTAAGCTACGACAAAAGAGTGAGGCCGAACTATGG 302

Qy    219 AGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTAT 278
          ||    |||    |  ||    ||  | ||   |||   |  | |  |  |  | |||
Db    303 AGGACCGCCAGTGGATGTGGGAGTCAACATGTACGTGCTCTCCATCAGCTCCTTATCTGA 362

Qy    279 CCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCT 338
            |  | |||||  | |||| |  ||   ||  ||||   ||    |||   |||    | ||
Db    363 AGTGAAAATGGATTTCACCCTGGATTTCTACTTCAGACAATTTTGGACAGACCCCAGGCT 422

Qy    339 CTGTTACAACGACACCT------TTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCA 392
            ||||||  | | |-      | ||| ||||     |         |  |  | ||  |
Db    423 TGCTTACAAAAAAAGCACGGGTGTGGAGACTCTGTCCGTCGGCTCGGAATTTATTAGAAA 482

Qy    393 GCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCAC 452
          |||||  | || |||||||| |||   ||    ||   | |  |    ||        ||
Db    483 CATATGGGTACCCGACACCTTCTTTGTTAACGAAAAACAGTCATATTTCCACATAGCTAC 542

Qy    453 CATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGAT 512
            |    |||| |  |  | |||||  |  |   |||     |        |  || ||  |
Db    543 TACAAGCAACGAATTCATACGCATTCATCATTCTGGATCTATTACTAGGAGTATAAGACT 602

Qy    513 GACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTG 572
          ||| ||    ||    ||  |  |  |  |||     ||||| |||||   ||| |  ||
Db    603 GACTATCACCGCTTCTTGTCCGATGGATTTGCAGTATTTTCCGATGGACCGTCAATTATG 662

Qy    573 CCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGA 629
          |  | |     ||   || |||  |||  |   |   || ||    |||||||||  |
Db    663 CAATATTGAAATCGAAAGTTTTGGCTACACCATGCGGGACATCCGATACAAGTGGAA 719


RESULT  14
US-08-554-659-3
; Sequence 3, Application US/08554659
; Patent No. 5767261
;  GENERAL INFORMATION:
;    APPLICANT:  Wingate, Vincent
;    APPLICANT:  Wolff, Mark
;    TITLE OF INVENTION:  LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
;    TITLE OF INVENTION:  AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/554,659
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9732
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1657 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  115..1581
US-08-554-659-3


  Query Match             7.9%;  Score 61.4;  DB 2;  Length 1657;
  Best Local Similarity   47.2%;  Pred. No. 8.6e-10;
  Matches  225;  Conservative    0;  Mismatches  246;  Indels    6;  Gaps    1;

Qy    159 CTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGG 218
          |||   |||  || |  |  |       |  || ||| | | | || | ||   |  |||
Db    243 CTCAGCCATTTTGGATTCGCTAAGTGTAAGCTACGACAAAAGAGTGAGGCCGAACTATGG 302

Qy    219 AGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTAT 278
          ||    |||    |  ||    ||  | ||   |||   |  | |  |  |  | |||
Db    303 AGGACCGCCAGTGGATGTGGGAGTCAACATGTACGTGCTCTCCATCAGCTCCTTATCTGA 362

Qy    279 CCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCT 338
            |  | |||||  | |||| |  ||   ||  ||||   ||    |||   |||    | ||
Db    363 AGTGAAAATGGATTTCACCCTGGATTTCTACTTCAGACAATTTTGGACAGACCCCAGGCT 422

Qy    339 CTGTTACAACGACACCT------TTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCA 392
            ||||||  | | |-      | ||| ||||     |         |  |  | ||  |
Db    423 TGCTTACAAAAAAAGCACGGGTGTGGAGACTCTGTCCGTCGGCTCGGAATTTATTAGAAA 482

Qy    393 GCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCAC 452
          |||||  | || |||||||| |||   ||    ||   | |  |    ||        ||
Db    483 CATATGGGTACCCGACACCTTCTTTGTTAACGAAAAACAGTCATATTTCCACATAGCTAC 542

Qy    453 CATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGAT 512
            |    |||| |  |  | |||||  |  |   |||     |        |  || ||  |
Db    543 TACAAGCAACGAATTCATACGCATTCATCATTCTGGATCTATTACTAGGAGTATAAGACT 602

Qy    513 GACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTG 572
          ||| ||    ||    ||  |  |  |  |||     ||||| |||||   ||| |  ||
Db    603 GACTATCACCGCTTCTTGTCCGATGGATTTGCAGTATTTTCCGATGGACCGTCAATTATG 662

Qy    573 CCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGA 629
          |  | |     ||   || |||  |||  |   |   || ||    |||||||||  |
Db    663 CAATATTGAAATCGAAAGTTTTGGCTACACCATGCGGGACATCCGATACAAGTGGAA 719


RESULT  15
US-08-249-112-2
; Sequence 2, Application US/08249112
; Patent No. 5527703
;  GENERAL INFORMATION:
;    APPLICANT:  Cully, Doris F.
;    APPLICANT:  Arena, Joseph P.
;    APPLICANT:  Liu, Ken K.
```

```
;    APPLICANT:  Vassilatis, Demetrios
;    TITLE OF INVENTION:  DNA ENCODING GLUTAMATE GATED CHLORIDE
;    TITLE OF INVENTION:  CHANNELS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wallen, John W.
;      STREET:  126 E. Lincoln Ave., P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/249,112
;      FILING DATE:  25-MAY-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wallen, John W.
;      REGISTRATION NUMBER:  35,403
;      REFERENCE/DOCKET NUMBER:  19194
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-3905
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1479 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-249-112-2


  Query Match             6.5%;  Score 50.4;  DB 1;  Length 1479;
  Best Local Similarity   50.8%;  Pred. No. 2.4e-06;
  Matches  120;  Conservative    0;  Mismatches  116;  Indels    0;  Gaps    0;

Qy     394 CTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACC 453
           |||||||| || ||||| || |||   |     ||     | ||    |||  |||
Db     359 CTATGGATTCCTGACACATTCTTTCCCACCGAAAAAGCAGCTCATAGACATTTGATTGAT 418

Qy     454 ATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATG 513
           |||   |||  | |  |  | || ||   |||||| ||  |  | ||||      ||||
Db     419 ATGGAAAACATGTTCTTGAGGATATATCCGGATGGAAAAATCCTCTACAGTTCCCGGATA 478

Qy     514 ACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGC 573
           |   |          ||| || | |   | |     |  ||| | || | ||| || ||
Db     479 AGTTTGACAAGTTCCTGCCCAATGCGTCTCCAACTCTACCCACTCGACTATCAATCGTGT 538

Qy     574 CCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGA 629
           |   | |    ||||   |  |  |   |||||| || || ||| |||||||
Db     539 AACTTTGATCTTGTCAGCTACGCGCACACAATGAATGATATCATGTACGAGTGGGA 594


Search completed: March  9, 2000, 13:40:02
Job time: 950 sec
```

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2000, 22:45:02 ; Search time 235.59 Seconds
(without alignments)
828.345 Million cell updates/sec

Title: US-09-030-832-41_COPY_95_874
Perfect score: 780
Sequence: 1 AGGGTCGAGGGACCTCAGAC.....ATGTGAGCAGGCGGTTTGGC 780

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	778.4	99.8	3123	1	V11776	GABA-A receptor ep
2	778.4	99.8	1552	1	V36319	Human GABA recepto
3	576.4	73.9	3026	1	V11777	Variant of GABA-A
4	301	38.6	10697	1	V11778	GABA-A receptor ep
5	240.8	30.9	1565	1	T02334	GABA-A receptor ga
6	177.8	22.8	1707	1	T28988	Human GABA-A recep
7	164.8	21.1	2310	1	Q33129	GABA-A receptor al
8	164.8	21.1	2310	1	Q69141	Human GABA recepto
9	159.2	20.4	1408	1	Q33130	GABA-A receptor al
10	159.2	20.4	1408	1	Q69142	Human GABA recepto
11	148	19.0	1638	1	Q69140	Human GABA recepto
12	146.4	18.8	1638	1	Q33128	GABA-A receptor al
13	140.8	18.1	2189	1	Q33127	GABA-A receptor al
14	140.8	18.1	2189	1	Q69139	Human GABA recepto
15	139.4	17.9	675	1	Q25720	OmpF signal peptid
16	129.6	16.6	2635	1	V84686	Insect GABA recept
17	125.6	16.1	1555	1	T28989	Human GABA-A recep
18	106.8	13.7	657	1	Q25722	GABA-A receptor be
19	105.4	13.5	660	1	Q25721	GABA-A receptor al
20	92.4	11.8	1884	1	V83111	Human GABA-A recep
21	92.4	11.8	1884	1	V83112	Human GABA-A recep
22	86.8	11.1	1866	1	Q33131	GABA-A receptor be
23	86.8	11.1	1866	1	Q69143	Human GABA recepto
24	72.6	9.3	1542	1	T09695	Caenorhabditis ele
25	70.4	9.0	1650	1	T10500	Human GABA-A recep
26	70.4	9.0	1650	1	T84630	Human GABA-A recep
27	70	9.0	3958	1	T43596	Glutamate-gated ch
28	61.4	7.9	1657	1	V55007	GABA gated chlorid
29	61.4	7.9	1657	1	V55008	GABA gated chlorid
30	58.2	7.5	1844	1	V64372	GABA-gated chlorid
31	55.6	7.1	1519	1	V64373	GABA-gated chlorid
32	50.4	6.5	1479	1	T09696	Caenorhabditis ele
33	50.2	6.4	1368	1	X24372	Cat flea glutamate
34	47.6	6.1	1491	1	Q99330	GABA receptor subu
35	47.6	6.1	1491	1	V84685	Insect GABA recept
36	46.8	6.0	1297	1	X24373	Cat flea glutamate
37	41.4	5.3	1823	1	X16065	DNA sequence of Lu
38	40.6	5.2	669	1	V64374	GABA-gated chlorid
39	36.6	4.7	2073	1	Q03099	Sequence encoding
40	36.6	4.7	2073	1	Q06140	Sequence encoding
41	35	4.5	1345	1	Q99225	Cavia porecellus t
c 42	35	4.5	9425	1	V74398	Staphylococcus aur
c 43	33.8	4.3	1638	1	Q13656	Encodes human brai
44	33.6	4.3	4680	1	V72211	Human heart hhNBC
45	33.6	4.3	3012	1	V72216	Human kidney hkNBC

ALIGNMENTS

RESULT 1
V11776
ID V11776 standard; cDNA; 3123 BP.
AC V11776;
DT 25-SEP-1998 (first entry)
DE GABA-A receptor epsilon sub-unit related gene.
KW ss; GABA-A receptor; diagnosis; therapy; drug screening.
OS Mammalia.
FH Key Location/Qualifiers
FT CDS 55. .1573
FT /*tag= a
FT /product= "GABA-A receptor epsilon sub-unit related
FT protein"
PN DE19644501-A1.
PD 30-APR-1998.
PF 25-OCT-1996; 044501.
PR 25-OCT-1996; DE-044501.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR WPI; 98-252096/23.
DR P-PSDB; W59048.
PT Protein related to GABA-A receptor sub-unit epsilon - useful for
PT diagnosis, therapy or drug screening
PS Example 1; Fig 1; 12pp; German.
CC The GABA-A receptor sub-unit epsilon related protein is used for the
CC diagnosis and/or therapy of related disorders. It can also be used to
CC screen for substances that modulate the activity of the protein.
SQ Sequence 3123 BP; 710 A; 877 C; 686 G; 849 T;

Query Match 99.8%; Score 778.4; DB 1; Length 3123;
Best Local Similarity 99.9%; Pred. No. 3.6e-240;
Matches 779; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     109 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 168

Qy      61 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     169 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 228

Qy     121 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     229 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 288

Qy     181 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     289 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 348

Qy     241 GTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATT 300
           ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     349 GTTGAGATCTCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATT 408

Qy     301 GACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     409 GACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAG 468

Qy     361 TCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     469 TCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGG 528
```

```
Qy    421 AATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTAC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    529 AATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTAC 588

Qy    481 AAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    589 AAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCAC 648

Qy    541 ATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTAT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    649 ATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTAT 708

Qy    601 CCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    709 CCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAAC 768

Qy    661 TCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    769 TCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACA 828

Qy    721 ACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    829 ACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 888
```

RESULT 2
V36319
ID V36319 standard; cDNA; 1552 BP.
AC V36319;
DT 12-OCT-1998 (first entry)
DE Human GABA receptor epsilon subunit cDNA.
KW GABA receptor; gamma-amino butyric acid receptor; human;
KW appetite; cognition; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 18. .1538
FT /*tag= a
PN WO9823742-A1.
PD 04-JUN-1998.
PF 18-NOV-1997; G03159.
PR 03-OCT-1997; GB-020995.
PR 25-NOV-1996; GB-024442.
PA (MERI) MERCK SHARP & DOHME LTD.
PI Whiting PJ;
DR WPI; 98-322722/28.
DR P-PSDB; W61045.
PT New isolated GABA receptor subunit, epsilon - used to develop
PT products for the screening and design of drugs, e.g. for modulating
PT appetite behaviours, hormonal interactions and cognition
PS Claim 5; Fig 1; 37pp; English.
CC This cDNA sequence codes for a novel class of subunit (see W61045),
CC classified as epsilon, within the human GABA receptor gene family.
CC It was generated from human brain cDNA by PCR using primers (see
CC V36322-23) derived from the 5' untranslated region (UTR) of an
CC anchored PCR product (see V36320-21) and from the 3'UTR of EST
CC R49718 (obtained from an EST database search using a GABA-A
CC receptor polypeptide). A stably co-transfected eukaryotic cell
CC line capable of expressing the GABA epsilon receptor subunit, at
CC least one alpha receptor subunit and at least one beta receptor
CC subunit is claimed. A recombinant expression vector, and protein
CC and membrane preparations of the GABA receptor obtained from the
CC co-transfected cells are also claimed. The new GABA-A receptor
CC epsilon subunit and products can be used in the screening and
CC design of drugs which act upon the GABA receptor. The ligands or
CC drug candidates identified may be used as therapeutic agents, e.g.
CC for the modulation of appetite behaviours, hormonal interactions
CC and cognition. They can also be used for the study of structure,
CC pharmacology and function of the various GABA receptor subtypes.
SQ Sequence 1552 BP; 344 A; 443 C; 349 G; 416 T;

Query Match 99.8%; Score 778.4; DB 1; Length 1552;
Best Local Similarity 99.9%; Pred. No. 2.4e-240;

Matches 779; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     72 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 131

Qy     61 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    132 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 191

Qy    121 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    192 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 251

Qy    181 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    252 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 311

Qy    241 GTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATT 300
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    312 GTTGAGATCTCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATT 371

Qy    301 GACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    372 GACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAG 431

Qy    361 TCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    432 TCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGG 491

Qy    421 AATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTAC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    492 AATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTAC 551

Qy    481 AAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    552 AAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCAC 611

Qy    541 ATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTAT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    612 ATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTAT 671

Qy    601 CCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    672 CCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAAC 731

Qy    661 TCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    732 TCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACA 791

Qy    721 ACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    792 ACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 851
```

RESULT 3
V11777
ID V11777 standard; DNA; 3026 BP.
AC V11777;
DT 25-SEP-1998 (first entry)
DE Variant of GABA-A receptor epsilon sub-unit related gene.
KW ss; GABA-A receptor; diagnosis; therapy; drug screening.
OS Mammalia.
FH Key Location/Qualifiers
FT CDS 55. .1479
FT /*tag= a
FT /product= "Variant of GABA-A receptor epsilon sub-unit
FT related protein"
PN DE19644501-A1.
PD 30-APR-1998.
PF 25-OCT-1996; 044501.
PR 25-OCT-1996; DE-044501.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

```
PI   Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR   WPI; 98-252096/23.
DR   P-PSDB; W59048.
PT   Protein related to GABA-A receptor sub-unit epsilon - useful for
PT   diagnosis, therapy or drug screening
PS   Disclosure; Fig 2; 12pp; German.
CC   The GABA-A receptor sub-unit epsilon related protein is used for the
CC   diagnosis and/or therapy of related disorders.  It can also be used to
CC   screen for substances that modulate the activity of the protein.
SQ   Sequence   3026 BP;    689 A;    853 C;    663 G;    821 T;


  Query Match             73.9%;  Score 576.4;  DB 1;  Length 3026;
  Best Local Similarity   87.6%;  Pred. No. 3.2e-175;
  Matches  683;  Conservative    0;  Mismatches    1;  Indels   96;  Gaps    1;

Qy      1 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    109 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 168

Qy     61 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    169 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 228

Qy    121 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 288

Qy    181 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    289 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 348

Qy    241 GTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATT 300
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349 GTTGAGATCTCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATT 408

Qy    301 GACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAG 360
          ||||||||||||||||||||||
Db    409 GACATCATCTTCTCCCAGACCT---------------------------------------- 431

Qy    361 TCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGG 420
                                                                    ||
Db    431 ------------------------------------------------------------GG 432

Qy    421 AATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTAC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    433 AATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTAC 492

Qy    481 AAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    493 AAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCAC 552

Qy    541 ATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTAT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    553 ATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTAT 612

Qy    601 CCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    613 CCTGAGAATGAGATGATCTACAAGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAAC 672

Qy    661 TCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    673 TCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAAATAATCACA 732

Qy    721 ACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    733 ACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 792


RESULT   4
V11778
ID   V11778 standard; DNA; 10697 BP.
AC   V11778;
DT   25-SEP-1998  (first entry)
DE   GABA-A receptor epsilon sub-unit related genomic sequence.
KW   ss; GABA-A receptor; diagnosis; therapy; drug screening.
OS   Mammalia.
FH   Key             Location/Qualifiers
FT   exon            1. .110
FT                   /*tag= a
FT                   /number= 1
FT   intron          111. .1217
FT                   /*tag= b
FT                   /number= 1
FT   exon            1218. .1435
FT                   /*tag= c
FT                   /number= 2
FT   intron          1436. .1883
FT                   /*tag= d
FT                   /number= 2
FT   exon            1884. .2172
FT                   /*tag= e
FT                   /number= 3
FT   intron          2173. .3169
FT                   /*tag= f
FT                   /number= 3
FT   exon            3170. .3252
FT                   /*tag= g
FT                   /number= 4
FT   intron          3253. .4559
FT                   /*tag= h
FT                   /number= 4
FT   exon            4560. .4697
FT                   /*tag= i
FT                   /number= 5
FT   intron          4698. .7962
FT                   /*tag= j
FT                   /number= 5
FT   exon            7963. .8115
FT                   /*tag= k
FT                   /number= 6
FT   intron          8116. .8255
FT                   /*tag= l
FT                   /number= 6
FT   exon            8256. .8455
FT                   /*tag= m
FT                   /number= 7
FT   intron          8456. .8738
FT                   /*tag= n
FT                   /number= 7
FT   exon            8739. .10697
FT                   /*tag= o
FT                   /number= 8
PN   DE19644501-A1.
PD   30-APR-1998.
PF   25-OCT-1996; 044501.
PR   25-OCT-1996; DE-044501.
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI   Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR   WPI; 98-252096/23.
PT   Protein related to GABA-A receptor sub-unit epsilon - useful for
PT   diagnosis, therapy or drug screening
PS   Disclosure; Fig 3; 12pp; German.
CC   The GABA-A receptor sub-unit epsilon related protein is used for the
CC   diagnosis and/or therapy of related disorders.  It can also be used to
CC   screen for substances that modulate the activity of the protein.
SQ   Sequence   10697 BP;    2524 A;    2704 C;    2471 G;    2991 T;


  Query Match             38.6%;  Score 301;  DB 1;  Length 10697;
  Best Local Similarity   98.4%;  Pred. No. 2.3e-86;
  Matches  304;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    202 CTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGC 261
          | || ||||| |||| ||||||||||||||||||||||||||||||| ||||||||||
Db   1865 CCGCCCCCTGCCATTAGAGAGAAGCCCACTGTGGTCACTGTTGAGATCTCCGTCAACAGC 1924
```

```
Qy    262 CTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACC 321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1925 CTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACC 1984

Qy    322 TGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAAT 381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1985 TGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAAT 2044

Qy    382 GTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAG 441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2045 GTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAG 2104

Qy    442 CATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTAC 501
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2105 CATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTAC 2164

Qy    502 ACAATTAGG 510
          |||||||||
Db   2165 ACAATTAGG 2173
```

```
RESULT   5
T02334
ID   T02334 standard; cDNA; 1565 BP.
AC   T02334;
DT   02-FEB-1996  (first entry)
DE   GABA-A receptor gamma-3 subunit cDNA.
KW   GABA-A receptor; gamma-aminobutyric acid receptor; gamma-3 subunit;
KW   ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             33. .1436
FT                   /*tag=  a
PN   WO9529234-A1.
PD   02-NOV-1995.
PF   12-APR-1995; G00834.
PR   22-APR-1994; GB-008064.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Whiting PJ;
DR   WPI; 95-382983/49.
DR   P-PSDB; R83968.
PT   New cell line expressing human GABA-A receptor sub-units - useful in
PT   drug screening and design
PS   Claim 5; Page 18-20; 30pp; English.
CC   A rat GABA-A receptor gamma-3 subunit cDNA probe was used to screen
CC   a human foetal brain cDNA library.  The single isolated clone
CC   lacked the 5' and 3' ends of the gamma-3 subunit coding region.
CC   These were obtd. by further PCR using primers based on the
CC   truncated sequence, giving a complete cDNA sequence (T02334).
CC   This can be used to express gamma-3 in transfected eukaryotic
CC   (pref. rodent fibroblast) cell lines for prodn. of hybrid GABA-A
CC   receptors having novel subunit compositions.
SQ   Sequence   1565 BP;    430 A;    397 C;    339 G;    399 T;
```

```
  Query Match           30.9%;  Score 240.8;  DB 1;  Length 1565;
  Best Local Similarity   61.5%;  Pred. No. 1.8e-67;
  Matches  386;  Conservative    0;  Mismatches  242;  Indels    0;  Gaps    0;

Qy    152 CAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTG 211
          | || |   |||  || || ||||   | || ||  | |||||  | || ||| | || |
Db    166 CCGACGTGACTCTTATTCTCAACAAGTTGCTAAGAGAGTATGATAAAAAGCTGAGGCCAG 225

Qy    212 GCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTC 271
            ||||||   || || || ||  |    ||||| ||    || |||||| ||||||||
Db    226 ATATTGGAATAAAACCGACCGTAATTGACGTTGACATTTATGTTAACAGCATTGGTCCTG 285

Qy    272 TCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACG 331
          | ||     || ||||||||||   ||||||||  | ||  | |||||||||   ||
Db    286 TGTCATCAATAAACATGGAATACCAAATTGACATATTTTTTGCTCAGACCTGGACAGATA 345

Qy    332 AACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCC 391
```

```
          |||||  | | ||||  |||  |  |   ||||  ||||||  ||||  ||||| |
Db    346 GTCGCCTTCGATTCAACAGCACAATGAAAATTCTTACTCTGAACAGCAACATGGTGGGGT 405

Qy    392 AGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCA 451
          | ||||||||  |||||| | ||  | ||||||||  |    |  | |  ||   |||||
Db    406 TAATCTGGATCCCAGACACCATCTTCCGCAATTCTAAAACCGCAGAGGCTCACTGGATCA 465

Qy    452 CCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGA 511
          |||  |||||  ||| |  ||||  || |  ||  || || ||  ||  | |||||  | |||
Db    466 CCACACCCAATCAGCTCCTCCGGATTTGGAATGACGGGAAAATCCTTTACACTTTGAGGC 525

Qy    512 TGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTT 571
          | |||||  ||||  |  |||   || ||  ||| ||  ||  || |||||    ||||| |
Db    526 TCACCATCAATGCTGAGTGCCAGCTGCAGCTGCACAACTTCCCCATGGACGAACACTCCT 585

Qy    572 GCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAA 631
          ||||  ||   |||||| |||| |  ||||||   |  |  | |||||  || |  |||  ||
Db    586 GCCCGCTGATTTTCTCCAGCTATGGCTATCCCAAAGAACAAATGATTTATAGATGGAGAA 645

Qy    632 ATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAG 691
          |        |  |       |||  |||| || |||  ||| |  ||||||||| || |  |
Db    646 AAAATTCAGTGCAGGCAGCTGACCAGAAATCATGGCGGCTTTATCAGTTTGACTTCATGG 705

Qy    692 GAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGA 751
          |  | || ||||  || |||||  | |||||  | |  |||||  |   | |||||||| |
Db    706 GCCTCAGAAACACCACAGAAATCGTGACAACGTCTGCAGGTGATTATGTTGTCATGACTA 765

Qy    752 TTTTCTTCAATGTGAGCAGGCGGTTTGG 779
          | |  ||  |  |||| |   |  | ||
Db    766 TATATTTTGAATTGAGTACAAGAATGGG 793
```

```
RESULT   6
T28988
ID   T28988 standard; cDNA; 1707 BP.
AC   T28988;
DT   06-JAN-1997  (first entry)
DE   Human GABA-A receptor alpha 4 subunit cDNA.
KW   GABA-A receptor; gamma-aminobutyric acid; alpha-4 subunit; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             39. .1703
FT                   /*tag=  a
PN   WO9610637-A1.
PD   11-APR-1996.
PF   29-SEP-1995; G02323.
PR   01-OCT-1994; GB-020010.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Le Bourdelles B,  Whiting PJ;
DR   WPI; 96-209359/21.
DR   P-PSDB; R97298.
PT   DNA encoding alpha-4 and delta subunit(s) of the human GABAa
PT   receptor  - also stably co-transfected eukaryotic cells expressing
PT   receptors contg. these subunit(s), used for screening and designing
PT   drugs
PS   Claim 9; Fig 2; 45pp; English.
CC   A cDNA clone (T28988) codes for the alpha-4 subunit (R97298) of the
CC   human GABA-A receptor.  It was isolated from human brain thalamus
CC   cDNA using primers (see also T28994-95) based on the 5' and 3'
CC   untranslated regions of a partial cDNA clone.  The cDNA can be
CC   incorporated into a vector and used to direct expression of the
CC   alpha-4 subunit in transfected cells, partic. rodent fibroblasts.
CC   Co-transfected host cells capable of expressing the alpha-4, delta
CC   (see also R97299) and beta subunits can be used to screen or design
CC   drugs that act on GABA-A receptors.
SQ   Sequence   1707 BP;    490 A;    373 C;    368 G;    476 T;
```

```
  Query Match           22.8%;  Score 177.8;  DB 1;  Length 1707;
  Best Local Similarity   56.5%;  Pred. No. 3.5e-47;
  Matches  354;  Conservative    0;  Mismatches  267;  Indels    6;  Gaps    1;

Qy    159 CTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGG 218
```

```
Db    182 CACCCGCATCCTGGACAGTTTGCTCGATGGTTATGACAACAGGCTGCGTCCTGGATTTGG 241

Qy    219 AGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTAT 278

Db    242 GGGTCCTGTTACAGAAGTGAAAACTGACATATATGTCACCAGCTTTGGACCTGTTTCTGA 301

Qy    279 CCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCT 338

Db    302 TGTTGAAGTGGAATACACAATGGATGTGTTCTTCAGGCAGACATGGATTGACAAAAGATT 361

Qy    339 CTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATG 398

Db    362 AAAATATGACGGCCCCATTGAAATTTTGAGATTGAACAATATGATGGTAACGAAAGTGTG 421

Qy    399 GATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCC 458

Db    422 GACCCCTGATACTTTCTTCAGGAATGGAAAGAAATCTGTCTCACATAATATGACAGCTCC 481

Qy    459 CAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCAT 518

Db    482 AAATAAGCTTTTTAGAATTATGAGAAATGGTACTATTTTATACACAATGAGACTCACCAT 541

Qy    519 TGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCT 578

Db    542 AAGTGCGGAGTGTCCCATGAGATTGGTGGATTTTCCCATGGATGGTCATGCATGCCCTGT 601

Qy    579 ATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA------ 633

Db    602 GAAATTCGGGAGTTATGCCTATCCAAAGAGTGAGATGATCTATACCTGGACAAAAGGTCC 661

Qy    633 TTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGG 692

Db    662 TGAGAAATCAGTTGAAGTTCCGAAGGAGTCTTCCAGCTTAGTTCAATATGATTTGATTGG 721

Qy    693 AGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGAT 752

Db    722 GCAAACCGTATCAAGTGAAACCATCAAATCAATTACGGGTGAATATATTGTTATGACGGT 781

Qy    753 TTTCTTCAATGTGAGCAGGCGGTTTGG 779

Db    782 TTACTTCCACCTCAGACGGAAGATGGG 808


RESULT   7
Q33129
ID   Q33129 standard; DNA; 2310 BP.
AC   Q33129;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-5 subunit gene.
KW   Primer; human; alpha-5; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             298. .1686
FT                   /*tag=  a
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   P-PSDB; R31186.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Claim 7; Fig 4; 43pp; English.
CC   The sequence given encodes the human alpha-5 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Rat alpha-5 cDNA was used as a probe
CC   and a human alpha-5 cDNA clone was isolated from a hippocampal cDNA
CC   library.  GABA-A receptor comprises a multimeric protein of molecular
CC   size 230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   2310 BP;    655 A;    582 C;    512 G;    561 T;


  Query Match             21.1%;  Score 164.8;  DB 1;  Length 2310;
  Best Local Similarity   53.8%;  Pred. No. 6.2e-43;
  Matches  365;  Conservative    0;  Mismatches  307;  Indels    6;  Gaps    1;

Qy    109 AAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATC 168

Db    394 ATGCCAACCAGTTCAGTGAAAGATGAGACCAATGACAACATCACGATATTTACCAGGATC 453

Qy    169 CTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCC 228

Db    454 TTGGATGGGCTCTTGGATGGCTACGACAACAGACTTCGGCCCGGGCTGGGAGAGCGCATC 513

Qy    229 ACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATG 288

Db    514 ACTCAGGTGAGGACCGACATCTACGTCACCAGCTTCGGCCCGGTGTCCGACACGGAAATG 573

Qy    289 GAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAAC 348

Db    574 GAGTACACCATAGACGTGTTTTTCCGACAAAGCTGGAAAGATGAAAGGCTTCGGTTTAAG 633

Qy    349 GACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGAC 408

Db    634 GGGCCCATGCAGCGCCTCCCTCTCAACAACCTCCTTGCCAGCAAGATCTGGACCCCAGAC 693

Qy    409 ACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATG 468

Db    694 ACGTTCTTCCACAACGGGAAGAAGTCCATCGCTCACAACATGACCACGCCCAACAAGCTG 753

Qy    469 GTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGA 528

Db    754 CTGCGGCTGGAGGACGACGGCACCCTGCTCTACACCATGCGCTTGACCATCTCTGCAGAG 813

Qy    529 TGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCT 588

Db    814 TGCCCCATGCAGCTTGAGGACTTCCCGATGGATGCGCACGCTTGCCCTCTGAAATTTGGC 873

Qy    589 AGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA------TTTCAAGCTT 642

Db    874 AGCTATGCGTACCCTAATTCTGAAGTCGTTTACGTCTGGACCAACGGCTCCACCAAGTCG 933

Qy    643 GAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAAC 702

Db    934 GTGGTGGTGGCGGAAGATGGCTCCAGACTGAACCAGTACCACCTGATGGGGCAGACGGTG 993

Qy    703 AAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAAT 762

Db    994 GGCACTGAGAACATCAGCACCAGCACAGGCGAATACACAATCATGACAGCTCACTTCCAC 1053

Qy    763 GTGAGCAGGCGGTTTGGC 780

Db   1054 CTGAAAAGGAAGATTGGC 1071


RESULT   8
Q69141
ID   Q69141 standard; DNA; 2310 BP.
AC   Q69141;
```

```
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha5 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             298. .1687
FT                   /*tag=  a
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   P-PSDB; R59864.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.4; 79pp; English.
CC   This receptor DNA may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   2310 BP;    654 A;    583 C;    513 G;    560 T;


  Query Match             21.1%;  Score 164.8;  DB 1;  Length 2310;
  Best Local Similarity   53.8%;  Pred. No. 6.2e-43;
  Matches  365;  Conservative    0;  Mismatches  307;  Indels    6;  Gaps    1;

Qy    109 AAGTCAACTGAGACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATC 168
Db    394 ATGCCAACCAGTTCAGTGAAAGATGAGACCAATGACAACATCACGATATTTACCAGGATC 453

Qy    169 CTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCC 228
Db    454 TTGGATGGGCTCTTGGATGGCTACGACAACAGACTTCGGCCCGGGCTGGGAGAGCGCATC 513

Qy    229 ACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATG 288
Db    514 ACTCAGGTGAGGACCGACATCTACGTCACCAGCTTCGGCCCGGTGTCCGACACGGAAATG 573

Qy    289 GAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAAC 348
Db    574 GAGTACACCATAGACGTGTTTTTCCGACAAAGCTGGAAAGATGAAAGGCTTCGGTTTAAG 633

Qy    349 GACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGAC 408
Db    634 GGGCCCATGCAGCGCCTCCCTCTCAACAACCTCCTTGCCAGCAAGATCTGGACCCCAGAC 693

Qy    409 ACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATG 468
Db    694 ACGTTCTTCCACAACGGGAAGAAGTCCATCGCTCACAACATGACCACGCCCAACAAGCTG 753

Qy    469 GTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGA 528
Db    754 CTGCGGCTGGAGGACGACGGCACCCTGCTCTACACCATGCGCTTGACCATCTCTGCAGAG 813

Qy    529 TGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCT 588
Db    814 TGCCCCATGCAGCTTGAGGACTTCCCGATGGATGCGCACGCTTGCCCTCTGAAATTTGGC 873

Qy    589 AGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA------TTTCAAGCTT 642
Db    874 AGCTATGCGTACCCTAATTCTGAAGTCGTTTACGTCTGGACCAACGGCTCCACCAAGTCG 933

Qy    643 GAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAAC 702
Db    934 GTGGTGGTGGCGGAAGATGGCTCCAGACTGAACCAGTACCACCTGATGGGGCAGACGGTG 993

Qy    703 AAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAAT 762
```

```
Db    994 GGCACTGAGAACATCAGCACCAGCACAGGCGAATACACAATCATGACAGCTCACTTCCAC 1053

Qy    763 GTGAGCAGGCGGTTTGGC 780
Db   1054 CTGAAAAGGAAGATTGGC 1071


RESULT   9
Q33130
ID   Q33130 standard; DNA; 1408 BP.
AC   Q33130;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-6 subunit gene.
KW   Primer; human; alpha-6; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             27. .1388
FT                   /*tag=  a
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   P-PSDB; R31187.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Claim 8; Fig 5; 43pp; English.
CC   The sequence given encodes the human alpha-6 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Rat alpha-6 cDNA was used as a probe
CC   and a human alpha-6 cDNA clone was isolated from a cerebellum cDNA
CC   library.  No full length cDNA's were isolated. To obtain a full length
CC   cDNA 3 clones were joined together using convenient restriction sites.
CC   GABA-A receptor comprises a multimeric protein of molecular size
CC   230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   1408 BP;    392 A;    321 C;    300 G;    395 T;


  Query Match             20.4%;  Score 159.2;  DB 1;  Length 1408;
  Best Local Similarity   54.4%;  Pred. No. 3e-41;
  Matches  345;  Conservative    0;  Mismatches  283;  Indels    6;  Gaps    1;

Qy    153 AGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGG 212
Db    116 AAACGTCAGTCGGATCCTGGACAACTTGCTTGAAGGCTATGACAATCGGCTGCGGCCGGG 175

Qy    213 CATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCT 272
Db    176 ATTTGGAGGTGCTGTCACTGAAGTCAAAACAGACATTTATGTGACCAGTTTTGGGCCCGT 235

Qy    273 CTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGA 332
Db    236 GTCAGATGTGGAGATGGAGTATACGATGGATGTTTTTTTTCGCCAGACCTGGACTGATGA 295

Qy    333 ACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCA 392
```

```
Db    296 GAGGTTGAAGTTTGGGGGGCCAACTGAGATTCTGAGTCTGAATAATTTGATGGTCAGTAA 355

Qy    393 GCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCAC 452
          | ||||  || |||||||||||| || |||  ||| | | ||    |  ||  | || ||
Db    356 AATCTGGACGCCTGACACCTTTTTCAGAAATGGTAAAAAGTCCATTGCTCACAACATGAC 415

Qy    453 CATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGAT 512
          |  || ||  |  |  || | ||      || |||| |    | || ||||| || ||| |
Db    416 AACTCCTAATAAACTCTTCAGAATAATGCAGAATGGAACCATTTTATACACCATGAGGCT 475

Qy    513 GACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTG 572
          |||||  |||| |  ||  |  |      || | |  ||||| ||||||   ||  ||||
Db    476 TACCATCAATGCTGACTGTCCCATGAGGCTGGTTAACTTTCCTATGGATGGGCATGCTTG 535

Qy    573 CCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA 632
          || ||    ||    |||| | | |||||  | | ||| || || || | |||| ||||
Db    536 TCCACTCAAGTTTGGGAGCTATGCTTATCCCAAAAGTGAAATCATATATACGTGGAAAAA 595

Qy    633 TTTCAAGCTTGAAATCAATGA------GAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 686
              ||| |       ||       | | || |  |  ||  |||||| |||| |
Db    596 AGGACCACTTTACTCAGTAGAAGTCCCAGAAGAATCTTCAAGCCTTCTCCAGTATGATCT 655

Qy    687 TACAGGAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCAT 746
          |  |||  |       | ||| | ||| | | |       |||||  | | |  | ||
Db    656 GATTGGACAAACAGTATCTAGTGAGACAATTAAATCTAACACAGGTGAATACGTTATAAT 715

Qy    747 GACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 780
          |||  ||| |||| |  ||   |||  | | |||
Db    716 GACAGTTTACTTCCACTTGCAAAGGAAGATGGGC 749


RESULT  10
Q69142
ID   Q69142 standard; DNA; 1408 BP.
AC   Q69142;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha6 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             27. .1388
FT                   /*tag=  a
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   P-PSDB; R59865.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.5; 79pp; English.
CC   This receptor DNA may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   1408 BP;    392 A;    321 C;    300 G;    395 T;


  Query Match             20.4%;  Score 159.2;  DB 1;  Length 1408;
  Best Local Similarity   54.4%;  Pred. No. 3e-41;
  Matches  345;  Conservative    0;  Mismatches  283;  Indels    6;  Gaps    1;

Qy    153 AGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGG 212
          | | | |  ||| |||||| |||   | ||       ||||||  |    ||||| || ||
Db    116 AAACGTCAGTCGGATCCTGGACAACTTGCTTGAAGGCTATGACAATCGGCTGCGGCCGGG 175

Qy    213 CATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCT 272
            ||||||       |||||  ||||     || ||    || | |||  |||| ||  |

Db    176 ATTTGGAGGTGCTGTCACTGAAGTCAAAACAGACATTTATGTGACCAGTTTTGGGCCCGT 235

Qy    273 CTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGA 332
          ||      | || ||||| || || || ||  |  | ||   |||||||||   || ||
Db    236 GTCAGATGTGGAGATGGAGTATACGATGGATGTTTTTTTTCGCCAGACCTGGACTGATGA 295

Qy    333 ACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCA 392
          |  |    |     |   |   ||||  |||   |||||||       ||||  ||  |
Db    296 GAGGTTGAAGTTTGGGGGGCCAACTGAGATTCTGAGTCTGAATAATTTGATGGTCAGTAA 355

Qy    393 GCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCAC 452
          | ||||  || |||||||||||| || |||  ||| | | ||    |  ||  | || ||
Db    356 AATCTGGACGCCTGACACCTTTTTCAGAAATGGTAAAAAGTCCATTGCTCACAACATGAC 415

Qy    453 CATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGAT 512
          |  || ||  |  |  || | ||      || |||| |    | || ||||| || ||| |
Db    416 AACTCCTAATAAACTCTTCAGAATAATGCAGAATGGAACCATTTTATACACCATGAGGCT 475

Qy    513 GACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTG 572
          |||||  |||| |  ||  |  |      || | |  |||||  ||||||   ||  ||||
Db    476 TACCATCAATGCTGACTGTCCCATGAGGCTGGTTAACTTTCCTATGGATGGGCATGCTTG 535

Qy    573 CCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA 632
          || ||    ||    |||| | | |||||  | | ||| || || || | |||| ||||
Db    536 TCCACTCAAGTTTGGGAGCTATGCTTATCCCAAAAGTGAAATCATATATACGTGGAAAAA 595

Qy    633 TTTCAAGCTTGAAATCAATGA------GAAGAACTCCTGGAAGCTCTTCCAGTTTGATTT 686
              ||| |       ||       | | || |  |  ||  |||||| |||| |
Db    596 AGGACCACTTTACTCAGTAGAAGTCCCAGAAGAATCTTCAAGCCTTCTCCAGTATGATCT 655

Qy    687 TACAGGAGTGAGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCAT 746
          |  |||  |       | ||| | ||| | | |       |||||  | | |  | ||
Db    656 GATTGGACAAACAGTATCTAGTGAGACAATTAAATCTAACACAGGTGAATACGTTATAAT 715

Qy    747 GACGATTTTCTTCAATGTGAGCAGGCGGTTTGGC 780
          |||  ||| |||| |  ||   |||  | | |||
Db    716 GACAGTTTACTTCCACTTGCAAAGGAAGATGGGC 749


RESULT  11
Q69140
ID   Q69140 standard; DNA; 1638 BP.
AC   Q69140;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha3 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             87. .1562
FT                   /*tag=  a
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   P-PSDB; R59863.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.3; 79pp; English.
CC   This receptor DNA may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   1638 BP;    430 A;    437 C;    364 G;    407 T;


  Query Match             19.0%;  Score 148;  DB 1;  Length 1638;
  Best Local Similarity   56.0%;  Pred. No. 1.3e-37;
```

```
  Matches  280;  Conservative    0;  Mismatches  220;  Indels    0;  Gaps    0;

Qy     128 CTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTA 187
           |||    |||   || |||   |  |       | |  | ||| || |    | | |||
Db     256 CTGATGACAGCACTGACAACATCACTATCTTCACCAGAATCTTGGATCGTCTTCTGGACG 315

Qy     188 ATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGA 247
             |||||| ||   ||||| |||||  |||||||        |||| || |    ||| |
Db     316 GCTATGACAACCGGCTGCGACCTGGGCTTGGAGATGCAGTGACTGAAGTGAAGACTGACA 375

Qy     248 TCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCA 307
           ||  ||| | |||  |||| ||| | ||   |   |||||||| ||||| |||||  |
Db     376 TCTACGTGACCAGTTTTGGCCCTGTGTCAGACACTGACATGGAGTACACTATTGATGTAT 435

Qy     308 TCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTG 367
           | ||    ||||| ||| | || ||| | ||     |   | | | || |  ||   |||
Db     436 TTTTTCGGCAGACATGGCATGATGAAAGACTGAAATTTGATGGCCCCATGAAGATCCTTC 495

Qy     368 TTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTA 427
             |||||        |||  ||  || | ||||  |||||||||| ||    |||   |
Db     496 CACTGAACAATCTCCTGGCTAGTAAGATCTGGACACCGGACACCTTCTTCCACAATGGCA 555

Qy     428 AGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATG 487
           |||   |   |  ||| | || |||| ||||||| || || || |  |     |  | |
Db     556 AGAAATCAGTGGCTCATAACATGACCACGCCCAACAAGCTGCTCAGATTGGTGGACAACG 615

Qy     488 GCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCA 547
           | |   | | || ||||| ||| | || ||| |||| |  ||  |  |||| ||  |||
Db     616 GAACCCTCCTCTATACAATGAGGTTAACAATTCATGCTGAGTGTCCCATCCATTTGGAAG 675

Qy     548 GATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGA 607
             ||||| ||||||   ||  | |||||  ||    ||    |||| | ||||| |
Db     676 ATTTTCCCATGGATGTGCATGCCTGCCCACTGAAGTTTGGAAGCTATGCCTATACAACAG 735

Qy     608 ATGAGATGATCTACAAGTGG 627
           |||  || | ||    |||
Db     736 CTGAAGTGGTTTATTCTTGG 755


RESULT  12
Q33128
ID   Q33128 standard; DNA; 1638 BP.
AC   Q33128;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-3 subunit gene.
KW   Primer; human; alpha-3; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             87. .1565
FT                   /*tag=  a
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   P-PSDB; R31185.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Claim 6; Fig 3; 43pp; English.
CC   The sequence given encodes the human alpha-3 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Bovine alpha-3 cDNA was used as a
CC   probe and an alpha-3 cDNA clone was isolated from a human foetal
CC   brain cDNA library, which was missing approx. 100 bp of the 5' end.
CC   This missing fragment was isolated by PCR.  The two fragments were
CC   ligated together to give a full length alpha-3 cDNA.    GABA-A
CC   receptor comprises a multimeric protein of molecular size 230-370 kD
CC   with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   1638 BP;    430 A;    436 C;    365 G;    407 T;


  Query Match           18.8%;  Score 146.4;  DB 1;  Length 1638;
  Best Local Similarity   55.8%;  Pred. No. 4.2e-37;
  Matches  279;  Conservative    0;  Mismatches  221;  Indels    0;  Gaps    0;

Qy     128 CTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTA 187
           |||    |||   || |||   |  |       | |  | ||| || |    | | |||
Db     256 CTGATGACAGCACTGACAACATCACTATCTTCACCAGAATCTTGGATCGTCTTCTGGACG 315

Qy     188 ATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGA 247
             |||||| ||   ||||| |||||  |||||||        |||| || |    ||| |
Db     316 GCTATGACAACCGGCTGCGACCTGGGCTTGGAGATGCAGTGACTGAAGTGAAGACTGACA 375

Qy     248 TCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCA 307
           ||  ||| | |||  |||| ||| | ||   |   |||||||| ||||| |||||  |
Db     376 TCTACGTGACCAGTTTTGGCCCTGTGTCAGACACTGACATGGAGTACACTATTGATGTAT 435

Qy     308 TCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTG 367
           | ||    ||||| ||| | || ||| | ||     |   | | | || |  ||   |||
Db     436 TTTTTCGGCAGACATGGCATGATGAAAGACTGAAATTTGATGGCCCCATGAAGATCCTTC 495

Qy     368 TTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTA 427
             |||||        |||  ||  || | ||||  |||||||||| ||    |||   |
Db     496 CACTGAACAATCTCCTGGCTAGTAAGATCTGGACACCGGACACCTTCTTCCACAATGGCA 555

Qy     428 AGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATG 487
           |||   |   |  ||| | || |||| ||||||| || || || |  |     |  | |
Db     556 AGAAATCAGTGGCTCATAACATGACCACGCCCAACAAGCTGCTCAGATTGGTGGACAACG 615

Qy     488 GCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCA 547
           | |   | | || ||||| ||| | || ||| |||| |  ||  |  |||| ||  |||
Db     616 GAACCCTCCTCTATACAATGAGGTTAACAATTCATGCTGAGTGTCCCATGCATTTGGAAG 675

Qy     548 GATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGA 607
             ||||| ||||||   ||  | |||||  ||    ||    |||| | ||||| |
Db     676 ATTTTCCCATGGATGTGCATGCCTGCCCACTGAAGTTTGGAAGCTATGCCTATACAACAG 735

Qy     608 ATGAGATGATCTACAAGTGG 627
           |||  || | ||    |||
Db     736 CTGAAGTGGTTTATTCTTGG 755


RESULT  13
Q33127
ID   Q33127 standard; DNA; 2189 BP.
AC   Q33127;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-2 subunit gene.
KW   Primer; human; alpha-3; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             214. .1569
FT                   /*tag=  a
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
```

```
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   P-PSDB; R31184.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Claim 5; Fig 2; 43pp; English.
CC   The sequence given encodes the human alpha-2 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Bovine alpha-2 cDNA was used as a
CC   probe and an alpha-2 cDNA clone was isolated from a human foetal
CC   brain cDNA library. GABA-A receptor comprises a multimeric protein
CC   of molecular size 230-270 kD with specific binding sites for various
CC   drugs including benzodiazepines, barbiturates, and beta-carbolines,
CC   in addition to the agonist ligand GABA.  The receptor is composed of
CC   several distinct types of subunit, which are divided into four classes
CC   (alpha, beta, gamma and delta) based on sequence homology.  To date
CC   six types of alpha, three types of beta, two types of gamma and one
CC   type of delta subunit have been identified.  It has been found that
CC   in addition to an alpha and a beta subunit, either gamma-1 or gamma-2
CC   is also required to confer benzodiazipine sensitivity.  The benzo-
CC   diazepine pharmacology of the receptor is largely dependent on the
CC   identity of the alpha and gamma subunits present.  Receptors
CC   containing a delta subunit do not appear to bind benzodiazepines.
SQ   Sequence   2189 BP;    640 A;    466 C;    418 G;    665 T;

  Query Match             18.1%;  Score 140.8;  DB 1;  Length 2189;
  Best Local Similarity   56.5%;  Pred. No. 3.1e-35;
  Matches  262;  Conservative    0;  Mismatches  202;  Indels    0;  Gaps    0;

Qy    164 GCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGA 223
          | || ||  |||   | |||  |  ||| ||  |    ||  | || ||  | ||||| |
Db    344 GAATTCTTGACAGACTTCTGGATGGTTACGATAATCGGCTTAGACCAGGACTGGGAGACA 403

Qy    224 AGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAG 283
              ||||  |||     | | |||  ||| | |||  |||| ||| ||||      ||
Db    404 GTATTACTGAAGTCTTCACTAACATCTACGTGACCAGTTTTGGCCCTGTCTCAGATACAG 463

Qy    284 ACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTT 343
          | ||||||||  || |||||  |  ||||    || |  ||| | || |||||  |    |
Db    464 ATATGGAATATACAATTGATGTTTTCTTTCGACAAAAATGGAAAGATGAACGTTTAAAAT 523

Qy    344 ACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCC 403
            || |   |  |  |    |||   || ||        |||  ||| |  | ||||  |
Db    524 TTAAAGGTCCTATGAATATCCTTCGACTAAACAATTTAATGGCTAGCAAAATCTGGACTC 583

Qy    404 CGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACC 463
          | || ||||||||   |||   ||||   |    |  ||| | || || ||||| ||
Db    584 CAGATACCTTTTTTCACAATGGGAAGAAATCAGTAGCTCATAATATGACAATGCCAAATA 643

Qy    464 AGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATG 523
          || || | || ||  |  | ||||| |   || |||| || || ||| | ||  || | |
Db    644 AGTTGCTTCGAATTCAGGATGATGGGACTCTGCTGTATACCATGAGGCTTACAGTTCAAG 703

Qy    524 CCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTT 583
          | | |||| || | ||| ||      || |||||||| |||| || || |||||    |
Db    704 CTGAATGCCCAATGCACTTGGAGGATTTCCCAATGGATGCTCATTCATGTCCTCTGAAAT 763

Qy    584 TCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGG 627
          |    |||| | | ||| |       ||| | |  || |  |||
Db    764 TTGGCAGCTATGCATATACAACTTCAGAGGTCACTTATATTTGG 807


RESULT  14
Q69139
ID   Q69139 standard; DNA; 2189 BP.
AC   Q69139;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha2 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             214. .1566
FT                   /*tag= a
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   P-PSDB; R59862.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.2; 79pp; English.
CC   This receptor DNA may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   2189 BP;    640 A;    466 C;    418 G;    665 T;

  Query Match             18.1%;  Score 140.8;  DB 1;  Length 2189;
  Best Local Similarity   56.5%;  Pred. No. 3.1e-35;
  Matches  262;  Conservative    0;  Mismatches  202;  Indels    0;  Gaps    0;

Qy    164 GCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGA 223
          | || ||  |||   | |||  |  ||| ||  |    ||  | || ||  | ||||| |
Db    344 GAATTCTTGACAGACTTCTGGATGGTTACGATAATCGGCTTAGACCAGGACTGGGAGACA 403

Qy    224 AGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAG 283
              ||||  |||     | | |||  ||| | |||  |||| ||| ||||      ||
Db    404 GTATTACTGAAGTCTTCACTAACATCTACGTGACCAGTTTTGGCCCTGTCTCAGATACAG 463

Qy    284 ACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTT 343
          | ||||||||  || |||||  |  ||||    || |  ||| | || |||||  |    |
Db    464 ATATGGAATATACAATTGATGTTTTCTTTCGACAAAAATGGAAAGATGAACGTTTAAAAT 523

Qy    344 ACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCC 403
            || |   |  |  |    |||   || ||        |||  ||| |  | ||||  |
Db    524 TTAAAGGTCCTATGAATATCCTTCGACTAAACAATTTAATGGCTAGCAAAATCTGGACTC 583

Qy    404 CGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACC 463
          | || ||||||||   |||   ||||   |    |  ||| | || || ||||| ||
Db    584 CAGATACCTTTTTTCACAATGGGAAGAAATCAGTAGCTCATAATATGACAATGCCAAATA 643

Qy    464 AGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATG 523
          || || | || ||  |  | ||||| |   || |||| || || ||| | ||  || | |
Db    644 AGTTGCTTCGAATTCAGGATGATGGGACTCTGCTGTATACCATGAGGCTTACAGTTCAAG 703

Qy    524 CCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTT 583
          | | |||| || | ||| ||      || |||||||| |||| || || |||||    |
Db    704 CTGAATGCCCAATGCACTTGGAGGATTTCCCAATGGATGCTCATTCATGTCCTCTGAAAT 763

Qy    584 TCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGG 627
          |    |||| | | ||| |       ||| | |  || |  |||
Db    764 TTGGCAGCTATGCATATACAACTTCAGAGGTCACTTATATTTGG 807


RESULT  15
Q25720
ID   Q25720 standard; DNA; 675 BP.
AC   Q25720;
DT   08-DEC-1992  (first entry)
DE   OmpF signal peptide coding sequence.
KW   Expression plasmid; gamma-aminobutyric acid; GABA; glycine; ss.
OS   Synthetic.
PN   J04144683-A.
PD   19-MAY-1992.
PF   05-OCT-1990; 267743.
PR   05-OCT-1990; JP-267743.
PA   (MITU ) MITSUBISHI KASEI CORP.
```

DR WPI; 92-214122/26.
PT Prepn. of N-terminal extracellular site protein - by culturing
PT E.coli transformed by a plasmid comprising the tac promoter, ribosome
PT binding site, etc.
PS Claim 1; Page 1; 12pp; Japanese.
CC The sequence given is the E. coli outer membrane protein OmpF signal
CC peptide coding sequence. This sequence is used in an expression
CC plasmid operably linked to the tac promoter, a ribosome binding
CC sequence and a sequence coding for the N-terminal extracellular site
CC of either the gamma-aminobutyric acid (GABA) A receptor alpha-
CC subunit, the GABA-A receptor beta-subunit or the glycine receptor
CC alpha-subunit. This expression plasmid can be used to transform E.
CC coli to produce an N-terminal extracellular site protein of ion
CC channel direct binding type receptor.
SQ Sequence 675 BP; 207 A; 145 C; 156 G; 167 T;

Query Match 17.9%; Score 139.4; DB 1; Length 675;
Best Local Similarity 56.1%; Pred. No. 4.6e-35;
Matches 263; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

```
Qy    159 CTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGG 218
          | |  | ||  || ||    ||||   |  ||||||| |    ||| | || ||  | ||
Db     45 CACCAGGATTTTGGACCGACTCCTAGATGGTTATGACAATCGCCTGAGACCGGGATTAGG 104

Qy    219 AGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTAT 278
          ||||      ||||  || |    ||| |||  ||||| |||  | || ||  | ||
Db    105 AGAGCGTGTAACTGAAGTGAAGACTGACATCTTCGTCACCAGTTTCGGACCCGTTTCAGA 164

Qy    279 CCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCT 338
          ||  || ||||||||| || || ||  |  | |||   || | |||| | || ||| |  |
Db    165 CCATGATATGGAATATACAATAGATGTATTTTTCCGTCAAAGCTGGAAGGATGAAAGGTT 224

Qy    339 CTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATG 398
              |  || |   |  |        ||     | ||| |    |||  ||  |  | ||
Db    225 AAAATTTAAAGGACCTATGACAGTACTCCGATTAAATAACCTAATGGCAAGTAAAATCTG 284

Qy    399 GATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCC 458
          ||  ||||| ||||||||    |||   |||| | |    |  ||  | || ||||||||
Db    285 GACTCCGGATACCTTTTTCCACAATGGAAAGAAGTCAGTGGCACACAACATGACCATGCC 344

Qy    459 CAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCAT 518
           ||| || |  | ||||||    |||| ||||   || |||||||| || ||  |||| |
Db    345 GAACAAGCTCCTGCGCATCACAGAGGACGGCACTTTGCTGTACACCATGAGACTGACGGT 404

Qy    519 TGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCT 578
              |||| |||  || | ||  ||       || || |||||| | ||  | ||||||||
Db    405 GAGAGCCGAATGTCCAATGCATTTGGAGGATTTCCCTATGGATGCCCATGCCTGCCCTCT 464

Qy    579 ATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGG 627
          |   ||    |||| | | ||| |       ||  |  | ||  |||||
Db    465 AAAATTTGGAAGCTATGCTTATACAAGAGCAGAAGTTGTTTATGAGTGG 513
```

Search completed: March 9, 2000, 22:45:20
Job time: 619 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2000, 02:00:26 ; Search time 3156.82 Seconds
(without alignments)
932.906 Million cell updates/sec

Title: US-09-030-832-41_COPY_95_874
Perfect score: 780
Sequence: 1 AGGGTCGAGGGACCTCAGAC.....ATGTGAGCAGGCGGTTTGGC 780

Scoring table: IDENTITY_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

Number of hits that pass the threshold : 9077268

1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*
44: gb_est25:*
45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_gss1:*
80: gb_gss2:*
81: gb_gss3:*
82: gb_gss4:*
83: em_gss1:*
84: em_gss2:*
85: em_gss3:*
86: em_gss4:*
87: gb_gss5:*
88: gb_gss6:*
89: gb_gss7:*
90: gb_gss8:*
91: gb_gss9:*
92: em_gss5:*
93: em_gss6:*
94: em_gss7:*
95: em_gss8:*
96: em_gss9:*
97: em_gss10:*
98: em_gss11:*
99: gb_gss10:*
100: gb_gss11:*
101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	283.8	36.4	436	26	W77939	W77939 zd71b07.r1
c	2	269.2	34.5	596	26	W72699	W72699 zd71b07.s1
	3	143.4	18.4	835	69	AU079558	AU079558 AU079558
	4	138.2	17.7	623	64	AW077068	AW077068 fj04d06.y
c	5	125.6	16.1	595	102	AQ411437	AQ411437 HS_5083_A
	6	120	15.4	900	50	AU067396	AU067396 AU067396
	7	118.8	15.2	780	50	AU066778	AU066778 AU066778

8	110.6	14.2	489	22	H10884	H10884 ym06c05.r1
9	106.4	13.6	730	47	AU051193	AU051193 AU051193
10	100.8	12.9	795	47	AU051757	AU051757 AU051757
11	99	12.7	790	69	AU080017	AU080017 AU080017
12	97.6	12.5	399	61	AI853304	AI853304 UI-M-BH0-
13	88.4	11.3	395	20	T28792	T28792 EST56588 Hu
14	88.2	11.3	649	61	AL035782	AL035782 DKFZp564O
c 15	85.2	10.9	1010	79	CNS00JJC	AL076351 Drosophil
16	84.2	10.8	780	40	AA981457	AA981457 ua35f10.r
17	78.4	10.1	363	22	R52300	R52300 yg79b08.r1
18	74.6	9.6	861	69	AU079488	AU079488 AU079488
19	72.4	9.3	559	64	AL120988	AL120988 DKFZp762J
20	71.4	9.2	382	22	R60404	R60404 yh04f08.r1
c 21	71.4	9.2	380	37	AA700894	AA700894 zj44a02.s
22	66.2	8.5	464	38	AA776176	AA776176 ae80c11.s
23	64.4	8.3	454	22	R25530	R25530 yg44g07.r1
c 24	63	8.1	203	74	AW204396	AW204396 UI-H-BI1-
25	61.6	7.9	526	47	AU051215	AU051215 AU051215
26	60.4	7.7	487	22	R24969	R24969 yg41f01.r1
27	60	7.7	430	64	AL119816	AL119816 DKFZp761H
c 28	58.2	7.5	914	87	AQ744135	AQ744135 HS_5507_A
29	47	6.0	272	31	AA317685	AA317685 EST19656
c 30	46.2	5.9	401	41	AI032204	AI032204 or96f07.s
c 31	46.2	5.9	538	79	FR0006685	Z90495 F.rubripes
32	44.6	5.7	419	21	R13383	R13383 yf76g06.r1
33	43	5.5	586	69	AW122941	AW122941 UI-M-BH2.
c 34	41.2	5.3	834	87	AQ748700	AQ748700 HS_5574_A
c 35	38	4.9	991	80	CNS015OV	AL105721 Drosophil
c 36	37.6	4.8	394	74	AW182872	AW182872 xp99a01.x
37	37.4	4.8	609	44	AU039865	AU039865 AU039865
38	37.4	4.8	564	50	AU061922	AU061922 AU061922
c 39	37.2	4.8	535	103	AQ482375	AQ482375 RPCI-11-2
c 40	37	4.7	547	88	AQ827943	AQ827943 HS_5437_B
c 41	36.6	4.7	424	90	AQ035081	AQ035081 CIT-HSP-2
42	36	4.6	421	42	AI098451	AI098451 uc05g03.r
43	36	4.6	340	69	AW120859	AW120859 UI-M-BH2.
c 44	35.8	4.6	1132	79	CNS007QP	AL050614 Drosophil
45	35.6	4.6	525	27	AA020424	AA020424 mh60e07.r

ALIGNMENTS

```
RESULT   1
W77939
LOCUS       W77939         436 bp    mRNA            EST       17-OCT-1996
DEFINITION  zd71b07.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
            IMAGE:346069 5' similar to SW:GAC4_CHICK P34904
            GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4 SUBUNIT PRECURSOR ;, mRNA
            sequence.
ACCESSION   W77939
VERSION     W77939.1  GI:1388445
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 436)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:838034.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Possible reversed clone: similarity on wrong strand
            Insert Length: 477    Std Error: 0.00
            Seq primer: mob.REGA+ET
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1. .436
                     /organism="Homo sapiens"
                     /db_xref="GDB:1271444"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:346069"
                     /clone_lib="Soares_fetal_heart_NbHH19W"
                     /sex="unknown"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTTT 3'),
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by
                     M.Fatima Bonaldo. This library was constructed from the
                     same fetus as the fetal lung library, Soares fetal lung
                     NbHL19W."
BASE COUNT      106 a    110 c    100 g    120 t
ORIGIN
```

```
  Query Match             36.4%;  Score 283.8;  DB 26;  Length 436;
  Best Local Similarity   99.3%;  Pred. No. 1.6e-74;
  Matches  285;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     149 AGGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTAT 208

Qy      61 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     209 GGCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAG 268

Qy     121 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATC 180
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     269 ACTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCTTGAACACTATC 328

Qy     181 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     329 CTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACT 388

Qy     241 GTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACAT 287
           ||||||||| |||||||||||||||||||||||||||||||||||||
Db     389 GTTGAGATCTCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACAT 435
```

```
RESULT   2
W72699/c
LOCUS       W72699         596 bp    mRNA            EST       17-OCT-1996
DEFINITION  zd71b07.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
            IMAGE:346069 3', mRNA sequence.
ACCESSION   W72699
VERSION     W72699.1  GI:1382696
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 596)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
```

```
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On May 18, 1995 this sequence version replaced gi:811335.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 477   Std Error: 0.00
            Seq primer: mob.REGA+ET
            High quality sequence stop: 425.
FEATURES             Location/Qualifiers
     source          1. .596
                     /organism="Homo sapiens"
                     /db_xref="GDB:1271444"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:346069"
                     /clone_lib="Soares_fetal_heart_NbHH19W"
                     /sex="unknown"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by
                     M.Fatima Bonaldo. This library was constructed from the
                     same fetus as the fetal lung library, Soares fetal lung
                     NbHL19W."
BASE COUNT      163 a    133 c    138 g    158 t      4 others
ORIGIN


  Query Match             34.5%;  Score 269.2;  DB 26;  Length 596;
  Best Local Similarity   97.6%;  Pred. No. 4.5e-70;
  Matches  282;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy       2 GGGTCGAGGGACCTCAGACTGAATCAAAGAATGAAGCCTCTTCCCGTGATGTTGTCTATG 61
           |||||||||||||||||||||| |||| || |||||| ||||||||||||||||||||||
Db     559 GGGTCGAGGGACCTCAGACTGANTCAAGGANTGAAGCNTCTTCCCGTGATGTTGTCTATG 500

Qy      62 GCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAGA 121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     499 GCCCCCAGCCCCAGCCTCTGGAAAATCAGCTCCTCTCTGAGGAAACAAAGTCAACTGAGA 440

Qy     122 CTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATCC 181
           ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     439 CTGAGACTGGGAGCAGAGTTGGCAAACTGCCAGAAGCCTCTCGCATCTTGAACACTATCC 380

Qy     182 TGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTC-ACT 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     379 TGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCAACT 320

Qy     241 GTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGG 289
           |||||||| |||||||||||||||||||||||||||||||||||||||
Db     319 GTTGAGATCTCCGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGG 271


RESULT   3
AU079558
LOCUS       AU079558      835 bp    mRNA            EST       20-OCT-1999
DEFINITION  AU079558 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-4466
            5', mRNA sequence.
ACCESSION   AU079558
VERSION     AU079558.1  GI:6084313
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 835)
  AUTHORS   Hashimoto,K., Kusuda,J., Toyoda,A., Tanuma,R., Ito,A., Hirata,M.,
            Suzuki,Y., Sasaki,M. and Sugano,S.
  TITLE     Isolation of full-length cDNA clones from a mouse brain cDNA
            library made by oligo-capping method
  JOURNAL   Unpublished (1999)
COMMENT     On Feb 18, 1999 this sequence version replaced gi:4299273.
            Contact: Katsuyuki Hashimoto
            Division of Genetic Resources
            National Institute of Infectious Diseases
            23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
            Email: khashi@nih.go.jp
            URL: http://www.nih.go.jp/yoken/genbank/.
FEATURES             Location/Qualifiers
     source          1. .835
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="MNCb-4466"
                     /clone_lib="Sugano mouse brain mncb"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="TOP10"
                     /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTT] double-stranded cDNA was
                     ligated to a DraIII adaptor [TGTTGGCCTACTGG] , digested
                     and cloned into dstinct DraIII sites of the pME18S-FL3.
                     XhoI sites just outside the DraIII sites can be used to
                     isolate the cDNA insert.  Size selection was performed to
                     exclude fragments <1.5 kb. Library was constructed by
                     Sugano et al. (University of Tokyo, Institute of Medical
                     Science).  Custom primer for sequencing: 5' end primer
                     [CTTCTGCTCTAAAAGCTGCG]"
BASE COUNT      221 a    180 c    209 g    212 t     13 others
ORIGIN


  Query Match             18.4%;  Score 143.4;  DB 69;  Length 835;
  Best Local Similarity   57.6%;  Pred. No. 3.1e-32;
  Matches  273;  Conservative    0;  Mismatches  199;  Indels    2;  Gaps    1;

Qy     161 CTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAG 220
           | || || ||| ||| | | ||| | |||||||| ||| ||||| ||||| |||| |
Db     282 CCCGTATTCTGGACAGTTTGCTGGATGGTTATGACAACAGGCTGCGTCCTGGATTTGGGG 341

Qy     221 AGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCC 280
               || |  || |    ||| ||    |||| |||| |||| ||  | |||
Db     342 GTCCTGTTACAGAAGTGAAAACTGATATATATGTCACCAGCTTTGGGCCCGTTTCTGATG 401

Qy     281 TAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCT 340
           | || |||||||||| || ||  | |||||   ||||| |||   ||| || | ||
Db     402 TTGAAATGGAATACACTATGGATGTGTTCTTCAGACAGACATGGATTGACAAAAGACTAA 461

Qy     341 GTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGA 400
             ||  ||| | |  |||| |   ||||||   |  |||| | | |  | ||||
Db     462 AATATGACGGCCCAATTGAAATCTTGAGGCTGAATAATATGATGGTCACCAAAGTTTGGA 521

Qy     401 TCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCA 460
           ||| || || || || |||||   ||||   |   |   ||| | || ||    || |
Db     522 CCCCTGATACTTTCTTCAGGAATGGAAAGAAATCTGTCTCACATAACATGACAGNTCCAA 581

Qy     461 ACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTG 520
           |  || |  |  | ||    |  ||||||   | || |||||||| ||  | |||||
Db     582 ATAAGCTTTTTAGAATTATGAGAAATGGCACTATTTTATACACAATGAGACTCACCATAA 641

Qy     521 ATGCCGGATGCTCACTCCACATGCTCAGATTTCC--AATGGATTCTCACTCTTGCCCTCT 578
           |||||||    | |   | |      ||||| |  |  |     |||  | |||||| |
```

```
Db    642 GTGCCGGAGTGCCCCATGAGACTGGNGGATTTTCCTATGGATGGGTCATGCCTGCCCTTT 701

Qy    579 ATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAA 632
          ||    || | ||||||| |  | | ||| |||||||||  |||   ||
Db    702 GAAATTTGGGAGTTATTCCTATNCCAAAAGTGAAATGATCTACACCTGGACCAA 755


RESULT  4
AW077068
LOCUS       AW077068      623 bp    mRNA            EST       14-OCT-1999
DEFINITION  fj04d06.y1 Zebrafish adult olfactory Danio rerio cDNA 5' similar to
            gb:X15376 GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT
            PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AW077068
VERSION     AW077068.1  GI:6032220
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
            Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
            Cyprinoidae; Cyprinidae; Rasborinae; Danio.
REFERENCE   1  (bases 1 to 623)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     On Dec 20, 1995 this sequence version replaced gi:1135328.
            Other_ESTs: fj04d06.x1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Seq primer: T3 ET from Amersham
            High quality sequence stop: 483.
FEATURES             Location/Qualifiers
     source          1. .623
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone_lib="Zebrafish adult olfactory"
                     /sex="mixed"
                     /tissue_type="Olfactory rosettes"
                     /dev_stage="adult"
                     /lab_host="D10Hb (Gibco BRL)"
                     /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; This
                     is a directionally cloned cDNA library from adult
                     Zebrafish olfactory epithelium."
BASE COUNT      145 a    151 c    146 g    179 t      2 others
ORIGIN


  Query Match           17.7%;  Score 138.2;  DB 64;  Length 623;
  Best Local Similarity   60.1%;  Pred. No. 9.8e-31;
  Matches  230;  Conservative    0;  Mismatches  153;  Indels    0;  Gaps    0;

Qy    397 TGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATG 456
          ||||| |||||||| |||||  | ||||||||  |   |  |||  |||  ||||||||
Db      1 TGGATTCCGGACACATTTTTCCGCAATTCTAAAAAAGCAGACGCCCATTGGATCACCACA 60

Qy    457 CCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACC 516
          |||||   |||| | || || |  || || ||      |  |||||||  | ||| |||||
Db     61 CCCAATAGGATGCTTCGGATATGGAATGACGGGCGTATACTGTACACTTTAAGGTTGACC 120

Qy    517 ATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCT 576
          ||||| || |  |||   ||  |  ||    |  ||||||||||||   || || || |||
Db    121 ATTGACGCAGAGTGCCAGCTTAAACTGAATAACTTTCCAATGGATGAGCATTCGTGTCCT 180

Qy    577 CTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGGAAAATTTC 636
          ||    ||||| || |    ||| ||  || | |||||  | |||||||| |       |
Db    181 CTCGAGTTCTCCAGTTACGGCTACCCCAAGGAGGAGATTGTATACAAGTGGAAGCGCAGC 240

Qy    637 AAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTG 696
            | ||| |    || |    |||||||   || | ||||||    |||   ||  ||
Db    241 TCTGTGGAAGTTGGAGATATCCGCTCCTGGCGTCTGTACCAGTTCTCCTTTGTTGGCCTG 300

Qy    697 AGCAACAAAACTGAAATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTC 756
          || || |   | ||  |  ||| ||        || || | | |||| | ||  | |||
Db    301 AGAAATACCTCAGAGGTTGTCAGGACTGTCTCAGGAGATTACGTGGTTCTTACAGTCTTC 360

Qy    757 TTCAATGTGAGCAGGCGGTTTGG 779
          ||  |  |||||||  |  | ||
Db    361 TTTGACCTGAGCAGAAGAATGGG 383


RESULT  5
AQ411437/c
LOCUS       AQ411437      595 bp    DNA             GSS       17-MAR-1999
DEFINITION  HS_5083_A1_A01_T7A RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=659 Col=1 Row=A, genomic survey sequence.
ACCESSION   AQ411437
VERSION     AQ411437.1  GI:4428630
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 595)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 659  row: A  column: 1
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 595.
FEATURES             Location/Qualifiers
     source          1. .595
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=659 Col=1 Row=A"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
BASE COUNT      181 a    156 c    137 g    110 t     11 others
ORIGIN
```

```
  Query Match            16.1%;  Score 125.6;  DB 102;  Length 595;
  Best Local Similarity   74.3%;  Pred. No. 5.8e-27;
  Matches  185;  Conservative    0;  Mismatches   60;  Indels    4;  Gaps    2;

Qy    252 CGTCAACAGCCTTGGTCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTT 311
          | ||  |||  |  || || |      | |  ||  ||||||| || | ||||||||||
Db    370 CATCCCCAGAGTGTGTGCTTTTCTGTCCTTCCACCAGGAATACCCCTTGGACATCATCTT 311

Qy    312 CT--CCCAGACCTGGTACGACGAACGCCTCT--GTTACAACGACACCTTTGAGTCTCTTG 367
           |  ||  ||| |||| ||| | |   || |  ||| | ||||||||||| || |||||
Db    310 TTTCCCAGGACGTGGTTCGATGTAGCGCTTTTGGTTGCTACGACACCTTTGGGTGTCTTG 251

Qy    368 TTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTA 427
          ||||| | ||||||||||||||||| | ||||| |||||| | ||||||||||  ||||||
Db    250 TTCTGTAGGGCAATGTGGTGAGCCTGTTATGGTTCCCGGCCGCCTTTTTTAGTGATTCTA 191

Qy    428 AGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATG 487
          |||| ||||||||||||| | || || ||||||  || | ||||||||||   || |||
Db    190 AGAGTACCCACGAGCATGNGTTCGCCGTGCCCACACAAAAGGTCCGCATCTCTCAGCATG 131

Qy    488 GCAAGGTGT 496
          |||||||||
Db    130 GCAAGGTGT 122


RESULT   6
AU067396
LOCUS       AU067396      900 bp    mRNA            EST       02-JUN-1999
DEFINITION  AU067396 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-3396
            5', mRNA sequence.
ACCESSION   AU067396
VERSION     AU067396.1  GI:4968133
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 900)
  AUTHORS   Hashimoto,K., Kusuda,J., Toyoda,A., Tanuma,R., Ito,A., Hirata,M.,
            Suzuki,Y., Sasaki,M. and Sugano,S.
  TITLE     Isolation of full-length cDNA clones from a mouse brain cDNA
            library made by oligo-capping method
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 5, 1998 this sequence version replaced gi:3189732.
            Contact: Katsuyuki Hashimoto
            Division of Genetic Resources
            National Institute of Infectious Diseases
            23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
            Email: khashi@nih.go.jp
            URL: http://www.nih.go.jp/yoken/genbank/.
FEATURES             Location/Qualifiers
     source          1. .900
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="MNCb-3396"
                     /clone_lib="Sugano mouse brain mncb"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="TOP10"
                     /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTTT] double-stranded cDNA was
                     ligated to a DraIII adaptor [TGTTGGCCTACTGG] , digested
                     and cloned into dstinct DraIII sites of the pME18S-FL3.
                     XhoI sites just outside the DraIII sites can be used to
                     isolate the cDNA insert.  Size selection was performed to
                     exclude fragments <1.5 kb. Library was constructed by
                     Sugano et al. (University of Tokyo, Institute of Medical
                     Science).  Custom primer for sequencing: 5' end primer
                     [CTTCTGCTCTAAAAGCTGCG]"
BASE COUNT      236 a    174 c    190 g    250 t     50 others
ORIGIN
```

```
  Query Match            15.4%;  Score 120;  DB 50;  Length 900;
  Best Local Similarity   57.0%;  Pred. No. 3.4e-25;
  Matches  266;  Conservative    0;  Mismatches  196;  Indels    5;  Gaps    3;

Qy    161 CTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAG 220
          | || || ||| ||| | | ||| | |||||||| |||  |||| ||||  |||| |
Db    216 CCCGTATTCTGGACAGTTTGCTGGATGGTTATGACAACAGGCTGCGTCCTGGATTTGGGG 275

Qy    221 AGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCC 280
              || |  || |    ||| ||    |||| |||| |||| ||  | |||
Db    276 GTCCTGTTACAGAAGTGAAAACTGATATATATGTCACCAGCTTTGGGCCCGTTTCTTATG 335

Qy    281 TAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCT 340
          | || ||||||||||| || ||  | ||||  |||| |||   ||| || | ||
Db    336 TTGAAATGGAATACACTATGGATGTGTTCTTCANACAGAC-TGGATTGACAAAAGACTAA 394

Qy    341 GTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGA 400
            ||  ||  | |  ||||    |    ||||||   |   |||| | | |    ||||
Db    395 AATATGACNGCCCAATTGAAATCTTGAGGCTGAATAATATGATGGTCACCAAAGNTTGGA 454

Qy    401 TCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCA 460
           ||| || |||||||| ||||||   ||||   |       ||| | || ||     |||
Db    455 CCCCTGATACCTTTTTCAGGAATGGAAAGAAATCTTGTCTNCATAACATGACAGCTTCCA 514

Qy    461 ACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTG 520
          |  || |  |  | ||    |  ||||||   | || ||| |||| ||  | |||||
Db    515 ATAAGCTTTTTAGAATTATGAGAAATGGCACTATTTTATACCCAATGAGACTCACCATAA 574

Qy    521 ATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTAT 580
           ||| |   || ||    |  ||      ||| | ||||||   ||  | |||| | |
Db    575 GTGCNGAGNGCCCA--TAAACTGGNGGATTTTTCTATGGATNGGCATGCCTGCCTTTTNA 632

Qy    581 CTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGG 627
            |  |      ||||||||||  | |  ||||| ||||||   |||
Db    633 AAT--TGGGAGNTTTCCTATCCCAAAAGGGAGATNATCTACCCCTGG 677


RESULT   7
AU066778
LOCUS       AU066778      780 bp    mRNA            EST       02-JUN-1999
DEFINITION  AU066778 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-2552
            5', mRNA sequence.
ACCESSION   AU066778
VERSION     AU066778.1  GI:4967515
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 780)
  AUTHORS   Hashimoto,K., Kusuda,J., Toyoda,A., Tanuma,R., Ito,A., Hirata,M.,
            Suzuki,Y., Sasaki,M. and Sugano,S.
  TITLE     Isolation of full-length cDNA clones from a mouse brain cDNA
            library made by oligo-capping method
  JOURNAL   Unpublished (1999)
COMMENT     On May 11, 1999 this sequence version replaced gi:4776633.
            Contact: Katsuyuki Hashimoto
            Division of Genetic Resources
            National Institute of Infectious Diseases
            23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
            Email: khashi@nih.go.jp
            URL: http://www.nih.go.jp/yoken/genbank/.
FEATURES             Location/Qualifiers
     source          1. .780
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="MNCb-2552"
                     /clone_lib="Sugano mouse brain mncb"
                     /sex="female"
                     /dev_stage="adult"
```

/lab_host="TOP10"
/note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT] double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG] , digested and cloned into dstinct DraIII sites of the pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer for sequencing: 5' end primer [CTTCTGCTCTAAAAGCTGCG]"
BASE COUNT 218 a 157 c 183 g 206 t 16 others
ORIGIN

Query Match 15.2%; Score 118.8; DB 50; Length 780;
Best Local Similarity 58.2%; Pred. No. 7.3e-25;
Matches 245; Conservative 0; Mismatches 173; Indels 3; Gaps 2;

```
Qy    161 CTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAG 220
          | || || ||| ||| | | |||  |  ||||||| |||  ||||| |||||  |||| |
Db    214 CCCGTATTCTGGACAGTTTGCTGGATGGTTATGACAACAGGCTGCGTCCTGGATTTGGGG 273

Qy    221 AGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCC 280
              || |  || |    ||| ||    |||| |||| |||| ||  | |||
Db    274 GTCCTGTTACAGAAGTGAAAACTGATATATATGTCACCAGCTTTGGGCCCGTTTCTGATG 333

Qy    281 TAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCT 340
          | || ||||||||||| || ||  | |||||   ||||| |||   ||| || | ||
Db    334 TTGAAATGGAATACACTATGGATGTGTTCTTCAGACAGACATGGATTGACAAAAGACTAA 393

Qy    341 GTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGA 400
            ||  ||| | |  ||||    |  ||||||   |  |||| | | |  | ||||
Db    394 AATATGACGGCCCAATTGAAATCTTGAGGCTGAATAATATGATGGTCACCAAAGTTTGGA 453

Qy    401 TCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCAC-CATGCCC 459
           ||| || ||||| || ||||||   ||||   |   |   ||| | || ||   | |
Db    454 CCCCTGATACCTTCTTCAGGAATGGAAAGAAATCTGTCTCACATAACATGACAGCTTCAA 513

Qy    460 AACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATT 519
          |   || |  |  | ||    |  ||||||  | || ||||||| ||  | |||||
Db    514 ATAAAGCTTTTTAGAATTATGAGAAATGGCACTATTTTATACACAATGAGACTNACCATA 573

Qy    520 GATGCCGGA--TGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTC 577
            |||||||    | ||    ||  |   |  ||||| ||||||   ||  | ||||||
Db    574 AGTGCCGGAATGCCCCATGAGACTGGTGGATTTTTCCTATGGATGGGCATGCCTGCCCTT 633

Qy    578 T 578
          |
Db    634 T 634
```

RESULT 8
H10884
LOCUS H10884 489 bp mRNA EST 26-JUN-1995
DEFINITION ym06c05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:47230 5' similar to gb:X14766 GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-1 SUBUNIT PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION H10884
VERSION H10884.1 GI:875704
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 489)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT On May 5, 1995 this sequence version replaced gi:798023.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1611
High quality sequence stops: 420
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1611 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 420.
FEATURES Location/Qualifiers
source 1. .489
/organism="Homo sapiens"
/db_xref="GDB:419771"
/db_xref="taxon:9606"
/clone="IMAGE:47230"
/clone_lib="Soares infant brain 1NIB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not I; Site_2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 142 a 101 c 120 g 124 t 2 others
ORIGIN

Query Match 14.2%; Score 110.6; DB 22; Length 489;
Best Local Similarity 56.9%; Pred. No. 1.7e-22;
Matches 203; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

```
Qy    159 CTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGG 218
          | |  | ||  || |||   ||||   |  ||||||| |    ||| | || ||  | ||
Db     23 CACCAGGATTTTGGACAGACTCCTAGATGGTTATGACAATCGCCTGAGACCAGGATTGGG 82

Qy    219 AGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTAT 278
          ||||      || |  || |    ||| |||  ||||| |||  | || ||  | ||
Db     83 AGAGCGTGTAACCGAAGTGAAGACTGATATCTTCGTCACCAGTTTCGGACCCGTTTCAGA 142

Qy    279 CCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCT 338
          ||  || ||||||||  || || ||  |  | |||   || | |||| | || ||| |  |
Db    143 CCATGATATGGAATATACAATAGATGTATTTTTCCGTCAAAGCTGGAAGGATGAAAGGTT 202

Qy    339 CTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATG 398
              |  || |   |  |       ||     | |||  |    |||  ||  |  | ||
Db    203 AAAATTTAAAGGACCTATGACAGTCCTCCGGTTAAATAACCTAATGGCAAGTAAAATCTG 262

Qy    399 GATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCC 458
          ||  |||||||| |||||    |||   |||| | |    |  ||  | || ||||||||
Db    263 GACTCCGGACACATTTTTCCACAATGGAAAGAAGTCAGTGGCCCACAACATGACCATGCC 322

Qy    459 CAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGAC 515
          |||| |  |  | || |||    |||||||||   || |||||| || ||| ||||
Db    323 CAACAAACTCCTGCGGATCACAGAGGATGGCACCTTGCTGTACACCATGAGGCTGAC 379
```

RESULT 9
AU051193
LOCUS AU051193 730 bp mRNA EST 18-MAR-1999
DEFINITION AU051193 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-1649 5', mRNA sequence.

```
ACCESSION   AU051193
VERSION     AU051193.1  GI:4434202
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 730)
  AUTHORS   Sasaki,M., Suzuki,Y., Watanabe,M., Imai,J., Shibui,A., Yoshida,K.,
            Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S.
  TITLE     Construction of mouse full length-enriched cDNA libraries by
            oligo-capping
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 22, 1998 this sequence version replaced gi:3246767.
            Contact: Katsuyuki Hashimoto
            Division of Genetic Resources
            National Institute of Infectious Diseases
            23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
            Email: khashi@nih.go.jp
            URL: http://www.nih.go.jp/yoken/genbank/
            Seq primer: 5' end primer: CTTCTGCTCTAAAAGCTGCG.
FEATURES             Location/Qualifiers
     source          1. .730
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="MNCb-1649"
                     /clone_lib="Sugano mouse brain mncb"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="TOP10"
                     /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTTT] double-stranded cDNA was
                     ligated to a DraIII adaptor [TGTTGGCCTACTGG] , digested
                     and cloned into dstinct DraIII sites of the pME18S-FL3.
                     XhoI sites just outside the DraIII sites can be used to
                     isolate the cDNA insert.  Size selection was performed to
                     exclude fragments <1.5 kb. Library was constructed by
                     Sugano et al. (University of Tokyo, Institute of Medical
                     Science).  Custom primer for sequencing: 5' end primer
                     [CTTCTGCTCTAAAAGCTGCG]"
BASE COUNT      166 a    196 c    187 g    157 t     24 others
ORIGIN
```

```
  Query Match             13.6%;  Score 106.4;  DB 47;  Length 730;
  Best Local Similarity   51.2%;  Pred. No. 3.7e-21;
  Matches  271;  Conservative    0;  Mismatches  255;  Indels    3;  Gaps    2;

Qy    163 CGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAG 222
          | || |||| |     |  ||      |||| ||  ||  | || || ||||||||||  |
Db    186 CCCAACCTGGATGGCTTAATGGAGGGCTATGCCCGAAACTTCCGACCAGGCATTGGAGGG 245

Qy    223 AAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTA 282
            ||      ||  |  |||   | |  ||   |||| |||  | | |||       |
Db    246 GCTCCTGNGAATGTGGCGCTTGCCCTAGAGGTGGCCAGCATTGACCATATCTNACAGGCA 305

Qy    283 GACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGT 342
          ||||||||||||||||     |  || |    || | ||||   |||    | || |
Db    306 NACATGGAATACACCATGACTGTGTTCCTGCATCANAGCTGGCGGGACAGCAGGCTGTCC 365

Qy    343 TACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATC 402
          ||||||  | ||    |||  |  |    ||| |  ||    | |||  | ||||||| ||
Db    366 TACAACCATACNAACGAGACCTTANGCCTGGACAGCCGCTTTGTGGACAAGCTATGGCTC 425

Qy    403 CCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAAC 462
          || ||||||||  |   |||| | ||     ||   |  |||||  | ||   |   |||
Db    426 CCTGACACCTTCATCGTGAATGCCAAATCTGCCTGGGTCCATGATGTGACTGNGGAAAAC 485

Qy    463 CAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGAT 522
          || |   |||  |  |    |||||   | | || ||||  ||  | || ||| |
Db    486 AAGCTTANCCGGCTACAGCCTGATGGGGNGATTTTATACAGCATNCGCATNACCTTCACA 545
```

```
Qy    523 GCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCT 582
          |  ||     |  || |   ||  |  ||| |||  |  ||    |||   ||
Db    546 ANGGCCTGTGACATGGACCTTGCCAAGTACCCACTGGGATGNCAGGANTGCATGCTGGAC 605

Qy    583 TTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACAAGTGGG--AAAATTTCAAGC 640
          |    |||| |  |||  ||    | || ||   |||  | ||||  | ||   | ||
Db    606 CT-ANAAGCTATNGCTACTCTTNTGAGGACATTGGCTATTATTGGGTCACAAAAACCAGA 664

Qy    641 TTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTAC 689
          ||||  |||  |  | ||      | ||    ||    || |||||||
Db    665 AGCTAATCCATGGGCTGGACAAGCTNNAACTTGGCCCAGTTCATTTTAC 713
```

```
RESULT  10
AU051757
LOCUS       AU051757      795 bp    mRNA            EST       18-MAR-1999
DEFINITION  AU051757 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-2436
            5', mRNA sequence.
ACCESSION   AU051757
VERSION     AU051757.1  GI:4434766
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 795)
  AUTHORS   Sasaki,M., Suzuki,Y., Watanabe,M., Imai,J., Shibui,A., Yoshida,K.,
            Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S.
  TITLE     Construction of mouse full length-enriched cDNA libraries by
            oligo-capping
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 22, 1998 this sequence version replaced gi:3247339.
            Contact: Katsuyuki Hashimoto
            Division of Genetic Resources
            National Institute of Infectious Diseases
            23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
            Email: khashi@nih.go.jp
            URL: http://www.nih.go.jp/yoken/genbank/
            Seq primer: 5' end primer: CTTCTGCTCTAAAAGCTGCG.
FEATURES             Location/Qualifiers
     source          1. .795
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="MNCb-2436"
                     /clone_lib="Sugano mouse brain mncb"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="TOP10"
                     /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTTT] double-stranded cDNA was
                     ligated to a DraIII adaptor [TGTTGGCCTACTGG] , digested
                     and cloned into dstinct DraIII sites of the pME18S-FL3.
                     XhoI sites just outside the DraIII sites can be used to
                     isolate the cDNA insert.  Size selection was performed to
                     exclude fragments <1.5 kb. Library was constructed by
                     Sugano et al. (University of Tokyo, Institute of Medical
                     Science).  Custom primer for sequencing: 5' end primer
                     [CTTCTGCTCTAAAAGCTGCG]"
BASE COUNT      171 a    190 c    171 g    179 t     84 others
ORIGIN
```

```
  Query Match             12.9%;  Score 100.8;  DB 47;  Length 795;
  Best Local Similarity   55.1%;  Pred. No. 1.9e-19;
  Matches  195;  Conservative    0;  Mismatches  159;  Indels    0;  Gaps    0;

Qy    163 CGCATCCTGAACACTATCCTGAGTAATTATGACCACAAACTGCGCCCTGGCATTGGAGAG 222
          | || |||| |     |  ||      |||| ||  ||  | || || ||||||||||
Db     84 CCCAACCTGGATGGNTTAATGGAGGGCTATGCCCGAAACTTCCGACCAGGCATTGGAGGT 143
```

```
Qy    223 AAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCCTTGGTCCTCTCTCTATCCTA 282
Db    144 GCTCCTGTGAATGTGGCGCTTGCCCTAGAGGTGGCCAGCATTGACCATATCTCAGAGGCA 203

Qy    283 GACATGGAATACACCATTGACATCATCTTCTCCCAGACCTGGTACGACGAACGCCTCTGT 342
Db    204 AACATGGAATACACCATGACTGTGTTCCTGCATCAGAGCTGGCGGGACAGCAGGCTGTCC 263

Qy    343 TACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATC 402
Db    264 TACAACCATACCAACGAGACCTTAGGCCTGGACAGCCGCTTTGTGGACAAGCTATGGCTC 323

Qy    403 CCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAAC 462
Db    324 CCTGACACCTTCATCGTGAATGCCAAATCTGCCTGGTTCCATGATGTGACTGTGGAAAAC 383

Qy    463 CAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACC 516
Db    384 AAGCTTATTCGCCTACAGCCTGATGGGGTGATTTTATACAGCATCCGCATNACC 437
```

```
RESULT  11
AU080017
LOCUS       AU080017      790 bp    mRNA            EST       20-OCT-1999
DEFINITION  AU080017 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-5087
            5', mRNA sequence.
ACCESSION   AU080017
VERSION     AU080017.1  GI:6084772
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 790)
  AUTHORS   Hashimoto,K., Kusuda,J., Toyoda,A., Tanuma,R., Ito,A., Hirata,M.,
            Suzuki,Y., Sasaki,M. and Sugano,S.
  TITLE     Isolation of full-length cDNA clones from a mouse brain cDNA
            library made by oligo-capping method
  JOURNAL   Unpublished (1999)
COMMENT     On Mar 10, 1998 this sequence version replaced gi:2948217.
            Contact: Katsuyuki Hashimoto
            Division of Genetic Resources
            National Institute of Infectious Diseases
            23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
            Email: khashi@nih.go.jp
            URL: http://www.nih.go.jp/yoken/genbank/.
FEATURES             Location/Qualifiers
     source          1. .790
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="MNCb-5087"
                     /clone_lib="Sugano mouse brain mncb"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="TOP10"
                     /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTTT] double-stranded cDNA was
                     ligated to a DraIII adaptor [TGTTGGCCTACTGG] , digested
                     and cloned into dstinct DraIII sites of the pME18S-FL3.
                     XhoI sites just outside the DraIII sites can be used to
                     isolate the cDNA insert.  Size selection was performed to
                     exclude fragments <1.5 kb. Library was constructed by
                     Sugano et al. (University of Tokyo, Institute of Medical
                     Science).  Custom primer for sequencing: 5' end primer
                     [CTTCTGCTCTAAAAGCTGCG]"
BASE COUNT      222 a    172 c    190 g    199 t      7 others
ORIGIN
```

```
  Query Match             12.7%;  Score 99;  DB 69;  Length 790;
  Best Local Similarity   49.0%;  Pred. No. 6.4e-19;
```

```
  Matches  264;  Conservative    0;  Mismatches  275;  Indels    0;  Gaps    0;

Qy    143 GCAAACTGCCAGAAGCCTCTCGCATCCTGAACACTATCCTGAGTAATTATGACCACAAAC 202
Db    114 GCAACATGTCATACGTGAAAGAGACAGTGGACCGACTGCTCAAAGGATATGACATTCGCT 173

Qy    203 TGCGCCCTGGCATTGGAGAGAAGCCCACTGTGGTCACTGTTGAGATCGCCGTCAACAGCC 262
Db    174 TGCGGCCGGACTTTGGAGGGCCCCCGGTGGACGTCGGGATGCGGATCGATGTCGCCAGCA 233

Qy    263 TTGGTCCTCTCTCTATCCTAGACATGGAATACACCATTGACATCATCTTCTCCCAGACCT 322
Db    234 TAGACATGGTCTCGGAAGTGAATATGGATTATACACTCACCATGTATTTCCAGCAGTCTT 293

Qy    323 GGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTTCTGAATGGCAATG 382
Db    294 GGAAGGACAAGAGGCTTTCATATTCTGGAATCCCATTAAATCTGACCCTTGACAACAGAG 353

Qy    383 TGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAGAGGACCCACGAGC 442
Db    354 TAGCTGACCAACTCTGGGTACCAGACACCTACTTTCTCAATGACAAGAAATCATTTGTGC 413

Qy    443 ATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGCAAGGTGTTGTACA 502
Db    414 ATGGGGTCACAGTGAAAAACCGAATGATCAGGCTGCATCCTGATGGAACTGTTCTCTATG 473

Qy    503 CAATTAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCAGATTTCCAATGGATT 562
Db    474 GACTACGGATCACAACCACTGCAGCATGCATGATGGATCTTCGAAGATACCCTCTGGATG 533

Qy    563 CTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGAATGAGATGATCTACA 622
Db    534 AGCAAAACTGCACCCTGGAGATTGAAAGTTATGGCTATACCACGGATGACATCGAATTTT 593

Qy    623 AGTGGGAAAATTTCAAGCTTGAAATCAATGAGAAGAACTCCTGGAAGCTCTTCCAGTTT 681
Db    594 ACTGGAATGGAGGAGAGGGAGCAGTAACTGGGGTCAATAAAATTGAGCTTCCCCAATTT 652
```

```
RESULT  12
AI853304
LOCUS       AI853304      399 bp    mRNA            EST       15-JUL-1999
DEFINITION  UI-M-BH0-ajl-g-02-0-UI.s1 NIH_BMAP_M_S1 Mus musculus cDNA clone
            UI-M-BH0-ajl-g-02-0-UI 3', mRNA sequence.
ACCESSION   AI853304
VERSION     AI853304.1  GI:5497210
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 399)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     On Dec 20, 1995 this sequence version replaced gi:1135354.
            Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to identify it as a clone from the
            normalized hypothalamus library cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
            available by the means that is soon to be determined. When NIH
```

```
           determines the means for distribution of the BMAP cDNA clones, this
           record will be updated accordingly when that means is determined.
           Seq primer: M13 Forward
           POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .399
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-BH0-ajl-g-02-0-UI"
                     /clone_lib="NIH_BMAP_M_S1"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_M_S1 library is a subtracted library derived from
                     a mixture of normalized libraries from ten regions of the
                     mouse brain (cerebellum, brain stems, olfactory bulbs,
                     hypothalamus, cortex, amygdala, basal ganglia, pineal
                     gland, striatum, hipoccampus). The driver used for
                     subtraction consisted of a pool of 20,000 cDNA clones
                     obtained from non-normalized and normalized libraries of
                     these ten regions of the mouse brain.
                     TAG_LIB=NIH_BMAP_M_S1
                     TAG_TISSUE=hypothalamus
                     TAG_SEQ=CGGTA"
BASE COUNT      117 a     89 c     89 g    104 t
ORIGIN


  Query Match             12.5%;  Score 97.6;  DB 61;  Length 399;
  Best Local Similarity   56.6%;  Pred. No. 1.2e-18;
  Matches  181;  Conservative    0;  Mismatches  139;  Indels    0;  Gaps    0;

Qy    308 TCTTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTG 367
          | || |  || |  ||| | || ||| |  |    | ||| |   || |       ||
Db     12 TTTTTTAACAAAGTTGGAAGGATGAAAGATTAAAATTCAAAGGACCCATGACAGTGCTCC 71

Qy    368 TTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTA 427
            || ||   |  | |||  ||  |  | ||||  || || || |||||    |||  |
Db     72 GGCTAAACAACCTTATGGCCAGTAAAATCTGGACTCCAGATACATTTTTCCACAATGGAA 131

Qy    428 AGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATG 487
          ||| | |    |  ||  | || |||||||| ||  || |  | || |||    ||||||
Db    132 AGAAGTCTGTGGCCCACAACATGACCATGCCTAATAAGCTCCTGCGTATCACAGAGGATG 191

Qy    488 GCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCA 547
          |||   || ||||||| || ||| ||||| |    || | |||| || | ||| ||
Db    192 GCACTCTGCTGTACACCATGAGGTTGACCGTGAGAGCTGAATGCCCAATGCACTTGGAAG 251

Qy    548 GATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCTATCCTGAGA 607
            || || |||||| | ||  | ||||| |||   |||   |||| | | ||| |
Db    252 ACTTCCCTATGGATGCCCATGCCTGCCCACTAAAATTCGGAAGCTATGCTTATACAAGAG 311

Qy    608 ATGAGATGATCTACAAGTGG 627
          ||  |  ||||  |||||
Db    312 CAGAAGTTGTCTATGAGTGG 331


RESULT  13
T28792
LOCUS       T28792         395 bp    mRNA            EST       06-SEP-1995
DEFINITION  EST56588 Human Brain Homo sapiens cDNA 5' end similar to
            gamma-aminobutyric acid (GABA) A receptor, alpha 5 (HT:911), mRNA
            sequence.
ACCESSION   T28792
VERSION     T28792.1  GI:610890
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 395)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,
            Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., HinkleJr,P.S.,
            Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
            Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T.,
            Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
            Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,
            Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A.,
            Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,
            Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
            Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,
            Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,
            Yu,G.-L., Ruben,S.M., , Dillon,P.J., Fannon,M.R., Rosen,C.A.,
            Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
  TITLE     Initial Assessment of Human Gene Diversity and Expression Patterns
            Based Upon 83 Million Basepairs of cDNA Sequence
  JOURNAL   Nature 377, 3-174 (1995)
  MEDLINE   96026280
COMMENT     Contact: Venter, JC
            The Institute for Genomic Research
            932 Clopper Rd, Gaithersburg, MD 20878
            Tel: 3018699056
            Fax: 3018699423
            Email: tdbinfo@tdb.tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please contact the TIGR Database
            (tdbinfo@tdb.tigr.org)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .395
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):103726"
                     /db_xref="taxon:9606"
                     /clone_lib="Human Brain"
                     /note="Organ: brain"
BASE COUNT       95 a    126 c     99 g     74 t      1 others
ORIGIN


  Query Match             11.3%;  Score 88.4;  DB 20;  Length 395;
  Best Local Similarity   57.7%;  Pred. No. 7.1e-16;
  Matches  158;  Conservative    0;  Mismatches  116;  Indels    0;  Gaps    0;

Qy    359 AGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTA 418
          ||   ||   ||| ||   |    | |  ||| || | |||| ||| ||||| || ||
Db      5 AGCGCCTCCCTCTCAACAACCTCCTTGCCAGCAAGATCTGGACCCCAGACACGTTCTTCC 64

Qy    419 GGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCT 478
            ||    |||| | ||  ||  ||  | || |||| ||||||| || || | ||  |
Db     65 ACAACGGGAAGAAGTCCATCGCTCACAACATGACCACGCCCAACAAGCTGCTGCGGCTGG 124

Qy    479 ACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCC 538
          |  | || ||||   || | ||||| ||  |  |||||||   ||| |  ||| |  | |
Db    125 AGGACGACGGCACCCTGCTCTACACCATGCGCTTGACCATCTCTGCAGAGTGCCCCATGC 184

Qy    539 ACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCCT 598
          |  |        || || |||||| | ||| ||||||||||    ||    |||| | | |
Db    185 AGCTTGAGGACTTCCCGATGGATGCGCACGCTTGCCCTCTGAAATTTGGCAGCTATGCGT 244

Qy    599 ATCCTGAGAATGAGATGATCTACAAGTGGGAAAA 632
          | ||| |   |||  |  | |||   |||   ||
Db    245 ACCCTAATTCTGAAGTCGTTTACGTCTGGACCAA 278


RESULT  14
AL035782
LOCUS       AL035782       649 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp564O1182_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
            DKFZp564O1182 5', mRNA sequence.
ACCESSION   AL035782
```

```
VERSION     AL035782.1  GI:5405419
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   Poustka,A., Klein,M., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Poustka, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 5, 1998 this sequence version replaced gi:3189585.
            Contact: Poustka A.J.
            Department Lehrach
            Max-Planck-Institute for Molecular Genetics
            Ihnestrasse 73, 14195 Berlin, Germany
            Tel: +49-30-84131623
            Fax: +49-30-84131128
            Email: poustka@mpimg-berlin-dahlem.mpg.de
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by DKFZ within the cDNA sequencing consortium of the
            German Genome Project.
            s1 sequence also available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .649
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp564O1182"
                     /clone_lib="564 (synonym: hfbr2)"
                     /tissue_type="brain"
                     /dev_stage="fetal"
                     /lab_host="Xl-2blue"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
BASE COUNT      141 a    214 c    179 g    115 t
ORIGIN
```

```
  Query Match             11.3%;  Score 88.2;  DB 61;  Length 649;
  Best Local Similarity   54.2%;  Pred. No. 1e-15;
  Matches  225;  Conservative    0;  Mismatches  183;  Indels    7;  Gaps    2;

Qy    358 GAGTCTCTTGTTCTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTT 417
          ||||  ||   ||| ||   |    | |  ||| || | |||| ||| ||||| || ||
Db    235 GAGTGCCTCCCTCTCAACAACCTCCTTGCCAGCAAGATCTGGACCCCAGACACGTTCTTC 294

Qy    418 AGGAATTCTAAGAGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATC 477
            ||    |||| | ||  ||  ||  | || |||| ||||||| || || | ||  |
Db    295 CACAACGGGAAGAAGTCCATCGCTCACAACATGACCACGCCCAACAAGCTGCTGCGGCTG 354

Qy    478 TACAAGGATGGCAAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTC 537
          | | || ||||   || | ||||| ||  |  |||||||   ||| |  ||| |  |
Db    355 GAGGACGACGGCACCCTGCTCTACACCATGCGCTTGACCATCTCTGCAGAGTGCCCCATG 414

Qy    538 CACATGCTCAGATTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTCTCTAGCTTTTCC 597
          ||  |     || |||| |||||| | ||| ||||||||||    ||    |||| | |
Db    415 CAGCT-TGAGGACTTCCGATGGATGCGCACGCTTGCCCTCTGAAATTTGGCAGCTATGCG 473

Qy    598 TATCCTGAGAATGAGATGATCTACAAGTGGGAAAA------TTTCAAGCTTGAAATCAAT 651
          || ||| |   |||  |  |||||   |||   ||          ||||   |   |
Db    474 TACCCTAATTCTGAAGTCGTCTACGTCTGGACCAACGGCTTCACCAAGTCGGTGGTGGTG 533

Qy    652 GAGAAGAACTCCTGGAAGCTCTTCCAGTTTGATTTTACAGGAGTGAGCAACAAAACTGAA 711
          | | |  |   ||  |  ||   |||||   |  | |  ||   ||        |||||
Db    534 GCGGAAGATGGCTTCAGACTGAACCAGTACCACCTGATGGGGCAGACGGTGGGCACTGAG 593

Qy    712 ATAATCACAACCCCAGTTGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGA 766
          |  ||||  |||      || || | ||   |||||||   |  |||  |  |||
Db    594 AACATCAGCACCAGCACAGGCGAATACACAATCATGACAGCTCACTTTCACCTGA 648
```

```
RESULT 15
CNS00JJC/c
LOCUS       CNS00JJC     1010 bp    DNA             GSS       03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR38F08 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL076351
VERSION     AL076351.1  GI:4955929
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1010)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1010
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR38F08"
                     /note="end : TET3"
BASE COUNT      321 a    162 c    168 g    242 t    117 others
ORIGIN
```

```
  Query Match             10.9%;  Score 85.2;  DB 79;  Length 1010;
  Best Local Similarity   54.3%;  Pred. No. 1e-14;
  Matches  150;  Conservative    9;  Mismatches  117;  Indels    0;  Gaps    0;

Qy    310 TTCTCCCAGACCTGGTACGACGAACGCCTCTGTTACAACGACACCTTTGAGTCTCTTGTT 369
          |||  |||  |||||   ||  |||: |||   | | | | | ||   ||  | || |
Db    456 TTCCGCCAATCCTGGGTGGATAAACKTCTCGCATTCGAGGGCGCCCAGGACMCGCTGGCA 397

Qy    370 CTGAATGGCAATGTGGTGAGCCAGCTATGGATCCCGGACACCTTTTTTAGGAATTCTAAG 429
          ||||    :  : || ||   | : | ||||  |||:  || ||||||   ||    |||
Db    396 CTGAKCTTYTCKWTGTTGGCACGKWTTTGGAAGCCGKTTACKTTTTTTTACAACGGCAAG 337

Qy    430 AGGACCCACGAGCATGAGATCACCATGCCCAACCAGATGGTCCGCATCTACAAGGATGGC 489
          || : :   |||   ||| |||| ||| ||  |: | ||  |  ||||  || | ||
Db    336 CAGAGYTWTTTGCACACGATTACCACGCCAAATAAKTTTGTGAGGTTCTATCAGAACGGA 277

Qy    490 AAGGTGTTGTACACAATTAGGATGACCATTGATGCCGGATGCTCACTCCACATGCTCAGA 549
          |||:||||| | |   || |||| ||| | ||||| ||| |  |  |  ||  |
Db    276 CGCGTGYTGTACTCCAGCCGGCTGACAATTAAAGCCGGCTGCCCCATGAATCTGGCCGAT 217

Qy    550 TTTCCAATGGATTCTCACTCTTGCCCTCTATCTTTC 585
          ||||||||||||   ||    || ||| |    |||
Db    216 TTTCCAATGGATATACAAAAGTGTCCTTTGAAATTC 181
```

Search completed: March 11, 2000, 02:00:34
Job time: 3222 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 10, 2000, 09:00:30 ; Search time 3678.19 Seconds
(without alignments)
-767.269 Million cell updates/sec

Title: US-09-030-832-41_COPY_880_1558
Perfect score: 679
Sequence: 1 TGCCTTTCAAAACTATGTCC.....GGCTTGTTTGCCTTAACTTG 679

Scoring table: IDENTITY_NUC

Searched: 4799332 seqs, -2078174120 residues

Database : Pending_Patents_NA:*

Word size : 0

Number of hits that pass the threshold : 9598654

1: /cgn2_6/ptodata/2/pna/PCTUS9_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US081A_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US081B_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US081C_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US081D_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US082A_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US082B_COMB.seq:*
10: /cgn2_6/ptodata/2/pna/US082C_COMB.seq:*
11: /cgn2_6/ptodata/2/pna/US083A_COMB.seq:*
12: /cgn2_6/ptodata/2/pna/US083B_COMB.seq:*
13: /cgn2_6/ptodata/2/pna/US084A_COMB.seq:*
14: /cgn2_6/ptodata/2/pna/US084B_COMB.seq:*
15: /cgn2_6/ptodata/2/pna/US084C_COMB.seq:*
16: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*
17: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*
18: /cgn2_6/ptodata/2/pna/US087A_COMB.seq:*
19: /cgn2_6/ptodata/2/pna/US087B_COMB.seq:*
20: /cgn2_6/ptodata/2/pna/US087C_COMB.seq:*
21: /cgn2_6/ptodata/2/pna/US088A_COMB.seq:*
22: /cgn2_6/ptodata/2/pna/US088B_COMB.seq:*
23: /cgn2_6/ptodata/2/pna/US088C_COMB.seq:*
24: /cgn2_6/ptodata/2/pna/US088D_COMB.seq:*
25: /cgn2_6/ptodata/2/pna/US089A_COMB.seq:*
26: /cgn2_6/ptodata/2/pna/US089B_COMB.seq:*
27: /cgn2_6/ptodata/2/pna/US089C_COMB.seq:*
28: /cgn2_6/ptodata/2/pna/US089D_COMB.seq:*
29: /cgn2_6/ptodata/2/pna/US089E_COMB.seq:*
30: /cgn2_6/ptodata/2/pna/US089F_COMB.seq:*
31: /cgn2_6/ptodata/2/pna/US089G_COMB.seq:*
32: /cgn2_6/ptodata/2/pna/US089H_COMB.seq:*
33: /cgn2_6/ptodata/2/pna/US089I_COMB.seq:*
34: /cgn2_6/ptodata/2/pna/US090A_COMB.seq:*
35: /cgn2_6/ptodata/2/pna/US090B_COMB.seq:*
36: /cgn2_6/ptodata/2/pna/US090C_COMB.seq:*
37: /cgn2_6/ptodata/2/pna/US090D_COMB.seq:*
38: /cgn2_6/ptodata/2/pna/US090E_COMB.seq:*
39: /cgn2_6/ptodata/2/pna/US091A_COMB.seq:*
40: /cgn2_6/ptodata/2/pna/US091B_COMB.seq:*
41: /cgn2_6/ptodata/2/pna/US091C_COMB.seq:*
42: /cgn2_6/ptodata/2/pna/US092A_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US092B_COMB.seq:*
44: /cgn2_6/ptodata/2/pna/US092C_COMB.seq:*
45: /cgn2_6/ptodata/2/pna/US092D_COMB.seq:*
46: /cgn2_6/ptodata/2/pna/US092E_COMB.seq:*
47: /cgn2_6/ptodata/2/pna/US093A_COMB.seq:*
48: /cgn2_6/ptodata/2/pna/US093B_COMB.seq:*
49: /cgn2_6/ptodata/2/pna/US093C_COMB.seq:*
50: /cgn2_6/ptodata/2/pna/US093D_COMB.seq:*
51: /cgn2_6/ptodata/2/pna/US093E_COMB.seq:*
52: /cgn2_6/ptodata/2/pna/US093F_COMB.seq:*
53: /cgn2_6/ptodata/2/pna/US094A_COMB.seq:*
54: /cgn2_6/ptodata/2/pna/US094B_COMB.seq:*
55: /cgn2_6/ptodata/2/pna/US6000_COMB.seq:*
56: /cgn2_6/ptodata/2/pna/US6001A_COMB.seq:*
57: /cgn2_6/ptodata/2/pna/US6001B_COMB.seq:*
58: /cgn2_6/ptodata/2/pna/US6002A_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6002B_COMB.seq:*
60: /cgn2_6/ptodata/2/pna/US6002C_COMB.seq:*
61: /cgn2_6/ptodata/2/pna/US6003A_COMB.seq:*
62: /cgn2_6/ptodata/2/pna/US6003B_COMB.seq:*
63: /cgn2_6/ptodata/2/pna/US6004A_COMB.seq:*
64: /cgn2_6/ptodata/2/pna/US6004B_COMB.seq:*
65: /cgn2_6/ptodata/2/pna/US6004C_COMB.seq:*
66: /cgn2_6/ptodata/2/pna/US6005_COMB.seq:*
67: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
68: /cgn2_6/ptodata/2/pna/US6007_COMB.seq:*
69: /cgn2_6/ptodata/2/pna/US6008A_COMB.seq:*
70: /cgn2_6/ptodata/2/pna/US6008B_COMB.seq:*
71: /cgn2_6/ptodata/2/pna/US6008C_COMB.seq:*
72: /cgn2_6/ptodata/2/pna/US6009A_COMB.seq:*
73: /cgn2_6/ptodata/2/pna/US6009B_COMB.seq:*
74: /cgn2_6/ptodata/2/pna/US6010A_COMB.seq:*
75: /cgn2_6/ptodata/2/pna/US6010B_COMB.seq:*
76: /cgn2_6/ptodata/2/pna/US6011A_COMB.seq:*
77: /cgn2_6/ptodata/2/pna/US6011B_COMB.seq:*
78: /cgn2_6/ptodata/2/pna/US6012A_COMB.seq:*
79: /cgn2_6/ptodata/2/pna/US6012B_COMB.seq:*
80: /cgn2_6/ptodata/2/pna/US6013A_COMB.seq:*
81: /cgn2_6/ptodata/2/pna/US6013B_COMB.seq:*
82: /cgn2_6/ptodata/2/pna/US6014A_COMB.seq:*
83: /cgn2_6/ptodata/2/pna/US6014B_COMB.seq:*
84: /cgn2_6/ptodata/2/pna/US6014C_COMB.seq:*
85: /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*
86: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:*
87: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:*
88: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
89: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
90: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
91: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
92: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	679	100.0	6146	24	US-08-888-012-1	Sequence 1, Appli
2	679	100.0	6146	35	US-09-030-832-1	Sequence 1, Appli
3	679	100.0	3154	35	US-09-030-832-41	Sequence 41, Appl
4	658	96.9	3268	87	US-60-172-373-15901	Sequence 15901, A
5	383	56.4	9631	24	US-08-888-012-5	Sequence 5, Appli
6	383	56.4	9631	35	US-09-030-832-5	Sequence 5, Appli
c 7	383	56.4	523	86	US-60-160-190-439	Sequence 439, App
8	252	37.1	268	29	US-08-951-198-2954	Sequence 2954, Ap
9	252	37.1	268	34	US-09-016-434-339	Sequence 339, App
10	252	37.1	268	60	US-60-027-249-2914	Sequence 2914, Ap
11	252	37.1	268	86	US-60-164-285-3990	Sequence 3990, Ap
12	242	35.6	599	86	US-60-168-603-89	Sequence 89, Appl
13	165.8	24.4	7479	24	US-08-888-012-6	Sequence 6, Appli
14	165.8	24.4	7479	35	US-09-030-832-6	Sequence 6, Appli
15	119.6	17.6	2434	50	US-09-354-899-7330	Sequence 7330, Ap
16	119.6	17.6	2434	51	US-09-371-168-7178	Sequence 7178, Ap
17	119.6	17.6	1332	68	US-60-070-771-92	Sequence 92, Appl
18	116	17.1	1980	54	US-09-471-275-1928	Sequence 1928, Ap
19	112	16.5	1565	18	US-08-716-396-7	Sequence 7, Appli
20	106.6	15.7	1408	2	US-07-971-767-17	Sequence 17, Appl

	21	106.6	15.7	1408	12	US-08-341-610-3 Sequence 3, Appli
	22	105	15.5	1893	87	US-60-172-373-2255 Sequence 2255, Ap
	23	99.6	14.7	1707	21	US-08-809-802-7 Sequence 7, Appli
c	24	98.4	14.5	1978	50	US-09-354-899-6566 Sequence 6566, Ap
c	25	98.4	14.5	1978	51	US-09-371-168-6154 Sequence 6154, Ap
	26	98	14.4	1679	34	US-09-016-434-1470 Sequence 1470, Ap
	27	97.4	14.3	445	52	US-09-399-720-17511 Sequence 17511, A
	28	97.4	14.3	1988	86	US-60-167-943-168 Sequence 168, App
	29	96.2	14.2	1640	54	US-09-471-275-2757 Sequence 2757, Ap
	30	96.2	14.2	1870	87	US-60-172-373-2198 Sequence 2198, Ap
	31	95.2	14.0	2310	2	US-07-971-767-15 Sequence 15, Appl
	32	95.2	14.0	2310	12	US-08-341-610-1 Sequence 1, Appli
	33	94.4	13.9	1834	54	US-09-471-275-2141 Sequence 2141, Ap
	34	94.4	13.9	4310	87	US-60-172-373-2841 Sequence 2841, Ap
	35	92.6	13.6	1917	38	US-09-083-194A-7 Sequence 7, Appli
	36	92	13.5	436	54	US-09-465-877-11303 Sequence 11303, A
	37	91.6	13.5	1638	2	US-07-971-767-13 Sequence 13, Appl
	38	91.6	13.5	1638	12	US-08-341-610-9 Sequence 9, Appli
	39	90.8	13.4	1866	2	US-07-971-767-19 Sequence 19, Appl
	40	90.8	13.4	1866	12	US-08-341-610-5 Sequence 5, Appli
	41	90.6	13.3	57201	86	US-60-161-932-161 Sequence 161, App
	42	90.6	13.3	57201	86	US-60-164-769-23689 Sequence 23689, A
	43	90.6	13.3	3729	86	US-60-167-216-421 Sequence 421, App
	44	90.6	13.3	1458	86	US-60-167-216-422 Sequence 422, App
	45	90.6	13.3	1458	87	US-60-173-464-13597 Sequence 13597, A

ALIGNMENTS

```
RESULT   1
US-08-888-012-1
; Sequence 1, Application US/08888012
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  ET2: An Alternative Transcript of the GABA-A
;    TITLE OF INVENTION:  Receptor n Subunit
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,012
;      FILING DATE:  Herewith
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950000/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6146 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3872..4597
US-08-888-012-1

  Query Match             100.0%;  Score 679;  DB 24;  Length 6146;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-194;
  Matches  679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3919 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 3978

Qy      61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3979 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 4038

Qy     121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4039 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 4098

Qy     181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4099 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 4158

Qy     241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4159 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 4218

Qy     301 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4219 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 4278

Qy     361 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4279 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 4338

Qy     421 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCCGCAGCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4339 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCCGCAGCCT 4398

Qy     481 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4399 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 4458

Qy     541 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4459 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 4518

Qy     601 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4519 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 4578

Qy     661 GCTTGTTTGCCTTAACTTG 679
          |||||||||||||||||||
Db    4579 GCTTGTTTGCCTTAACTTG 4597
```

```
RESULT   2
US-09-030-832-1
; Sequence 1, Application US/09030832
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
```

```
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/030,832
;       FILING DATE:  Herewith
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/888,012
;       FILING DATE:  03-JUL-1997
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Steffe, Eric K.
;       REGISTRATION NUMBER:  36,688
;       REFERENCE/DOCKET NUMBER:  1488.0950001/EKS/SGW
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 371-2600
;       TELEFAX:  (202) 371-2540
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6146 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  3872..4597
US-09-030-832-1


  Query Match             100.0%;  Score 679;  DB 35;  Length 6146;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-194;
  Matches  679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3919 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 3978

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3979 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 4038

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4039 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 4098

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4099 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 4158

Qy    241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4159 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 4218

Qy    301 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4219 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 4278

Qy    361 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4279 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 4338

Qy    421 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4339 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 4398

Qy    481 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4399 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 4458

Qy    541 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4459 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 4518

Qy    601 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4519 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 4578

Qy    661 GCTTGTTTGCCTTAACTTG 679
          ||||||||||||||||||
Db   4579 GCTTGTTTGCCTTAACTTG 4597


RESULT   3
US-09-030-832-41
; Sequence 41, Application US/09030832
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/030,832
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/888,012
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950001/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3154 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  41..1558
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  41..94
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  95..1558
US-09-030-832-41


  Query Match             100.0%;  Score 679;  DB 35;  Length 3154;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-194;
  Matches  679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    880 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 939

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
```

```
Db    940 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 999

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
Db   1000 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 1059

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
Db   1060 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 1119

Qy    241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 300
Db   1120 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 1179

Qy    301 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 360
Db   1180 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 1239

Qy    361 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 420
Db   1240 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 1299

Qy    421 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 480
Db   1300 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 1359

Qy    481 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 540
Db   1360 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 1419

Qy    541 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 600
Db   1420 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 1479

Qy    601 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 660
Db   1480 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 1539

Qy    661 GCTTGTTTGCCTTAACTTG 679
Db   1540 GCTTGTTTGCCTTAACTTG 1558
```

RESULT 4
US-60-172-373-15901
; Sequence 15901, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymorp
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 15901
; LENGTH: 3268
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 331742.2
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3257, 3265
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-15901

Query Match 96.9%; Score 658; DB 87; Length 3268;
Best Local Similarity 98.4%; Pred. No. 6e-188;
Matches 679; Conservative 0; Mismatches 0; Indels 11; Gaps 1;

```
Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
Db    975 tgcctttcaaaactatgtcccttcttccgtgaccacgatgctctcctgggtttccttttg 1034

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
Db   1035 gatcaagacagagtctgctccagcccggacctctctagggatcacctctgttctgaccat 1094

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
Db   1095 gaccacgttgggcacctttttctcgtaagaatttcccgcgtgtctcctatatcacagcctt 1154

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
Db   1155 ggatttctatatcgccatctgcttcgtcttctgcttctgcgctctgttggagtttgctgt 1214

Qy    241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCAT-- 299
Db   1215 gctcaacttcctgatctacaaccagacaaaagcccatgcttctcctaaactccgccatgt 1274

Qy    299 ---------CCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCC 349
Db   1275 atgagctggcctcgtatcaatagccgtgcccatgcccgtacccgtgcacgttcccgagcc 1334

Qy    350 TGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGAT 409
Db   1335 tgtgcccgccaacatcaggaagcttttgtgtgccagattgtcaccactgagggaagtgat 1394

Qy    410 GGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGT 469
Db   1395 ggagaggagcgcccgtcttgctcagcccagcagcccccctagcccaggtagccctgagggt 1454

Qy    470 CCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTAC 529
Db   1455 ccccgcagcctctgctccaagctggcctgctgtgagtggtgcaagcgttttaagaagtac 1514

Qy    530 TTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCAT 589
Db   1515 ttctgcatggtccccgattgtgagggcagtacctggcagcagggccgcctctgcatccat 1574

Qy    590 GTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAAT 649
Db   1575 gtctaccgcctggataactactcgagagttgttttcccagtgactttcttcttcttcaat 1634

Qy    650 GTGCTCTACTGGCTTGTTTGCCTTAACTTG 679
Db   1635 gtgctctactggcttgtttgccttaacttg 1664
```

RESULT 5
US-08-888-012-5
; Sequence 5, Application US/08888012
; GENERAL INFORMATION:
; APPLICANT: Hanna, Michael C.
; APPLICANT: Kirkness, Ewen F.
; TITLE OF INVENTION: ET2: An Alternative Transcript of the GABA-A
; TITLE OF INVENTION: Receptor n Subunit
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Avenue, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,012
;      FILING DATE:  Herewith
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950000/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9631 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-888-012-5


  Query Match             56.4%;  Score 383;  DB 24;  Length 9631;
  Best Local Similarity   96.3%;  Pred. No. 1.5e-104;
  Matches  392;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    273 CCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 332
          ||||    | ||||   |      | ||||||||||||||||||||||||||||||||||
Db   7832 CCCACTTCTTTCCTTGTCCATTTTAGCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 7891

Qy    333 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7892 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 7951

Qy    393 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7952 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 8011

Qy    453 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8012 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 8071

Qy    513 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8072 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 8131

Qy    573 GCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8132 GCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 8191

Qy    633 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTG 679
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   8192 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTG 8238


RESULT   6
US-09-030-832-5
; Sequence 5, Application US/09030832
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/030,832
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/888,012
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950001/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9631 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-030-832-5


  Query Match             56.4%;  Score 383;  DB 35;  Length 9631;
  Best Local Similarity   96.3%;  Pred. No. 1.5e-104;
  Matches  392;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    273 CCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 332
          ||||    | ||||   |      | ||||||||||||||||||||||||||||||||||
Db   7832 CCCACTTCTTTCCTTGTCCATTTTAGCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 7891

Qy    333 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7892 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 7951

Qy    393 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7952 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 8011

Qy    453 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8012 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 8071

Qy    513 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8072 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 8131

Qy    573 GCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8132 GCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 8191

Qy    633 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTG 679
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   8192 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTG 8238


RESULT   7
US-60-160-190-439/c
; Sequence 439, Application US/60160190
; GENERAL INFORMATION:
;  APPLICANT: BONAZZI, VIVIEN
;  TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: CL000115
;  CURRENT APPLICATION NUMBER: US/60/160,190
;  CURRENT FILING DATE: 1998-10-19
;  NUMBER OF SEQ ID NOS: 2384
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 439
```

```
;   LENGTH: 523
;   TYPE: DNA
;   ORGANISM: HUMAN
US-60-160-190-439


  Query Match             56.4%;  Score 383;  DB 86;  Length 523;
  Best Local Similarity   96.3%;  Pred. No. 3.4e-105;
  Matches  392;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    273 CCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 332
          ||||    | ||||   |       | ||||||||||||||||||||||||||||||||
Db    473 CCCACTTCTTTCCTTGTCCATTTTAGCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 414

Qy    333 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    413 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 354

Qy    393 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    353 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 294

Qy    453 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 234

Qy    513 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 174

Qy    573 GCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    173 GCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 114

Qy    633 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTG 679
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    113 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTG 67


RESULT   8
US-08-951-198-2954
; Sequence 2954, Application US/08951198
;  GENERAL INFORMATION:
;    APPLICANT:  Gooding, Douglas H.
;    APPLICANT:  Stuv , Laura L.
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Ito, Laura Y.
;    APPLICANT:  Akerblom, Ingrid E.
;    APPLICANT:  Delegeane, Angelo M.
;    APPLICANT:  Naughton, Rebecca E.
;    APPLICANT:  Klingler, Tod M.
;    TITLE OF INVENTION:  POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
;    TITLE OF INVENTION:  HUMAN BREAST
;    NUMBER OF SEQUENCES:  6047
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/951,198
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/027,249
;      FILING DATE:  OCTOBER 1, 1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/839,968
;      FILING DATE:  APRIL 24, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CERRONE, MICHAEL C.
;      REGISTRATION NUMBER:  39,132
;      REFERENCE/DOCKET NUMBER:  PD-0150-1 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  2954:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  268 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    IMMEDIATE SOURCE:
;      CLONE:  1961860
US-08-951-198-2954


  Query Match             37.1%;  Score 252;  DB 29;  Length 268;
  Best Local Similarity   100.0%;  Pred. No. 1e-65;
  Matches  252;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     17 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 76

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     77 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 136

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    137 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 196

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    197 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 256

Qy    241 GCTCAACTTCCT 252
          ||||||||||||
Db    257 GCTCAACTTCCT 268


RESULT   9
US-09-016-434-339
; Sequence 339, Application US/09016434
;  GENERAL INFORMATION:
;    APPLICANT:  Janice Au-Young
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;    TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;    NUMBER OF SEQUENCES:  1490
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HEREWITH
```

```
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  339:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  268 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  BRSTNOT04
;      CLONE:  1961860
US-09-016-434-339


  Query Match             37.1%;  Score 252;  DB 34;  Length 268;
  Best Local Similarity   100.0%;  Pred. No. 1e-65;
  Matches  252;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     17 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 76

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     77 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 136

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    137 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 196

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    197 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 256

Qy    241 GCTCAACTTCCT 252
          ||||||||||||
Db    257 GCTCAACTTCCT 268


RESULT  10
US-60-027-249-2914
; Sequence 2914, Application US/60027249
;  GENERAL INFORMATION:
;    APPLICANT:  Gooding, Douglas H.
;    APPLICANT:  Stuve, Laura L.
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Ito, Laura Y.
;    APPLICANT:  Akerblom, Ingrid E.
;    APPLICANT:  Delegeane, Angelo M.
;    APPLICANT:  Naughton, Rebecca E.
;    APPLICANT:  Klingler, Tod M.
;    TITLE OF INVENTION:  POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
;    TITLE OF INVENTION:  HUMAN BREAST
;    NUMBER OF SEQUENCES:  6007
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/027,249
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CERRONE, MICHAEL C., Ph.D.
;      REGISTRATION NUMBER:  39132
;      REFERENCE/DOCKET NUMBER:  PD-0241P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 855-0555
;      TELEFAX:  (415) 845-4166
;  INFORMATION FOR SEQ ID NO:  2914:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  268 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    IMMEDIATE SOURCE:
;      CLONE:  1961860
US-60-027-249-2914


  Query Match             37.1%;  Score 252;  DB 60;  Length 268;
  Best Local Similarity   100.0%;  Pred. No. 1e-65;
  Matches  252;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     17 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 76

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     77 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 136

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    137 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 196

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    197 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 256

Qy    241 GCTCAACTTCCT 252
          ||||||||||||
Db    257 GCTCAACTTCCT 268


RESULT  11
US-60-164-285-3990
; Sequence 3990, Application US/60164285
; GENERAL INFORMATION:
;  APPLICANT: Ma, Xiao-Jun
;  TITLE OF INVENTION: Tumor Associated Molecules (TAMs): Targets for diagnosis, trea
;  FILE REFERENCE: 3214
;  CURRENT APPLICATION NUMBER: US/60/164,285
;  CURRENT FILING DATE: 1999-11-05
;  NUMBER OF SEQ ID NOS: 8259
; SEQ ID NO 3990
;   LENGTH: 268
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-164-285-3990


  Query Match             37.1%;  Score 252;  DB 86;  Length 268;
  Best Local Similarity   100.0%;  Pred. No. 1e-65;
  Matches  252;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
```

```
Db     17 tgcctttcaaaactatgtcccttcttccgtgaccacgatgctctcctgggtttccttttg 76

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
Db     77 gatcaagacagagtctgctccagcccggacctctctagggatcacctctgttctgaccat 136

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
Db    137 gaccacgttgggcacctttttctcgtaagaatttcccgcgtgtctcctatatcacagcctt 196

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
Db    197 ggatttctatatcgccatctgcttcgtcttctgcttctgcgctctgttggagtttgctgt 256

Qy    241 GCTCAACTTCCT 252
Db    257 gctcaacttcct 268


RESULT 12
US-60-168-603-89
; Sequence 89, Application US/60168603
; GENERAL INFORMATION:
;  APPLICANT: Hodgson, David M.                Jones, Anissa L.
;  APPLICANT: Lincoln, Stephen E.              Yu, Jimmy Y.
;  APPLICANT: Russo, Frank D.                  Greenawalt, Lila B.
;  APPLICANT: Spiro, Peter A.                  Panzer, Scott R.
;  APPLICANT: Banville, Steve C.               Roseberry, Ann M.
;  APPLICANT: Bratcher, Shawn R.               Wright, Rachel J.
;  APPLICANT: Dufour, Gerard E.                Chen, Wensheng
;  APPLICANT: Cohen, Howard J.                 Liu, Tommy
;  APPLICANT: Rosen, Bruce                     Yap, Pierre E.
;  APPLICANT: Shah, Purvi                      Stockdreher, Theresa K.
;  APPLICANT: Chalup, Michael S.               Amshey, Stefan
;  APPLICANT: Hillman, Jennifer L.             Fong, Willy Tuen
;  TITLE OF INVENTION: MEMBRANE TRANSPORT MOLECULES
;  FILE REFERENCE: PT-0095 P
;  CURRENT APPLICATION NUMBER: US/60/168,603
;  CURRENT FILING DATE: 1999-12-01
;  NUMBER OF SEQ ID NOS: 153
;  SOFTWARE: PERL Program
; SEQ ID NO 89
;   LENGTH: 599
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 425535.2
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 35
;   OTHER INFORMATION: a, t, c, g, or other
US-60-168-603-89


  Query Match           35.6%;  Score 242;  DB 86;  Length 599;
  Best Local Similarity  99.6%;  Pred. No. 1.6e-62;
  Matches  253;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
Db    347 tgcctttcaaaactatgtcccttcttccgtgaccacgatgctctcctgggtttccttttg 406

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
Db    407 gatcaagacagagtctgctccagcccggacctctctagggatcacctctgttctgaccat 466

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
Db    467 gaccacgttgggcacctttttctcgtaagaatttcccgcgtgtctcctatatcacagcctt 526

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
Db    527 ggatttctatatcgccatctgcttcgtcttctgcttctgcgctctgttggag-ttgctgt 585

Qy    241 GCTCAACTTCCTGA 254
Db    586 gctcaacttcctga 599


RESULT 13
US-08-888-012-6
; Sequence 6, Application US/08888012
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  ET2: An Alternative Transcript of the GABA-A
;    TITLE OF INVENTION:  Receptor n Subunit
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,012
;      FILING DATE:  Herewith
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950000/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7479 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-888-012-6


  Query Match           24.4%;  Score 165.8;  DB 24;  Length 7479;
  Best Local Similarity  67.9%;  Pred. No. 6.3e-39;
  Matches  271;  Conservative    0;  Mismatches  107;  Indels   21;  Gaps    2;

Qy    281 TCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGT 340
Db   6654 TTTCCAACCAATAGCCGTGCTAATGCACGTACTCGTGCTCGTGCCCGCACTCGTGCTCGT 6713

Qy    341 TCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAG 400
Db   6714 GCTCGTGCCCGTGCTCGTCAGCAGCAGGAAGTGTTTGTGTGTGAGATTGTTACCTATGAG 6773

Qy    401 GGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGC 460
Db   6774 GAAAATGCTGAAGAGG--------------GTTACCAGTGGTCTCCAAGATCAAGAAGA 6818

Qy    461 CCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTT 520
Db   6819 CCTCAGTGTCCCTGGAGGCGATGTGGC------CGAAGCTATGTGTGCTTCAGGGTTCTC 6872

Qy    521 AAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTC 580
Db   6873 AGGAAGTATTTCTGCATGGTTCCTGGTTGTGAGGGCAACAGCTGGCAGCGGGGCCGCATC 6932
```

```
Qy    581 TGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTC 640
          |||||||| || || |||||||||||||||||| | ||  |||||||  | || ||||||
Db   6933 TGCATCCACGTTTATCGCCTGGATAACTACTCGCGGGTGCTTTTCCCCATTACATTCTTC 6992

Qy    641 TTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTG 679
          ||||| |||||| |||||||| |  ||||||||||| ||
Db   6993 TTCTTTAATGTGGTCTACTGGGTGATTTGCCTTAACCTG 7031


RESULT 14
US-09-030-832-6
; Sequence 6, Application US/09030832
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/030,832
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/888,012
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950001/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7479 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-030-832-6


  Query Match             24.4%;  Score 165.8;  DB 35;  Length 7479;
  Best Local Similarity   67.9%;  Pred. No. 6.3e-39;
  Matches  271;  Conservative    0;  Mismatches  107;  Indels   21;  Gaps    2;

Qy    281 TCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGT 340
          | ||| |      ||| | ||  |     ||  ||||| | |||||| || ||||| |||
Db   6654 TTTCCAACCAATAGCCGTGCTAATGCACGTACTCGTGCTCGTGCCCGCACTCGTGCTCGT 6713

Qy    341 TCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAG 400
          | || ||| |||| || || || |||||||  ||||||||  |||||||  |||  ||||
Db   6714 GCTCGTGCCCGTGCTCGTCAGCAGCAGGAAGTGTTTGTGTGTGAGATTGTTACCTATGAG 6773

Qy    401 GGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGC 460
          | || || || |||||                    ||||  | | || ||  || | ||
Db   6774 GAAAATGCTGAAGAGG--------------GTTACCAGTGGTCTCCAAGATCAAGAAGA 6818

Qy    461 CCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTT 520
          ||| || ||||| | || |  ||   |          ||| || ||| | || |  | |
Db   6819 CCTCAGTGTCCCTGGAGGCGATGTGGC------CGAAGCTATGTGTGCTTCAGGGTTCTC 6872

Qy    521 AAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTC 580
          | |||||| |||||||||| || | ||||||||||  | |||||||| |||||| ||
Db   6873 AGGAAGTATTTCTGCATGGTTCCTGGTTGTGAGGGCAACAGCTGGCAGCGGGGCCGCATC 6932

Qy    581 TGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTC 640
          ||||||||| || || |||||||||||||||||| | ||  |||||||  | || ||||||
Db   6933 TGCATCCACGTTTATCGCCTGGATAACTACTCGCGGGTGCTTTTCCCCATTACATTCTTC 6992

Qy    641 TTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTG 679
          ||||| |||||| |||||||| |  ||||||||||| ||
Db   6993 TTCTTTAATGTGGTCTACTGGGTGATTTGCCTTAACCTG 7031


RESULT 15
US-09-354-899-7330
; Sequence 7330, Application US/09354899
; GENERAL INFORMATION:
;  APPLICANT: Glucksmann, M. Alexandra
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
;  TITLE OF INVENTION: HUMAN BRAIN LIBRARY
;  FILE REFERENCE: MLN98-35pA
;  CURRENT APPLICATION NUMBER: US/09/354,899
;  CURRENT FILING DATE: 1999-07-09
;  EARLIER APPLICATION NUMBER: 60/092,406
;  EARLIER FILING DATE: 1998-07-10
;  NUMBER OF SEQ ID NOS: 8631
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7330
;   LENGTH: 2434
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(2434)
;   OTHER INFORMATION: n = A,T,C or G
US-09-354-899-7330


  Query Match             17.6%;  Score 119.6;  DB 50;  Length 2434;
  Best Local Similarity   64.4%;  Pred. No. 3.3e-25;
  Matches  179;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          | || | || | |||| |||| |   |  | |      | || ||||||||| || || ||
Db    813 taccatccagacctatatccctgcacactcattgtcgtcctatcctgggtgtctttctg 872

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          ||||||  |  ||  ||| ||||||| | || ||| |||| |||||| |||| ||||| ||
Db    873 gatcaataaggatgctgttccagccagaacatctttaggtatcaccactgtcctgacaat 932

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||  |  ||||| || | || ||     ||||    |||||||| |||||||  |
Db    933 gaccaccctcagcaccattgcccggaaatcgctccccaaggtctcctatgtcacagcgat 992

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          |||| ||| | |  |  | || ||| ||||   |||||  |||||| |||||| ||
Db    993 ggatctctttgtatctgtttgtttcatctttgtcttctctgctctggtggagtatggcac 1052

Qy    241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATG 278
          |  | |   |  ||  ||||| || |  |  | | |
Db   1053 cttgcattattttgtcagcaaccggaaaccaagcaagg 1090


Search completed: March 10, 2000, 09:00:51
Job time: 9129 sec
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2000, 01:35:15 ; Search time 4946.18 Seconds
(without alignments)
-416.828 Million cell updates/sec

Title: US-09-030-832-41_COPY_880_1558
Perfect score: 679
Sequence: 1 TGCCTTTCAAAACTATGTCC.....GGCTTGTTTGCCTTAACTTG 679

Scoring table: IDENTITY_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl:*

Word size : 0

Number of hits that pass the threshold : 1642386

1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_prl:*
10: gb_pr2:*
11: gb_pr3:*
12: gb_ro:*
13: gb_sts:*
14: gb_sy:*
15: gb_un:*
16: gb_vi:*
17: em_fun:*
18: em_huml:*
19: em_hum2:*
20: em_in:*
21: em_om:*
22: em_or:*
23: em_ov:*
24: em_pat:*
25: em_ph:*
26: em_pl:*
27: em_ro:*
28: em_sts:*
29: em_sy:*
30: em_un:*
31: em_vi:*
32: gb_htg1:*
33: gb_htg2:*
34: gb_in1:*
35: gb_in2:*
36: em_ba1:*
37: em_ba2:*
38: em_hum3:*
39: em_hum4:*
40: gb_pr4:*
41: gb_htg3:*
42: gb_htg4:*
43: gb_htg5:*
44: gb_htg6:*
45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_hum5:*
50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	679	100.0	3153	9	HSGABACHL	Y07637 H.sapiens m
2	679	100.0	3154	10	HSU66661	U66661 Human GABA-
3	679	100.0	3150	10	HSY09765	Y09765 Homo sapien
4	679	100.0	6146	11	HSU92285	U92285 Human GABA-
5	383	56.4	9631	11	HSGABRE3	U92283 Human GABA-
c 6	383	56.4	158898	11	U82696	U82696 Homo sapien
7	379.8	55.9	10897	10	HSY09764	Y09764 Homo sapien
8	165.8	24.4	7479	12	RNU92284	U92284 Rattus norv
9	144.4	21.3	1572	4	GGGABAA	X73533 G.domesticu
10	119.6	17.6	1745	9	HSGABAAS	X15376 Human mRNA
11	119.2	17.6	1428	3	BOVGABAARG	M55563 Bovine gamm
12	113.6	16.7	1838	12	RATGABAAI	L08497 Rattus ratt
13	112.2	16.5	1654	12	RATGABAA	M81142 Rat GABA-A
14	112.2	16.5	1930	12	RNGABAG3	X63324 R.norvegicu
15	112	16.5	1565	5	A46959	A46959 Sequence 7
16	112	16.5	1536	10	S82769	S82769 GABAA recep
17	112	16.5	2231	12	MUSGABAAG2	M62374 Mus musculu
18	112	16.5	2036	12	MUSGABAAR	M86572 Mouse gamma
19	109.4	16.1	1629	34	LSGABAA	X58638 L.stagnalis
20	109	16.1	1598	12	MMGSGABA	X59300 Mouse mRNA
21	107.6	15.8	1843	12	RATGABAAE	L08493 Rattus ratt
22	107.6	15.8	1843	12	S55933	S55933 GABAA recep
23	106.6	15.7	1408	5	A28106	A28106 Human GABAa
24	106.6	15.7	1408	5	A39278	A39278 Sequence 3
25	106.6	15.7	1732	5	I88880	I88880 Sequence 17
26	105	15.5	1732	10	S81944	S81944 gamma-amino
27	102.2	15.1	1345	4	CAGABANTS	X94342 C.auratus m
28	101.8	15.0	2206	4	GDGABAAR	X54944 Chicken mRN
29	101.4	14.9	2228	12	MMGABAB1	X55273 Mouse mRNA
30	101.4	14.9	2228	12	MMU14418	U14418 Mus musculu
31	100.4	14.8	1439	4	GGGABAA6S	X94343 G.gallus mR
32	99.6	14.7	1707	5	A50024	A50024 Sequence 7
33	98.4	14.5	1628	9	HUMGABARHO	M86868 Human gamma
34	98.4	14.5	1634	9	HUMGABRB3A	M82919 Human gamma
35	98.2	14.5	1628	4	DRE5812	AJ005812 Danio rer
36	98	14.4	1679	10	HSU30461	U30461 Human GABAA
37	97.4	14.3	1989	9	HUMGABAR	M62400 Human gamma
38	96.2	14.2	1866	9	HSGABAAB1	X14767 Human mRNA
39	95.6	14.1	2000	12	RSGARB2	X15467 Rat mRNA fo
40	95.2	14.0	1480	4	GDGABAAA	X72806 G.domesticu
41	95.2	14.0	2310	5	A28104	A28104 Human GABAa
42	95.2	14.0	2310	5	A39276	A39276 Sequence 1
43	95.2	14.0	2310	5	I88879	I88879 Sequence 15
44	95.2	14.0	2318	9	HUMGABRA5Y	L08485 Human GABA-
45	95.2	14.0	346	12	AF090376	AF090376 Mus muscu

ALIGNMENTS

RESULT 1
HSGABACHL
LOCUS HSGABACHL 3153 bp mRNA PRI 03-MAR-1997
DEFINITION H.sapiens mRNA for putative GABA-gated chloride channel.
ACCESSION Y07637
VERSION Y07637.1 GI:1747370
KEYWORDS GABA-gated chloride channel.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3153)

```
  AUTHORS   Garret,M., Bascles,L., Boue-Grabot,E., Sartor,P., Charron,G.,
            Bloch,B. and Margolskee,R.F.
  TITLE     An mRNA encoding a putative GABA-gated chloride channel is
            expressed in the human cardiac conduction system
  JOURNAL   J. Neurochem. 68 (4), 1382-1389 (1997)
  MEDLINE   97238072
REFERENCE   2  (bases 1 to 3153)
  AUTHORS   Garret,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-AUG-1996) M. Garret, CNRS UMR5543, Laboratoire de
            Neurophysiologie, Universite de Bordeaux2, 146 rue Leo Saignat,
            33076 Bordeaux Cedex, FRANCE
FEATURES             Location/Qualifiers
     source          1. .3153
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             51. .1568
                     /function="expressed in cardiac conduction system"
                     /codon_start=1
                     /product="putative GABA-gated chloride channel"
                     /protein_id="CAA68914.1"
                     /db_xref="GI:1747371"
                     /db_xref="SPTREMBL:Q99520"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIA
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPGDFMVMTIFFNVSRRF
                     GYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVS
                     YITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRAR
                     SRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCK
                     RFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
     polyA_signal    3118. .3123
BASE COUNT      726 a    885 c    687 g    855 t
ORIGIN
```

```
  Query Match             100.0%;  Score 679;  DB 9;  Length 3153;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-179;
  Matches  679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     887 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 946

Qy      61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     947 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 1006

Qy     121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1007 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 1066

Qy     181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1067 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 1126

Qy     241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1127 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 1186

Qy     301 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1187 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 1246

Qy     361 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1247 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 1306

Qy     421 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1307 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 1366

Qy     481 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1367 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 1426

Qy     541 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1427 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 1486

Qy     601 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1487 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 1546

Qy     661 GCTTGTTTGCCTTAACTTG 679
          |||||||||||||||||||
Db    1547 GCTTGTTTGCCTTAACTTG 1565
```

```
RESULT   2
HSU66661
LOCUS       HSU66661     3154 bp    mRNA            PRI       11-MAR-1997
DEFINITION  Human GABA-A receptor epsilon subunit mRNA, complete cds.
ACCESSION   U66661
VERSION     U66661.1  GI:1857125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3154)
  AUTHORS   Davies,P.A., Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Insensitivity to anaesthetic agents conferred by a class of GABA(A)
            receptor subunit
  JOURNAL   Nature 385 (6619), 820-823 (1997)
  MEDLINE   97192095
REFERENCE   2  (bases 1 to 3154)
  AUTHORS   Davies,P.A., Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-1996) Department of Cellular and Molecular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .3154
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             41. .1561
                     /codon_start=1
                     /product="GABA-A receptor epsilon subunit"
                     /protein_id="AAB49284.1"
                     /db_xref="GI:1857126"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIA
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRR
                     FGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV
                     SYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRA
                     RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWC
                     KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
BASE COUNT      725 a    886 c    686 g    857 t
ORIGIN
```

```
  Query Match             100.0%;  Score 679;  DB 10;  Length 3154;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-179;
  Matches  679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 939

Qy      61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 999
```

```
Qy     121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 1059

Qy     181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 1119

Qy     241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1120 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 1179

Qy     301 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1180 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 1239

Qy     361 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1240 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 1299

Qy     421 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1300 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 1359

Qy     481 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1360 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 1419

Qy     541 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1420 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 1479

Qy     601 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1480 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 1539

Qy     661 GCTTGTTTGCCTTAACTTG 679
           ||||||||||||||||||||
Db    1540 GCTTGTTTGCCTTAACTTG 1558
```

```
RESULT   3
HSY09765
LOCUS       HSY09765     3150 bp    mRNA            PRI       31-OCT-1997
DEFINITION  Homo sapiens mRNA for putative GABA receptor epsilon subunit.
ACCESSION   Y09765
VERSION     Y09765.1  GI:2285960
KEYWORDS    GABA receptor; GABRE gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3150)
  AUTHORS   Wilke,K., Gaul,R., Klauck,S.M. and Poustka,A.
  TITLE     A gene in human chromosome band Xq28 (GABRE) defines a putative new
            subunit class of the GABAA neurotransmitter receptor
  JOURNAL   Genomics 45 (1), 1-10 (1997)
  MEDLINE   97480709
REFERENCE   2  (bases 1 to 3150)
  AUTHORS   Wilke,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1996) K. Wilke, Deutsches Krebsforschungszentrum,
            Abteilung Molekulare Genomanalyse (840), Im Neuenheimer Feld 280,
            D-69120 Heidelberg, FRG
FEATURES             Location/Qualifiers
     source          1. .3150
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /map="q28"
     CDS             55. .1575
                     /note="putative"
                     /codon_start=1
                     /product="GABA receptor epsilon subunit"
                     /protein_id="CAA70904.1"
                     /db_xref="GI:2285961"
                     /db_xref="SPTREMBL:O15346"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIS
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRR
                     FGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV
                     SYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRA
                     RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWC
                     KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
BASE COUNT      712 a    889 c    690 g    859 t
ORIGIN
```

```
  Query Match           100.0%;  Score 679;  DB 10;  Length 3150;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-179;
  Matches  679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     894 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 953

Qy      61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     954 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 1013

Qy     121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1014 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 1073

Qy     181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1074 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 1133

Qy     241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1134 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 1193

Qy     301 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1194 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 1253

Qy     361 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1254 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 1313

Qy     421 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1314 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 1373

Qy     481 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1374 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 1433

Qy     541 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1434 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 1493

Qy     601 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1494 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 1553

Qy     661 GCTTGTTTGCCTTAACTTG 679
           ||||||||||||||||||||
Db    1554 GCTTGTTTGCCTTAACTTG 1572
```

```
RESULT   4
HSU92285
LOCUS       HSU92285     6146 bp    mRNA            PRI       04-FEB-1998
DEFINITION  Human GABA-A receptor epsilon subunit (GABRE) RNA, alternative
            transcript.
ACCESSION   U92285
VERSION     U92285.1  GI:2735330
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 6146)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6146)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .6146
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq28"
     misc_RNA        1. .6146
                     /gene="GABRE"
                     /note="RNA transcript is initiated from within the GABRE
                     gene, and therefore contains intron sequence with respect
                     to the subunit transcript"
     misc_feature    1. .3863
                     /gene="GABRE"
                     /note="intron 6 of GABRE; GABRE gene sequence deposited in
                     GenBank Accession Number U92283"
     gene            1. .6146
                     /gene="GABRE"
     stem_loop       12. .96
                     /gene="GABRE"
     stem_loop       1065. .1147
                     /gene="GABRE"
     misc_feature    3864. .6146
                     /gene="GABRE"
                     /note="exons 7, 8 and 9 of GABRE; GABRE gene sequence
                     deposited in GenBank Accession Number U92283"
BASE COUNT     1440 a   1519 c   1458 g   1729 t
ORIGIN


  Query Match             100.0%;  Score 679;  DB 11;  Length 6146;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-179;
  Matches  679;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3919 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 3978

Qy      61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3979 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 4038

Qy     121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4039 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 4098

Qy     181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4099 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 4158

Qy     241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4159 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 4218

Qy     301 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4219 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 4278

Qy     361 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4279 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 4338

Qy     421 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4339 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 4398

Qy     481 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4399 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 4458

Qy     541 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4459 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 4518

Qy     601 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4519 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 4578

Qy     661 GCTTGTTTGCCTTAACTTG 679
          ||||||||||||||||||||
Db    4579 GCTTGTTTGCCTTAACTTG 4597


RESULT   5
HSGABRE3
LOCUS       HSGABRE3     9631 bp    DNA             PRI       03-JAN-1998
DEFINITION  Human GABA-A receptor epsilon subunit (GABRE) gene, exons 4-9, and
            complete cds.
ACCESSION   U92283
VERSION     U92283.1  GI:2735347
KEYWORDS    .
SEGMENT     3 of 3
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9631)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 9631)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .9631
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq28"
     mRNA            join(U92281.1:<162. .256,U92282.1:64. .281,
                     U92282.1:730. .797,301. .521,1577. .1659,2966. .3103,
                     7082. .7234,7375. .7574,7858. .>9631)
                     /gene="GABRE"
                     /product="GABA-A receptor epsilon subunit"
     gene            order(U92281.1:<162. .556,U92282.1:1. .1097,1. .>9631)
                     /gene="GABRE"
     CDS             join(U92281.1:201. .256,U92282.1:64. .281,U92282.1:730. .797,
                     301. .521,1577. .1659,2966. .3103,7082. .7234,7375. .7574,
                     7858. .8241)
                     /gene="GABRE"
```

```
                     /codon_start=1
                     /product="GABA-A receptor epsilon subunit"
                     /protein_id="AAB94645.1"
                     /db_xref="GI:2735349"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIS
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRR
                     FGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV
                     SYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRA
                     RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWC
                     KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
     intron          <1. .300
                     /gene="GABRE"
     exon            301. .521
                     /gene="GABRE"
     intron          522. .1576
                     /gene="GABRE"
     repeat_region   1095. .1134
                     /rpt_type=tandem
                     /rpt_unit=ttttg
     exon            1577. .1659
                     /gene="GABRE"
     intron          1660. .2965
                     /gene="GABRE"
     exon            2966. .3103
                     /gene="GABRE"
     intron          3104. .7081
                     /gene="GABRE"
     stem_loop       3230. .3314
                     /gene="GABRE"
     stem_loop       4283. .4365
                     /gene="GABRE"
     exon            7082. .7234
                     /gene="GABRE"
     intron          7235. .7374
                     /gene="GABRE"
     exon            7375. .7574
                     /gene="GABRE"
     intron          7575. .7857
                     /gene="GABRE"
     exon            7858. .>9631
                     /gene="GABRE"
     3'UTR           8242. .>9631
                     /gene="GABRE"
BASE COUNT     2267 a   2381 c   2249 g   2734 t
ORIGIN


  Query Match           56.4%;  Score 383;  DB 11;  Length 9631;
  Best Local Similarity  96.3%;  Pred. No. 1.8e-96;
  Matches  392;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     273 CCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 332
           ||||    | ||||   |       | ||||||||||||||||||||||||||||||||||
Db    7832 CCCACTTCTTTCCTTGTCCATTTTAGCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 7891

Qy     333 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7892 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 7951

Qy     393 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 452
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7952 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 8011

Qy     453 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 512
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8012 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 8071

Qy     513 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 572
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8072 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 8131

Qy     573 GCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 632
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8132 GCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 8191

Qy     633 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTG 679
           |||||||||||||||||||||||||||||||||||||||||||||||
Db    8192 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTG 8238


RESULT   6
U82696/c
LOCUS       U82696     158898 bp    DNA             PRI       01-JAN-1998
DEFINITION  Homo sapiens chromosome X map Xq28, complete sequence.
ACCESSION   U82696
VERSION     U82696.1  GI:2735037
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Hinzmann,B., Bauer,D., Drescher,B., Knop,A., Nordsiek,D.,
            Kioschis,P., Poustka,A., Rosenthal,A. and Gloeckner,G.
  TITLE     Location of GABA receptor gamma-4 subunit (GABRG4) on Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 158898)
  AUTHORS   Gloeckner,G., Rosenthal,A., Drescher,B., Schattevoy,R., Hinzmann,B.
            and Poustka,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-DEC-1996) Genome Analysis, Institut for Molecular
            Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
FEATURES             Location/Qualifiers
     source          1. .158898
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq28"
     misc_feature    1. .39138
                     /note="Region: cosmid IF064"
     repeat_region   1. .106
                     /rpt_family="L1PA11"
                     /evidence=not_experimental
     repeat_region   213. .282
                     /rpt_family="L1MB3"
                     /evidence=not_experimental
     exon            complement(1180. .1284)
                     /note="GRAIL, score = 43.000%, comment = marginal"
                     /evidence=not_experimental
     exon            complement(1683. .1767)
                     /note="MZEF, score = 60%"
                     /evidence=not_experimental
     exon            complement(2062. .2120)
                     /note="FEXHB, score = 11.76%"
                     /evidence=not_experimental
     repeat_region   complement(2637. .2710)
                     /rpt_family="L1ME2"
                     /evidence=not_experimental
     repeat_region   complement(2859. .3028)
                     /rpt_family="L1ME3A"
                     /evidence=not_experimental
     exon            complement(2911. .2978)
                     /note="MZEF, score = 79.7%"
                     /evidence=not_experimental
     exon            4250. .4431
                     /note="GRAIL, score = 52.000%, comment = good shadow"
                     /evidence=not_experimental
     repeat_region   complement(4639. .4866)
                     /rpt_family="L1MA2"
                     /evidence=not_experimental
     repeat_region   complement(4893. .5203)
                     /rpt_family="L1MA2"
                     /evidence=not_experimental
```

```
exon            complement(4974. .5117)
                /note="GRAIL, score = 61.000%, comment = good"
                /evidence=not_experimental
repeat_region   complement(5206. .5561)
                /rpt_family="L1MA2"
                /evidence=not_experimental
repeat_region   complement(5562. .5602)
                /rpt_family="L1MA9"
                /evidence=not_experimental
repeat_region   complement(5619. .5655)
                /rpt_family="L1MA5"
                /evidence=not_experimental
repeat_region   complement(6084. .6254)
                /rpt_family="MLT1D"
                /evidence=not_experimental
repeat_region   complement(6262. .6322)
                /rpt_family="MLT1D"
                /evidence=not_experimental
repeat_region   complement(6384. .6549)
                /rpt_family="MLT1D"
                /evidence=not_experimental
repeat_region   6664. .6771
                /note="homology = 89.80%, score = 82, counts = 27"
                /rpt_type=tandem
                /rpt_unit=cctt
                /evidence=not_experimental
exon            6807. .6884
                /note="FEXHB, score = 10.83%"
                /evidence=not_experimental
repeat_region   7337. .7454
                /rpt_family="L1"
                /evidence=not_experimental
exon            7483. .7533
                /note="FEXHB, score = 12.95%"
                /evidence=not_experimental
repeat_region   7950. .8010
                /rpt_family="MSTA"
                /evidence=not_experimental
repeat_region   8147. .8238
                /rpt_family="MSTA"
                /evidence=not_experimental
repeat_region   8245. .8286
                /rpt_family="MSTA"
                /evidence=not_experimental
repeat_region   8287. .8361
                /rpt_family="MSTC"
                /evidence=not_experimental
repeat_region   8878. .8921
                /note="homology = 97.70%, score = 20, counts = 2"
                /rpt_type=tandem
                /rpt_unit=gattttaccttgtcaagtgcta
                /evidence=not_experimental
exon            complement(9471. .9526)
                /note="MZEF, score = 85.6%"
                /evidence=not_experimental
exon            complement(9474. .9529)
                /note="FEXHB, score = 12.02%"
                /evidence=not_experimental
repeat_region   9618. .9660
                /rpt_family="MER3"
                /evidence=not_experimental
exon            10066. .10099
                /note="GRAIL, score = 61.000%, comment = good"
                /evidence=not_experimental
exon            11110. .11190
                /note="GRAIL, score = 76.000%, comment = excellent"
                /evidence=not_experimental
exon            11257. .11275
                /note="FEXHB, score = 19.61%"
                /evidence=not_experimental
repeat_region   11360. .11419
                /note="homology = 91.70%, score = 20, counts = 2"
                /rpt_type=tandem
                /rpt_unit=agggcaaatagctagaactattcatcaggc
                /evidence=not_experimental
exon            11613. .11637
                /note="Xpound exon prediction, score = 68% (0%)"
                /evidence=not_experimental
exon            complement(12630. .12662)
                /note="FEXHB, score = 13.07%"
                /evidence=not_experimental
repeat_region   13530. .13600
                /rpt_family="MLT2B2"
                /evidence=not_experimental
repeat_region   13607. .13760
                /rpt_family="MLT2B2"
                /evidence=not_experimental
exon            13820. .13947
                /note="GRAIL, score = 88.000%, comment = excellent"
                /evidence=not_experimental
repeat_region   13924. .13977
                /rpt_family="MLT2D"
                /evidence=not_experimental
repeat_region   13978. .14043
                /note="homology = 75.80%, score = 23, counts = 6"
                /rpt_type=tandem
                /rpt_unit=ctctctccttt
                /evidence=not_experimental
repeat_region   14054. .14087
                /note="homology = 94.10%, score = 28, counts = 17"
                /rpt_type=tandem
                /rpt_unit=tg
                /evidence=not_experimental
exon            complement(15048. .15137)
                /note="FEXHB, score = 12.14%"
                /evidence=not_experimental
exon            complement(15049. .15138)
                /note="MZEF, score = 83.8%"
                /evidence=not_experimental
misc_feature    15192. .57359
                /note="Region: Cosmid IG0799"
exon            complement(15720. .15884)
                /note="GRAIL, score = 53.000%, comment = good"
                /evidence=not_experimental
repeat_region   16505. .16631
                /rpt_family="L1MA9"
                /evidence=not_experimental
repeat_region   16659. .16746
                /rpt_family="MER4A"
                /evidence=not_experimental
repeat_region   16798. .16851
                /rpt_family="MER4A"
                /evidence=not_experimental
repeat_region   complement(16851. .16910)
                /rpt_family="THE1B"
                /evidence=not_experimental
repeat_region   complement(16920. .16972)
                /rpt_family="THE1B"
                /evidence=not_experimental
exon            complement(16931. .16963)
                /note="FEXHB, score = 12.61%"
                /evidence=not_experimental
repeat_region   complement(17023. .17178)
                /rpt_family="THE1B"
                /evidence=not_experimental
repeat_region   complement(17252. .17279)
                /rpt_family="THE1BR"
                /evidence=not_experimental
repeat_region   complement(17282. .17495)
```

Query Match 56.4%; Score 383; DB 11; Length 158898;
Best Local Similarity 96.3%; Pred. No. 2.5e-96;
Matches 392; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```
Qy    273 CCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 332
          ||||    | ||||    |       | ||||||||||||||||||||||||||||||||||
```

```
Db  92564 CCCACTTCTTTCCTTGTCCATTTTAGCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 92505

Qy    333 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92504 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 92445

Qy    393 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92444 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 92385

Qy    453 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92384 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 92325

Qy    513 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92324 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 92265

Qy    573 GCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  92264 GCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 92205

Qy    633 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTG 679
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  92204 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTG 92158


RESULT   7
HSY09764
LOCUS       HSY09764     10897 bp    DNA             PRI       31-OCT-1997
DEFINITION  Homo sapiens GABRE gene, exon 2-8.
ACCESSION   Y09764
VERSION     Y09764.1  GI:2285959
KEYWORDS    GABA receptor; GABRE gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10897)
  AUTHORS   Wilke,K., Gaul,R., Klauck,S.M. and Poustka,A.
  TITLE     A gene in human chromosome band Xq28 (GABRE) defines a putative new
            subunit class of the GABAA neurotransmitter receptor
  JOURNAL   Genomics 45 (1), 1-10 (1997)
  MEDLINE   97480709
REFERENCE   2  (bases 1 to 10897)
  AUTHORS   Wilke,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1996) K. Wilke, Deutsches Krebsforschungszentrum,
            Abteilung Molekulare Genomanalyse (840), Im Neuenheimer Feld 280,
            D-69120 Heidelberg, FRG
FEATURES             Location/Qualifiers
     source          1. .10897
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="q28"
                     /clone="cosmid Qc11C8"
     gene            1334. .10897
                     /gene="GABRE"
     exon            1334. .1551
                     /gene="GABRE"
                     /number=2
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            2000. .2288
                     /gene="GABRE"
                     /number=3
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            3346. .3428
                     /gene="GABRE"
                     /number=4
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            4736. .4873
                     /gene="GABRE"
                     /number=5
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            8163. .8315
                     /gene="GABRE"
                     /number=6
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            8456. .8655
                     /gene="GABRE"
                     /number=7
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            8939. .10897
                     /gene="GABRE"
                     /number=8
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
BASE COUNT     2630 a    2703 c    2465 g    3099 t
ORIGIN


  Query Match             55.9%;  Score 379.8;  DB 10;  Length 10897;
  Best Local Similarity   95.8%;  Pred. No. 1.4e-95;
  Matches  390;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy    273 CCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 332
          ||||    | ||||   |       | ||||||||||||||||||||||||||||||||||||
Db   8913 CCCACTTCTTTCCTTGTCCATTTTAGCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 8972

Qy    333 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8973 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 9032

Qy    393 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9033 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 9092

Qy    453 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9093 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 9152

Qy    513 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9153 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 9212

Qy    573 GCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9213 CCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 9272

Qy    633 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTG 679
          |||||||||||||||||||||||||||||| ||||||||||||||
Db   9273 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTTTTTGCCTTAACTTG 9319


RESULT   8
RNU92284
LOCUS       RNU92284     7479 bp    DNA             ROD       01-JAN-1998
DEFINITION  Rattus norvegicus GABA-A receptor epsilon subunit gene, partial
            cds.
ACCESSION   U92284
VERSION     U92284.1  GI:2735328
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 7479)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
```

```
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 7479)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .7479
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
     mRNA            join(<1. .200,895. .977,2138. .2275,5938. .6090,6207. .6406,
                     6654. .>7479)
                     /product="GABA-A receptor epsilon subunit"
     exon            <1. .200
                     /number=4
     CDS             join(<1. .200,895. .977,2138. .2275,5938. .6090,6207. .6406,
                     6654. .7034)
                     /codon_start=1
                     /product="GABA-A receptor epsilon subunit"
                     /protein_id="AAB93879.1"
                     /db_xref="GI:2735329"
                     /translation="FYQTWYDERLCYNDTFETLILHGNVVSQLWIPDTFFRNSKRTQE
                     YDITIPNQMALIHKDGKVLYTVRMTIDARCSLHMLNFPMDSHSCPLSFSSFSYDEHEM
                     IYKWENFKLKIDAKNTWKLLEFDFTGVNNKTEIISTPVGDFMVMTFFFNVSRRFGFIV
                     FQNYIPSSVTTMLSWVSFWIKIEAAAARASVGVSSVLTMATLGTFSRKNFPRVSYLTA
                     LDFYIAICFVLCFCTLLEFTVLNFLTYNNIERQASPKFYQFPTNSRANARTRARARTR
                     ARARARARQQQEVFVCEIVTYEENAEEGYQWSPRSRRPQCPWRRCGRSYVCFRVLRKY
                     FCMVPGCEGNSWQRGRICIHVYRLDNYSRVLFPITFFFFNVVYWVICLNL"
     intron          201. .894
                     /number=4
     exon            895. .977
                     /number=5
     intron          978. .2137
                     /number=5
     exon            2138. .2275
                     /number=6
     intron          2276. .5937
                     /number=6
     stem_loop       2412. .2496
     stem_loop       3389. .3472
     exon            5938. .6090
                     /number=7
     intron          6091. .6206
                     /number=7
     exon            6207. .6406
                     /number=8
     intron          6407. .6653
                     /number=8
     exon            6654. .>7479
                     /number=9
     3'UTR           7032. .>7479
BASE COUNT     1931 a   1620 c   1557 g   2371 t
ORIGIN
```

```
  Query Match           24.4%;  Score 165.8;  DB 12;  Length 7479;
  Best Local Similarity  67.9%;  Pred. No. 7.2e-36;
  Matches  271;  Conservative    0;  Mismatches  107;  Indels   21;  Gaps    2;

Qy     281 TCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGT 340
           | ||| |     ||| | ||  |     ||  ||||| | |||||| || ||||| |||
Db    6654 TTTCCAACCAATAGCCGTGCTAATGCACGTACTCGTGCTCGTGCCCGCACTCGTGCTCGT 6713

Qy     341 TCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAG 400
           | || ||| |||| || || || |||||||  ||||||||  |||||||  ||| |||
Db    6714 GCTCGTGCCCGTGCTCGTCAGCAGCAGGAAGTGTTTGTGTGTGAGATTGTTACCTATGAG 6773

Qy     401 GGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGC 460
           | || || || |||||                    ||||  | | || ||  || | ||
Db    6774 GAAAATGCTGAAGAGG--------------GTTACCAGTGGTCTCCAAGATCAAGAAGA 6818

Qy     461 CCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTT 520
           ||| || ||||| | || |  ||   |          ||| || ||| | || |  | |
Db    6819 CCTCAGTGTCCCTGGAGGCGATGTGGC------CGAAGCTATGTGTGCTTCAGGGTTCTC 6872

Qy     521 AAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTC 580
           | |||||| |||||||||| || | ||||||||||  | ||||||| |||||| ||
Db    6873 AGGAAGTATTTCTGCATGGTTCCTGGTTGTGAGGGCAACAGCTGGCAGCGGGGCCGCATC 6932

Qy     581 TGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTC 640
           |||||||| || || ||||||||||||||||| | ||  |||||||  | || ||||||
Db    6933 TGCATCCACGTTTATCGCCTGGATAACTACTCGCGGGTGCTTTTCCCCATTACATTCTTC 6992

Qy     641 TTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTG 679
           ||||| |||||| |||||||| |  ||||||||||| ||
Db    6993 TTCTTTAATGTGGTCTACTGGGTGATTTGCCTTAACCTG 7031
```

```
RESULT   9
GGGABAA
LOCUS       GGGABAA      1572 bp    mRNA            VRT       26-SEP-1994
DEFINITION  G.domesticus mRNA for GABA-A receptor gamma-4 subunit.
ACCESSION   X73533
VERSION     X73533.1  GI:414021
KEYWORDS    GABA-A receptor; GABA-A receptor gamma-4 subunit; glycoprotein;
            ligand gated ion channel; membrane spanning; multigene family;
            neurotransmitter receptor.
SOURCE      chicken.
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
            Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1572)
  AUTHORS   Harvey,R.J., Kim,H.C. and Darlison,M.G.
  TITLE     Molecular cloning reveals the existence of a fourth gamma subunit
            of the vertebrate brain GABAA receptor
  JOURNAL   FEBS Lett. 331 (3), 211-216 (1993)
  MEDLINE   93387470
REFERENCE   2  (bases 1 to 1572)
  AUTHORS   Darlison,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUN-1993) M. Darlison, Inst. fuer Zellbiochemie und
            Klinische Neurobiologie, Universitaet-Krankenhaus Eppendorf, Univ.
            Hamburg, 2000 Hamburg 20, FRG
FEATURES             Location/Qualifiers
     source          1. .1572
                     /organism="Gallus gallus"
                     /strain="Commercial Rhode Island cross"
                     /db_xref="taxon:9031"
                     /dev_stage="embryonic"
                     /tissue_type="whole brain"
                     /clone_lib="lambda gt10 cDNA library"
                     /clone="pcGR lambda4.1"
     CDS             88. .1461
                     /note="gamma-4 subunit"
                     /codon_start=1
                     /product="GABA-A receptor"
                     /protein_id="CAA51939.1"
                     /db_xref="GI:414022"
                     /db_xref="SWISS-PROT:P34904"
                     /translation="MPAMVLLLCLALGPALRSARCESTEEYDYDYLSINKTWVLTPKA
                     QETDATQILNSLLKNYDNKLRPDIGIKPTFIDVDIYVNSIGPVSVIQMEYTIDIFFAQ
                     TWYDRRLRFNSTLKALTLNTNMVSRIWIPDTFFRNSKRADSHWITTPNQLLRIWNDGK
                     VLYTLRLTIEAECLLQLQNFPMDTHSCPLVFSSYGYPREEIVYRWRRYSIEVSDQRTW
                     RLYQFDFTGLRNTSEVLRTGAGEYMVMTVSFDLSRRMGYFAIQTYIPCILTVVLSWVS
                     FWIKRDSTPARTSLGITTVLTMTTLSTISRKHLPRVSYITAMDLFVSVCFIFVFAALM
                     EYATLNYLVGNKKPLEHSSRKARLPPAGAQVMPSFTAININNNIMHWPPEIEEDEDD
                     DPGSPCLEGKECERFFCCIEDCQTGMWREGRVRIHISRLDSYSRVFFPTAFLLFNIVY
                     WIAYLYL"
     sig_peptide     88. .150
     mat_peptide     151. .1458
                     /product="GABA A receptor"
     misc_feature    151. .858
                     /note="large extracellular domain; putative"
     misc_feature    190. .198
```

```
                     /note="N-linked glycosylation site; putative"
     misc_feature    421. .429
                     /note="N-linked glycosylation site; putative"
     misc_feature    604. .648
                     /note="dicysteine loop; putative"
     misc_feature    775. .783
                     /note="N-linked glycosylation site; putative"
     misc_feature    859. .924
                     /note="membrane spanning domain; putative"
     misc_feature    937. .1002
                     /note="membrane spanning domain; putative"
     misc_feature    1036. .1104
                     /note="membrane spanning domain; putative"
     misc_feature    1105. .1386
                     /note="large intracellular loop; putative"
     misc_feature    1135. .1146
                     /note="casein kinase I phosphorylation site; putative"
     misc_feature    1141. .1149
                     /note="protein C kinase phosphorylation site; putative"
     misc_feature    1144. .1152
                     /note="protein C kinase phosphorylation site; putative"
     misc_feature    1375. .1386
                     /note="multifunctional calmodulin-dependent protein kinase
                     II phosphorylation site; putative"
     misc_feature    1387. .1458
                     /note="membrane spanning domain; putative"
BASE COUNT      356 a    443 c    385 g    388 t
ORIGIN
```

```
  Query Match             21.3%;  Score 144.4;  DB 4;  Length 1572;
  Best Local Similarity   71.4%;  Pred. No. 5.6e-30;
  Matches  190;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          |||| |||| | |||  | || |    | ||||     | || ||||||||||||||| ||
Db    861 TGCCATTCAGACCTACATTCCCTGCATCCTGACTGTTGTTCTGTCCTGGGTTTCCTTCTG 920

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          |||||||| ||| ||| | |||||| |||| || || || |||||| |||| || || ||
Db    921 GATCAAGAGAGACTCTACACCAGCCAGGACATCCCTCGGTATCACCACTGTGCTAACAAT 980

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||| || | ||| | || || ||| |  | || ||||| ||||||||||||||| |
Db    981 GACCACGCTGAGTACCATCTCCCGCAAGCACCTTCCACGTGTTTCCTATATCACAGCCAT 1040

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          |||  ||| | |  |  | |||||| |||||  |||    |||||  |||||| ||||
Db   1041 GGACCTCTTTGTGTCTGTGTGCTTCATCTTCGTCTTTGCAGCTCTCATGGAGTATGCTAC 1100

Qy    241 GCTCAACTTCCTGATCTACAACCAGA 266
           ||||||| |||| |    ||| |||
Db   1101 ACTCAACTACCTGGTGGGAAACAAGA 1126
```

```
RESULT  10
HSGABAAS
LOCUS       HSGABAAS     1745 bp    mRNA            PRI       15-MAR-1991
DEFINITION  Human mRNA for GABA-A receptor, gamma 2 subunit.
ACCESSION   X15376
VERSION     X15376.1  GI:31636
KEYWORDS    GABA-A receptor; gamma subunit receptor; gamma-aminobutyric acid
            receptor.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1745)
  AUTHORS   Pritchett,D.B., Sontheimer,H., Shivers,B.D., Ymer,S.,
            Kettenmann,H., Schofield,P.R. and Seeburg,P.H.
  TITLE     Importance of a novel GABAA receptor subunit for benzodiazepine
            pharmacology
  JOURNAL   Nature 338 (6216), 582-585 (1989)
  MEDLINE   89181956
FEATURES             Location/Qualifiers
     source          1. .1745
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /dev_stage="fetal"
                     /tissue_type="brain"
                     /tissue_lib="fetal brain cDNA"
     mRNA            1. .>1745
                     /note="for GABA-A receptor gamma 2 subunit"
     sig_peptide     226. .342
     CDS             227. .1630
                     /codon_start=1
                     /product="GABA-A receptor gamma 2 subunit"
                     /protein_id="CAA33437.1"
                     /db_xref="GI:31637"
                     /db_xref="SWISS-PROT:P18507"
                     /translation="MSSPNIWSTGSSVYSTPVFSQKMTVWILLLLSLYPGFTSQKSDD
                     DYEDYASNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIG
                     PVNAINMEYTIDIFFAQMWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADA
                     HWITTPNRMLRIWNDGRVLYSLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEI
                     VYQWKRSSVEVGDTRSWRLYQFSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFT
                     IQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTA
                     MDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPAPTIDIRPRSATIQMN
                     NATHLQERDEEYGYECLDGKDCASFFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFP
                     TAFCLFNLVYWVSYLYL"
     mat_peptide     341. .1627
                     /product="GABA-A receptor gamma 2 subunit"
BASE COUNT      492 a    389 c    378 g    486 t
ORIGIN
```

```
  Query Match             17.6%;  Score 119.6;  DB 9;  Length 1745;
  Best Local Similarity   64.4%;  Pred. No. 4.7e-23;
  Matches  179;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          | || | || | |||| |||| |   |  | |      | || |||||||| || || ||
Db   1051 TACCATCCAGACCTATATCCCCTGCACACTCATTGTCGTCCTATCCTGGGTGTCTTTCTG 1110

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          ||||||  |  ||  ||| ||||||| | || ||| |||| |||||| |||| ||||| ||
Db   1111 GATCAATAAGGATGCTGTTCCAGCCAGAACATCTTTAGGTATCACCACTGTCCTGACAAT 1170

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||  |  ||||| || | || ||     ||||    |||||||| |||||||  |
Db   1171 GACCACCCTCAGCACCATTGCCCGGAAATCGCTCCCCAAGGTCTCCTATGTCACAGCGAT 1230

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||||  ||| | |  |  | || ||| ||||   |||||  |||||| ||||||  ||
Db   1231 GGATCTCTTTGTATCTGTTTGTTTCATCTTTGTCTTCTCTGCTCTGGTGGAGTATGGCAC 1290

Qy    241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATG 278
            |  | |   |  ||  ||||| || |  |  | | |
Db   1291 CTTGCATTATTTTGTCAGCAACCGGAAACCAAGCAAGG 1328
```

```
RESULT  11
BOVGABAARG
LOCUS       BOVGABAARG   1428 bp    mRNA            MAM       27-APR-1993
DEFINITION  Bovine gamma-aminobutyrate receptor type A gamma-2 subunit mRNA,
            complete cds.
ACCESSION   M55563
VERSION     M55563.1  GI:163069
KEYWORDS    GABA-alpha receptor; gamma-aminobutyrate receptor type A.
SOURCE      Bovine cortex, cDNA to mRNA.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 1428)
  AUTHORS   Whiting,P.J., McKernan,R.M. and Iversen,L.L.
  TITLE     Another mechanism for creating diversity in gamma-aminobutyrate
```

```
            type A receptors: RNA splicing directs expression of two forms of
            gamma-2 subunit, one of which contains a protein kinase C
            phosphorylation site
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 87, 9966-9970 (1990)
  MEDLINE   91088632
FEATURES             Location/Qualifiers
     source          1. .1428
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /tissue_type="cortex"
     sig_peptide     1. .117
                     /gene="GABA-alpha receptor gamma-2 subunit"
     CDS             1. .1428
                     /gene="GABA-alpha receptor gamma-2 subunit"
                     /codon_start=1
                     /product="gamma-aminobutyrate receptor type A gamma-2
                     subuni"
                     /protein_id="AAA30531.1"
                     /db_xref="GI:163070"
                     /translation="MSSPNIWSTGSSVYSTPVFSQKMTLWILLLLSLYPGLTRQKSDD
                     DYEDYASNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIG
                     PVNAINMEYTIDIFFGQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADA
                     HWITTPNRMLRIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEI
                     VYQWKRSSVEVSDTRSWRLYQFSFVGLRNTTEVVKTTSGDYVVMTVYFDLSRRMGYFT
                     IQTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTA
                     MDLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPLLRMFSFKAPTIDIRP
                     RSATIQMNNATHLQERDEEYGYECLDGKDCASFFCCFEDCRTGAWRHGRIHIRIAKMD
                     SYARIFFPTAFCLFNLVYWVSYLYL"
     gene            1. .1428
                     /gene="GABA-alpha receptor gamma-2 subunit"
     mat_peptide     118. .1425
                     /gene="GABA-alpha receptor gamma-2 subunit"
                     /product="gamma-aminobutyrate receptor type A gamma-2
                     subuni"
BASE COUNT      399 a    325 c    303 g    401 t
ORIGIN
```

```
  Query Match           17.6%;  Score 119.2;  DB 3;  Length 1428;
  Best Local Similarity   64.5%;  Pred. No. 6e-23;
  Matches  178;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy       3 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 62
           || | || | |||  |||| | | |  | |      | || || ||||| || || ||||
Db     827 CCATCCAGACCTACATCCCCTGTACACTCATTGTTGTCCTATCTTGGGTGTCTTTCTGGA 886

Qy      63 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 122
           |||| |  ||  ||| |||||||  | || ||| |||| |||||| |||| ||||| ||||
Db     887 TCAATAAGGATGCTGTTCCAGCCAGAACTTCTTTAGGAATCACCACTGTCCTGACAATGA 946

Qy     123 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGG 182
           | ||  |  ||||| || | || |||  | ||||    ||||||||  |||||||  |||
Db     947 CTACCCTCAGCACCATTGCCCGGAAGTCTCTCCCCAAGGTCTCCTACGTCACAGCGATGG 1006

Qy     183 ATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGC 242
           || ||| | |  |  | |||||| ||||   |||||  ||| || |||||| ||     |
Db    1007 ATCTCTTTGTATCTGTTTGCTTCATCTTTGTCTTCTCTGCTTTGGTGGAGTATGGCACTC 1066

Qy     243 TCAACTTCCTGATCTACAACCAGACAAAAGCCCATG 278
           | | |   |  ||  ||||| || |  |  | | |
Db    1067 TGCATTATTTTGTCAGCAACCGGAAACCAAGCAAGG 1102
```

```
RESULT  12
RATGABAAI
LOCUS       RATGABAAI     1838 bp    DNA             ROD       27-APR-1993
DEFINITION  Rattus rattus GABA-A receptor gamma-2 subunit gene, complete cds.
ACCESSION   L08497
VERSION     L08497.1  GI:204217
KEYWORDS    GABA-alpha receptor gamma-2 subunit.
SOURCE      Rattus rattus (library: lambda-cDNA) brain DNA.
  ORGANISM  Rattus rattus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 1838)
  AUTHORS   Shivers,B.D., Killisch,I., Sprengel,R., Sontheimer,H., Koehler,M.,
            Schofield,P.R. and Seeburg,P.H.
  TITLE     Two novel GABA-A receptor subunits exist in distinct neuronal
            subpopulations
  JOURNAL   Neuron 3, 327-337 (1989)
  MEDLINE   90380375
REFERENCE   2  (bases 1 to 1838)
  AUTHORS   Seeburg,P.H., Wisden,W., Verdoorn,T.A., Pritchett,D., Werner,P.,
            Herb,A., Lueddens,H., Sprengel,R. and Sakmann,B.
  TITLE     The GABA-A receptor family: Molecular and functional diversity
  JOURNAL   Cold Spring Harb. Symp. Quant. Biol. 55, 29-40 (1990)
  MEDLINE   92111149
REFERENCE   3  (bases 1 to 1838)
  AUTHORS   Draguhn,A., Verdoorn,T.A., Ewert,M., Seeburg,P.H. and Sakmann,B.
  TITLE     Functional and molecular distinction between recombinant rat GABA-A
            receptor subtypes by Zn(2+)
  JOURNAL   Neuron 5, 781-788 (1990)
  MEDLINE   91097789
REFERENCE   4  (bases 1 to 1838)
  AUTHORS   Wisden,W. and Seeburg,P.H.
  TITLE     GABAA receptor channels: from subunits to functional entities
  JOURNAL   Curr. Opin. Neurobiol. 2 (3), 263-269 (1992)
  MEDLINE   92353623
REFERENCE   5  (bases 1 to 1838)
  AUTHORS   Wisden,W., Laurie,D.J., Monyer,H. and Seeburg,P.H.
  TITLE     The distribution of 13 GABA-A receptor subunit mRNAs in the rat
            brain - I. Telencephalon, diencephalon, mesencephalon
  JOURNAL   J. Neurosci. 12, 1040-1062 (1992)
  MEDLINE   92185508
REFERENCE   6  (bases 1 to 1838)
  AUTHORS   Laurie,D.J., Wisden,W. and Seeburg,P.H.
  TITLE     The distribution of 13 GABA-A receptor subunit mRNAs in the rat
            brain - II. Olfactory bulb and cerebellum
  JOURNAL   J. Neurosci. 12, 1063-1076 (1992)
  MEDLINE   92185509
FEATURES             Location/Qualifiers
     source          1. .1838
                     /organism="Rattus rattus"
                     /db_xref="taxon:10117"
                     /tissue_type="brain"
                     /tissue_lib="lambda-cDNA"
     CDS             45. .1445
                     /codon_start=1
                     /product="GABA-A receptor gamma-2 subunit"
                     /protein_id="AAC42036.1"
                     /db_xref="GI:204218"
                     /translation="MSSPNTWSTGSTVYSPVFSQKMTLWILLLLSLYPGFTSQKSDDD
                     YEDYASNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGP
                     VNAINMEYTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAH
                     WITTPNRMLRIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIV
                     YQWKRSSVEVGDTRSWRLYQFSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTI
                     QTYIPCTLIVVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAM
                     DLFVSVCFIFVFSALVEYGTLHYFVSNRKPSKDKDKKKKNPAPTIDIRPRSATIQMNN
                     ATHLQERDEEYGYECLDGKDCASFFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPT
                     AFCLFNLVYWVSYLYL"
BASE COUNT      509 a    404 c    408 g    517 t
ORIGIN
```

```
  Query Match           16.7%;  Score 113.6;  DB 12;  Length 1838;
  Best Local Similarity   62.9%;  Pred. No. 2.3e-21;
  Matches  176;  Conservative    0;  Mismatches  104;  Indels    0;  Gaps    0;

Qy       1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
           | || | || | |||  | || |   |  | | |    | | || |||||||| ||||| ||
Db     866 TACCATCCAGACCTACATTCCCTGCACACTCATTGTGGTTCTGTCCTGGGTGTCCTTCTG 925

Qy      61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
           ||||||  ||  |||  || ||  | || ||| |||| |||||  |||| ||||| ||
Db     926 GATCAATAAGGATGCTGTCCCTGCAAGAACATCTTTAGGAATCACGACTGTCCTGACGAT 985
```

```
Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||  |  ||||| |  | || |||  | | ||    |||||||| |||||||  |
Db    986 GACCACTCTCAGCACCATAGCCCGGAAGTCTCTGCCCAAGGTCTCCTATGTCACAGCAAT 1045

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          |||| |||   || |  | |||||| ||||    || |  ||| || |||||| || |
Db   1046 GGATCTCTTCGTCTCTGTTTGCTTCATCTTTGTGTTTTCAGCTTTGGTGGAGTATGGTAC 1105

Qy    241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCT 280
          ||  |||   |  |   ||||| || |  |  | | | |
Db   1106 CCTGCACTATTTTGTGAGCAACCGGAAACCAAGCAAGGAT 1145


RESULT  13
RATGABAA
LOCUS       RATGABAA     1654 bp    mRNA            ROD       27-APR-1993
DEFINITION  Rat GABA-A receptor gamma-3 subunit mRNA, complete cds.
ACCESSION   M81142
VERSION     M81142.1  GI:204199
KEYWORDS    GABA-alpha receptor gamma-3 subunit.
SOURCE      Rattus rattus unknown adult fore brain cDNA to mRNA.
  ORGANISM  Rattus rattus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 1654)
  AUTHORS   Herb,A., Wisden,W., Lueddens,H., Puia,G., Vicini,S. and
            Seeburg,P.H.
  TITLE     The third gamma subunit of the gamma-aminobutyric acid type A
            receptor family
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89, 1433-1437 (1992)
  MEDLINE   92159063
FEATURES             Location/Qualifiers
     source          1. .1654
                     /organism="Rattus rattus"
                     /db_xref="taxon:10117"
                     /dev_stage="adult"
                     /sex="unknown"
                     /tissue_type="fore brain"
     sig_peptide     103. .153
                     /gene="GABA-alpha receptor gamma-3 subunit"
     CDS             103. .1506
                     /gene="GABA-alpha receptor gamma-3 subunit"
                     /codon_start=1
                     /product="GABA-alpha receptor gamma-3 subunit"
                     /protein_id="AAA41181.1"
                     /db_xref="GI:204200"
                     /translation="MAAKLLLLLCLFSGLHARSRRVEEDDSEDSPSNQKWVLAPKSQD
                     TDVTLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSINMEYQIDIFFAQTW
                     TDSRLRFNSTMKILTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQLLRIWNDGKIL
                     YTLRLTINAECQLQLHNFPMDAHACPLTFSSYGYPKEEMIYRWRKNSVEAADQKSWRL
                     YQFDFMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFW
                     IKKDATPARTTLGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEY
                     ATLNYYSSCRKPTIRKKKTSLLHPDSTRWIPDRISLQAPSNYSLLDMRPPPPVMITLN
                     NSMYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSWRRGRIHIDVSELDSYSRVFFP
                     TSFLLFNLVYWVGYLYL"
     gene            103. .1506
                     /gene="GABA-alpha receptor gamma-3 subunit"
     mat_peptide     154. .1503
                     /gene="GABA-alpha receptor gamma-3 subunit"
                     /product="GABA-alpha receptor gamma-3 subunit"
BASE COUNT      449 a    414 c    374 g    417 t
ORIGIN


  Query Match             16.5%;  Score 112.2;  DB 12;  Length 1654;
  Best Local Similarity   66.1%;  Pred. No. 5.5e-21;
  Matches  162;  Conservative    0;  Mismatches   83;  Indels    0;  Gaps    0;

Qy      6 TTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCA 65
          | || |  ||| |||| |      ||||   | | || |||||||| || ||||||||||
Db    875 TCCAGACGTATATCCCCTGCATACTGACTGTGGTTCTGTCCTGGGTATCATTTTGGATCA 934

Qy     66 AGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCA 125
          |  | |||  |  | |||||  | ||  |  |||| |||||| | || || ||||||||||
Db    935 AAAAAGATGCGACACCAGCAAGAACAACATTAGGCATCACCACGGTGCTAACCATGACCA 994

Qy    126 CGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATT 185
          |  |  ||||| || |  | |||    | || || || |||||| |||| ||| ||||
Db    995 CACTCAGCACCATTGCCAGGAAGTCCCTGCCTCGGGTGTCCTATGTCACTGCCATGGACC 1054

Qy    186 TCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCA 245
          ||| | |  |  | ||||||  | ||   |||   ||| ||| ||||||  ||||   ||||
Db   1055 TCTTTGTGACTGTGTGCTTCTTGTTTGTCTTTGCCGCACTGATGGAGTATGCTACTCTCA 1114

Qy    246 ACTTC 250
          ||| |
Db   1115 ACTAC 1119


RESULT  14
RNGABAG3
LOCUS       RNGABAG3     1930 bp    mRNA            ROD       18-AUG-1992
DEFINITION  R.norvegicus mRNA for GABA-receptor gamma 3 subunit sequence.
ACCESSION   X63324
VERSION     X63324.1  GI:56181
KEYWORDS    GABA-A receptor gamma-3 subunit.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 1930)
  AUTHORS   Knoflach,F., Rhyner,T., Villa,M., Kellenberger,S., Drescher,U.,
            Malherbe,P., Sigel,E. and Mohler,H.
  TITLE     The gamma 3-subunit of the GABAA-receptor confers sensitivity to
            benzodiazepine receptor ligands
  JOURNAL   FEBS Lett. 293 (1-2), 191-194 (1991)
  MEDLINE   92070559
REFERENCE   2  (bases 1 to 1930)
  AUTHORS   Villa,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-AUG-1992) M. Villa, Parmacology, ETH and Univ of
            Zurich, Gloriastrasse 32, CH-8006 Zurich, SWITZERLAND
FEATURES             Location/Qualifiers
     source          1. .1930
                     /organism="Rattus norvegicus"
                     /strain="Zur-Siv"
                     /db_xref="taxon:10116"
                     /dev_stage="newborn"
                     /tissue_type="brain"
     CDS             177. .1580
                     /codon_start=1
                     /product="GABA-A receptor gamma-3 subunit"
                     /protein_id="CAA44930.1"
                     /db_xref="GI:56182"
                     /db_xref="SWISS-PROT:P28473"
                     /translation="MAAKLLLLLCLFSGLHARSRRVEEDDSEDSPSNQKWVLAPKSQD
                     TDVTLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSINMEYQIDIFFAQTW
                     TDSRLRFNSTMKILTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQLLRIWNDGKIL
                     YTLRLTINAECQLQLHNFPMDAHACPLTFSSYGYPKEEMIYRWRKNSVEAADQKSWRL
                     YQFDFMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFW
                     IKKDATPARTTLGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEY
                     ATLNYYSSCRKPTIRKKKTSLLHPDSTRWIPDRISLQAPSNYSLLDMRPPPPVMITLN
                     NSMYWQEFEDTCVYECLDGKDCQTFFCCYEECKSGSWRRGRIHIDVSELDSYSRVFFP
                     TSFLLFNLVYWVGYLYL"
BASE COUNT      554 a    520 c    398 g    458 t
ORIGIN


  Query Match             16.5%;  Score 112.2;  DB 12;  Length 1930;
  Best Local Similarity   66.1%;  Pred. No. 5.6e-21;
  Matches  162;  Conservative    0;  Mismatches   83;  Indels    0;  Gaps    0;

Qy      6 TTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCA 65
          | || |  ||| |||| |      ||||   | | || |||||||| || ||||||||||
Db    949 TCCAGACGTATATCCCCTGCATACTGACTGTGGTTCTGTCCTGGGTATCATTTTGGATCA 1008
```

```
Qy      66 AGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCA 125
           | | |||  |  | |||||  | ||  |  |||| |||||| | || || ||||||||||
Db    1009 AAAAAGATGCGACACCAGCAAGAACAACATTAGGCATCACCACGGTGCTAACCATGACCA 1068

Qy     126 CGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATT 185
           |  |  ||||| || |  | |||    | || || || |||||| |||| ||| ||||
Db    1069 CACTCAGCACCATTGCCAGGAAGTCCCTGCCTCGGGTGTCCTATGTCACTGCCATGGACC 1128

Qy     186 TCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCA 245
           ||| | |  |  | |||||| | ||   |||   ||| ||| |||||| ||||   ||||
Db    1129 TCTTTGTGACTGTGTGCTTCTTGTTTGTCTTTGCCGCACTGATGGAGTATGCTACTCTCA 1188

Qy     246 ACTTC 250
           ||| |
Db    1189 ACTAC 1193


RESULT  15
A46959
LOCUS       A46959       1565 bp    DNA             PAT       07-MAR-1997
DEFINITION  Sequence 7 from Patent WO9529234.
ACCESSION   A46959
VERSION     A46959.1  GI:2300979
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1565)
  AUTHORS   Whiting,P.J.
  TITLE     HUMAN GAMMA 3 GABA-A RECEPTOR SUBUNIT AND STABLY CO-TRANSFECTED
            CELL LINES
  JOURNAL   Patent: WO 9529234-A 7 02-NOV-1995;
            MERCK SHARP & DOHME (GB)
FEATURES             Location/Qualifiers
     source          1. .1565
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     CDS             33. .1436
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAA02960.1"
                     /db_xref="GI:2300980"
                     /translation="MAPKLLLLLCLFSGLHARSRKVEEDEYEDSSSNQKWVLAPKSQD
                     TDVTLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSINMEYQIDIFFAQTW
                     TDSRLRFNSTMKILTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQLLRIWNDGKIL
                     YTLRLTINAECQLQLHNFPMDEHSCPLIFSSYGYPKEEMIYRWRKNSVEAADQKSWRL
                     YQFDFMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFW
                     IKKDATPARTALGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEY
                     ATLNYYSSCRKPTTTKKTTSLLHPDSSRWIPERISLQAPSNYSLLDMRPPPPAMITLN
                     NSVYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSWRKGRIHIDILELDSYSRVFFP
                     TSFLLFNLVYWVGYLYL"
BASE COUNT      430 a    393 c    343 g    399 t
ORIGIN


  Query Match           16.5%;  Score 112;  DB 5;  Length 1565;
  Best Local Similarity  65.7%;  Pred. No. 6.2e-21;
  Matches  163;  Conservative    0;  Mismatches   85;  Indels    0;  Gaps    0;

Qy       3 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 62
           || |||| |  ||  | || | |    ||||   | |  | |||||||| || |||||||
Db     802 CCATTCAGACATACATTCCCTGTATACTGACTGTGGTTTTATCCTGGGTGTCATTTTGGA 861

Qy      63 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 122
           |||| | |||  || | |||||  | ||  |  |||| |||||| | || ||||||||||
Db     862 TCAAAAAAGATGCTACGCCAGCAAGAACAGCATTAGGCATCACCACGGTGCTGACCATGA 921

Qy     123 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGG 182
           ||||  || ||||| |  |  | |||   || || || || |||||  | || ||| |||
Db     922 CCACCCTGAGCACCATCGCCAGGAAGTCCTTGCCACGCGTGTCCTACGTGACCGCCATGG 981

Qy     183 ATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGC 242
           |  | | | |  | | |||||| | ||   ||||  ||| ||| |||||| |||    |

Db     982 ACCTTTTTGTGACTGTGTGCTTCCTGTTTGTCTTCGCCGCGCTGATGGAGTATGCCACCC 1041

Qy     243 TCAACTTC 250
           |||||| |
Db    1042 TCAACTAC 1049


Search completed: March  9, 2000, 01:36:26
Job time: 7169 sec
```

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2000, 13:40:02 ; Search time 147.28 Seconds
(without alignments)
551.952 Million cell updates/sec

Title: US-09-030-832-41_COPY_880_1558
Perfect score: 679
Sequence: 1 TGCCTTTCAAAACTATGTCC.....GGCTTGTTTGCCTTAACTTG 679

Scoring table: IDENTITY_NUC

Searched: 214294 seqs, 59861208 residues

Database : Issued_Patents_NA:*

Word size : 0

Number of hits that pass the threshold : 428588
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	106.6	15.7	1732	2	US-08-417-330A-17	Sequence 17, Appl
	2	95.2	14.0	2310	2	US-08-417-330A-15	Sequence 15, Appl
	3	91.6	13.5	1638	2	US-08-417-330A-13	Sequence 13, Appl
	4	90.8	13.4	1866	2	US-08-417-330A-19	Sequence 19, Appl
	5	89.6	13.2	1491	1	US-08-137-614A-3	Sequence 3, Appli
	6	89.6	13.2	1491	3	US-08-768-301-1	Sequence 1, Appli
	7	85.6	12.6	2191	2	US-08-417-330A-11	Sequence 11, Appl
	8	81	11.9	2635	3	US-08-768-301-3	Sequence 3, Appli
	9	72.8	10.7	1542	1	US-08-249-112-1	Sequence 1, Appli
	10	72.8	10.7	1542	6	PCT-US95-06556-1	Sequence 1, Appli
	11	72	10.6	1657	2	US-08-554-659-1	Sequence 1, Appli
	12	70.4	10.4	1657	2	US-08-554-659-3	Sequence 3, Appli
	13	65.6	9.7	2066	5	US-08-072-064-3	Sequence 3, Appli
	14	65.6	9.7	2066	5	US-08-072-064-5	Sequence 5, Appli
	15	64.8	9.5	7218	1	US-08-232-463-14	Sequence 14, Appl
	16	64	9.4	2066	5	US-08-072-064-2	Sequence 2, Appli
	17	64	9.4	1970	5	US-08-072-064-9	Sequence 9, Appli
	18	64	9.4	2059	6	PCT-US92-08558-2	Sequence 2, Appli
	19	64	9.4	1970	6	PCT-US92-08558-3	Sequence 3, Appli
	20	62.4	9.2	2066	5	US-08-072-064-7	Sequence 7, Appli
	21	62.2	9.2	3958	2	US-08-435-933-5	Sequence 5, Appli
	22	62.2	9.2	3958	6	PCT-US96-06035-5	Sequence 5, Appli
	23	58.2	8.6	1650	1	US-08-459-100A-1	Sequence 1, Appli
	24	58.2	8.6	1650	6	PCT-US94-09589-1	Sequence 1, Appli
	25	56	8.2	1479	1	US-08-249-112-2	Sequence 2, Appli
	26	56	8.2	1479	6	PCT-US95-06556-2	Sequence 2, Appli
	27	39.2	5.8	152	2	US-08-435-933-4	Sequence 4, Appli
	28	39.2	5.8	152	6	PCT-US96-06035-4	Sequence 4, Appli
	29	36.4	5.4	575	2	US-08-554-659-11	Sequence 11, Appl
c	30	33	4.9	2791	4	US-09-016-000-8	Sequence 8, Appli
	31	32.6	4.8	128	2	US-08-554-659-7	Sequence 7, Appli
	32	31.8	4.7	1140	1	US-08-236-427-1	Sequence 1, Appli
c	33	31.6	4.7	2277	2	US-08-676-967-2	Sequence 2, Appli
c	34	31.6	4.7	2277	2	US-08-676-974-2	Sequence 2, Appli
c	35	31.6	4.7	2277	4	US-09-098-487-2	Sequence 2, Appli
c	36	31	4.6	1373	4	US-08-394-189B-3	Sequence 3, Appli
c	37	31	4.6	1373	6	PCT-US93-05705-3	Sequence 3, Appli
	38	30.8	4.5	1907	1	US-08-462-884A-2	Sequence 2, Appli
	39	30.8	4.5	1908	2	US-08-461-881B-2	Sequence 2, Appli
	40	30.8	4.5	1908	4	US-09-123-960-2	Sequence 2, Appli
	41	30.6	4.5	1373	4	US-08-907-674-2	Sequence 2, Appli
c	42	30.6	4.5	15328	4	US-08-888-497-33	Sequence 33, Appl
	43	30.6	4.5	1373	4	US-09-215-087-2	Sequence 2, Appli
c	44	30.6	4.5	15328	6	PCT-US94-07926-33	Sequence 33, Appl
c	45	30	4.4	2085	1	US-08-164-839-3	Sequence 3, Appli

ALIGNMENTS

```
RESULT   1
US-08-417-330A-17
; Sequence 17, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1732 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  27...1385
;      OTHER INFORMATION:
US-08-417-330A-17


  Query Match             15.7%;  Score 106.6;  DB 2;  Length 1732;
```

```
  Best Local Similarity   62.6%;  Pred. No. 4.3e-23;
  Matches  166;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy       6 TTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCA 65
           | || |  ||    ||||     ||||    || || |||  ||| || || |||||  |
Db     760 TACAGATATACACTCCTTGCATTATGACAGTCATTCTTTCCCAGGTGTCTTTCTGGATTA 819

Qy      66 AGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCA 125
           | |  ||||| |  |||||  | ||   ||| |||||||||| ||||| | || |||||||
Db     820 ATAAGGAGTCCGTCCCAGCAAGAACTGTTCTTGGGATCACCACTGTTTTAACTATGACCA 879

Qy     126 CGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATT 185
           | ||| ||| |  | | ||  |   ||| ||    || || ||| ||| ||| ||||||
Db     880 CTTTGAGCATCAGTGCCCGGCACTCTTTGCCAAAAGTGTCATATGCCACTGCCATGGATT 939

Qy     186 TCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCA 245
             |  || ||  | ||||| |  |||  |||||  |||||  | ||||| || |   |||
Db     940 GGTTCATAGCTGTTTGCTTTGCATTCGTCTTCTCTGCTCTTATCGAGTTCGCAGCTGTCA 999

Qy     246 ACTTCCTGATCTACAACCAGACAAA 270
           |||  | | | | |    |||||| |
Db    1000 ACTACTTTACCAATCTTCAGACACA 1024


RESULT   2
US-08-417-330A-15
; Sequence 15, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2310 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  298...1683
;      OTHER INFORMATION:
US-08-417-330A-15


  Query Match             14.0%;  Score 95.2;  DB 2;  Length 2310;
  Best Local Similarity   60.4%;  Pred. No. 1.4e-19;
  Matches  157;  Conservative    0;  Mismatches  103;  Indels    0;  Gaps    0;

Qy       1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
           || | | || | |||  | || |      |||||  |||  | ||   ||| |||||||||
Db    1077 TGTCATCCAGACCTACCTTCCCTGCATAATGACCGTGATCTTATCACAGGTGTCCTTTTG 1136

Qy      61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
           | | ||    || || |  |||||| ||||   | | ||| ||||| | || |||||||||
Db    1137 GCTGAACCGGGAATCAGTCCCAGCCAGGACAGTTTTTGGGGTCACCACGGTGCTGACCAT 1196

Qy     121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
           ||| ||  |  ||| |    |  | ||   | | ||    ||  ||||   ||| ||| |
Db    1197 GACGACCCTCAGCATCAGCGCCAGGAACTCTCTGCCCAAAGTGGCCTACGCCACCGCCAT 1256

Qy     181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
           ||| |  |  || ||  | ||||  | ||||  |||||  || ||| | ||||||||
Db    1257 GGACTGGTTCATAGCTGTGTGCTATGCCTTCGTCTTCTCGGCGCTGATAGAGTTTGCCAC 1316

Qy     241 GCTCAACTTCCTGATCTACA 260
           | |||| | | | | | | |
Db    1317 GGTCAATTACTTTACCAAGA 1336


RESULT   3
US-08-417-330A-13
; Sequence 13, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1638 base pairs
```

```
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  87...1562
;      OTHER INFORMATION:
US-08-417-330A-13


  Query Match             13.5%;  Score 91.6;  DB 2;  Length 1638;
  Best Local Similarity   59.7%;  Pred. No. 1.5e-18;
  Matches  154;  Conservative    0;  Mismatches  104;  Indels    0;  Gaps    0;

Qy       1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
           ||   | || | |||  | || | |  | ||||    || || ||    || || || ||
Db     920 TGTGATCCAGACCTACTTGCCATGTATCATGACTGTCATTCTGTCACAAGTGTCGTTCTG 979

Qy      61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
           | |||| | |||||||| ||| ||||| ||     | ||  ||||| |||| || |||||
Db     980 GCTCAACAGAGAGTCTGTTCCTGCCCGTACAGTCTTTGGTGTCACCACTGTGCTTACCAT 1039

Qy     121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
           |||||| ||| | | |  | | |  || ||    || ||    ||  | |||   || ||| |
Db    1040 GACCACCTTGAGTATCAGTGCCAGAAATTCCTTACCTAAAGTGGCATATGCGACGGCCAT 1099

Qy     181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
           ||| |  |  || ||| |||| |  | |||    || |  || ||| | || |||||
Db    1100 GGACTGGTTCATAGCCGTCTGTTATGCCTTTGTATTTTCTGCACTGATTGAATTTGCCAC 1159

Qy     241 GCTCAACTTCCTGATCTA 258
             ||||||   | | | |
Db    1160 TGTCAACTATTTCACCAA 1177


RESULT   4
US-08-417-330A-19
; Sequence 19, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1866 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  225...1646
;      OTHER INFORMATION:
US-08-417-330A-19


  Query Match             13.4%;  Score 90.8;  DB 2;  Length 1866;
  Best Local Similarity   59.8%;  Pred. No. 2.8e-18;
  Matches  152;  Conservative    0;  Mismatches  102;  Indels    0;  Gaps    0;

Qy       4 CTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGAT 63
           | | ||||  ||  | |||||   | |||  || || ||||||||||| ||||| |||||
Db     962 CCTGCAAACATACATGCCTTCCATCCTGATTACCATCCTCTCCTGGGTCTCCTTCTGGAT 1021

Qy      64 CAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGAC 123
             ||    ||  || |  | ||  ||    |  |||| |||||  |||| || || |||||
Db    1022 TAATTACGATGCTTCAGCTGCAAGGGTGGCATTAGGAATCACAACTGTCCTCACAATGAC 1081

Qy     124 CACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGA 183
           |||  |   ||||      ||  | | | ||||     || ||||| | |  ||| | ||
Db    1082 CACAATCAACACCCACCTCCGGGAAACTCTCCCTAAAATCCCCTATGTGAAGGCCATTGA 1141

Qy     184 TTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCT 243
             | ||  |       ||||| ||||||   |||   || ||  |||| | |||   |  |
Db    1142 CATGTACCTGATGGGGTGCTTTGTCTTCGTTTTCATGGCCCTTCTGGAATATGCCCTAGT 1201

Qy     244 CAACTTCCTGATCT 257
           ||||| | |  |||
Db    1202 CAACTACATCTTCT 1215


RESULT   5
US-08-137-614A-3
; Sequence 3, Application US/08137614A
; Patent No. 5487976
;  GENERAL INFORMATION:
;    APPLICANT:  Soderlund, David M.
;    APPLICANT:  Knipple, Douglas C.
;    APPLICANT:  Henderson, Joseph E.
;    TITLE OF INVENTION:  Gene Encoding An Insect
;    TITLE OF INVENTION:  Gamma-Aminobutyric Acid (GABA) Receptor Subunit
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,614A
;      FILING DATE:  15-OCT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/120
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716)263-1636
;      TELEFAX:  (716)263-1600
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-137-614A-3


  Query Match             13.2%;  Score 89.6;  DB 1;  Length 1491;
  Best Local Similarity   60.1%;  Pred. No. 5.9e-18;
  Matches  149;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||  || ||||  ||| | ||         ||| |   ||||| || ||||| || || ||
Db    777 TGTATTCCAAACTTATCTGCCCAGCATTCTGATCGTAATGCTGTCGTGGGTCTCGTTCTG 836

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          ||| ||    ||| |  |    ||||||    |  | || |||||| | || || |||||
Db    837 GATTAACCACGAGGCGACGAGTGCCCGGGTTGCATTGGGCATCACCACGGTGCTCACCAT 896

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||  |  ||||  |  ||| |      | |||||  | || ||| | |  ||  |
Db    897 GACCACCATTAGCACGGGTGTTCGCAGCTCACTGCCGCGCATATCGTATGTGAAGGCGAT 956

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||  | ||| | | ||| |||||||| |||   |||   || || ||||| |  ||||
Db    957 CGACATTTATCTGGTCATGTGCTTCGTTTTCGTGTTCGCAGCCCTCTTGGAATACGCTGC 1016

Qy    241 GCTCAACT 248
          | ||||
Db   1017 CGTTAACT 1024


RESULT   6
US-08-768-301-1
; Sequence 1, Application US/08768301
; Patent No. 5854002
;  GENERAL INFORMATION:
;    APPLICANT:  Tomalski, Michael D.
;    APPLICANT:  Gant, Daniel B.
;    TITLE OF INVENTION:  METHOD OF IDENTIFYING COMPOUNDS THAT BIND
;    TITLE OF INVENTION:  TO THE INSECT GABA RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brumbaugh, Graves, Donohue & Raymond
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  10112-0228
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/768,301
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacLeod, Janet M
;      REGISTRATION NUMBER:  35,263
;      REFERENCE/DOCKET NUMBER:  A30693
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-408-2500
;      TELEFAX:  212-765-2519
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
US-08-768-301-1


  Query Match             13.2%;  Score 89.6;  DB 3;  Length 1491;
  Best Local Similarity   60.1%;  Pred. No. 5.9e-18;
  Matches  149;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||  || ||||  ||| | ||         ||| |   ||||| || ||||| || || ||
Db    777 TGTATTCCAAACTTATCTGCCCAGCATTCTGATCGTAATGCTGTCGTGGGTCTCGTTCTG 836

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          ||| ||    ||| |  |    ||||||    |  | || |||||| | || || |||||
Db    837 GATTAACCACGAGGCGACGAGTGCCCGGGTTGCATTGGGCATCACCACGGTGCTCACCAT 896

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||  |  ||||  |  ||| |      | |||||  | || ||| | |  ||  |
Db    897 GACCACCATTAGCACGGGTGTTCGCAGCTCACTGCCGCGCATATCGTATGTGAAGGCGAT 956

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||  | ||| | | ||| |||||||| |||   |||   || || ||||| |  ||||
Db    957 CGACATTTATCTGGTCATGTGCTTCGTTTTCGTGTTCGCAGCCCTCTTGGAATACGCTGC 1016

Qy    241 GCTCAACT 248
          | ||||
Db   1017 CGTTAACT 1024


RESULT   7
US-08-417-330A-11
; Sequence 11, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2191 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  214...1566
;      OTHER INFORMATION:
US-08-417-330A-11


  Query Match             12.6%;  Score 85.6;  DB 2;  Length 2191;
  Best Local Similarity   58.1%;  Pred. No. 1.2e-16;
  Matches  151;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy       1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
           ||   |||||| |||| | ||||    | ||||    || ||||||   ||||| || ||
Db     972 TGTGATTCAAACCTATCTGCCTTGCATCATGACTGTCATTCTCTCCCAAGTTTCATTCTG 1031

Qy      61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
           | | || | ||| ||||  || ||  | ||     | ||  | ||  |||| || || ||
Db    1032 GCTTAACAGAGAATCTGTGCCTGCAAGAACTGTGTTTGGAGTAACAACTGTCCTAACAAT 1091

Qy     121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
           ||| ||  |  ||| |  | |||| ||   | ||||    ||  | |||   || ||| |
Db    1092 GACAACTCTAAGCATCAGTGCTCGGAATTCTCTCCCCAAAGTGGCTTATGCAACTGCCAT 1151

Qy     181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
           ||| |  | ||| ||  | || |  |  ||    ||||  || ||  | || |||||
Db    1152 GGACTGGTTTATTGCTGTTTGTTATGCATTTGTGTTCTCTGCCCTAATTGAATTTGCAAC 1211

Qy     241 GCTCAACTTCCTGATCTACA 260
             | || | | | | | | |
Db    1212 TGTTAATTACTTCACCAAAA 1231


RESULT   8
US-08-768-301-3
; Sequence 3, Application US/08768301
; Patent No. 5854002
;  GENERAL INFORMATION:
;    APPLICANT:  Tomalski, Michael D.
;    APPLICANT:  Gant, Daniel B.
;    TITLE OF INVENTION:  METHOD OF IDENTIFYING COMPOUNDS THAT BIND
;    TITLE OF INVENTION:  TO THE INSECT GABA RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brumbaugh, Graves, Donohue & Raymond
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  10112-0228
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/768,301
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacLeod, Janet M
;      REGISTRATION NUMBER:  35,263
;      REFERENCE/DOCKET NUMBER:  A30693
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-408-2500
;      TELEFAX:  212-765-2519
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2635 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
US-08-768-301-3


  Query Match             11.9%;  Score 81;  DB 3;  Length 2635;
  Best Local Similarity   57.8%;  Pred. No. 3.2e-15;
  Matches  144;  Conservative    0;  Mismatches  105;  Indels    0;  Gaps    0;

Qy      14 TATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGAG 73
           || |  || |  | | ||     | | |||   ||||| ||||| ||| | ||    |||
Db    1553 TACGGTCCCTGCTGCCTGCTGGTGGTCCTCAGTTGGGTGTCCTTCTGGCTGAACCGCGAG 1612

Qy      74 TCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGGC 133
             | || | |  |||   || || ||||||||  | || |||||  ||||||    | ||
Db    1613 GCCACTGCTGATCGGGTTTCCCTCGGGATCACTACCGTGCTGACGATGACCTTTCTCGGA 1672

Qy     134 ACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATC 193
               |||| | | || | ||    || ||||||  ||| ||| |||| ||||   |
Db    1673 CTGGAGGCTCGCACGGATCTGCCCAAGGTGTCCTATCCCACGGCCCTGGACTTCTTCGTG 1732

Qy     194 GCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCTG 253
             | |||  |||| |||   |||   | |  |  || ||||||| ||| |  ||| |
Db    1733 TTCCTCTCGTTCGGCTTTATCTTTGCCACAATCCTGCAGTTTGCCGTGGTGCACTACTAC 1792

Qy     254 ATCTACAAC 262
           | | |  ||
Db    1793 ACCAAGTAC 1801


RESULT   9
US-08-249-112-1
; Sequence 1, Application US/08249112
; Patent No. 5527703
;  GENERAL INFORMATION:
;    APPLICANT:  Cully, Doris F.
;    APPLICANT:  Arena, Joseph P.
;    APPLICANT:  Liu, Ken K.
;    APPLICANT:  Vassilatis, Demetrios
;    TITLE OF INVENTION:  DNA ENCODING GLUTAMATE GATED CHLORIDE
;    TITLE OF INVENTION:  CHANNELS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wallen, John W.
;      STREET:  126 E. Lincoln Ave., P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

```
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/249,112
;      FILING DATE:  25-MAY-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wallen, John W.
;      REGISTRATION NUMBER:  35,403
;      REFERENCE/DOCKET NUMBER:  19194
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-3905
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1542 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-249-112-1


  Query Match             10.7%;  Score 72.8;  DB 1;  Length 1542;
  Best Local Similarity   55.0%;  Pred. No. 7.6e-13;
  Matches  143;  Conservative    0;  Mismatches  117;  Indels    0;  Gaps    0;

Qy       6 TTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCA 65
           | |||  |||  |||| || | | ||      ||  | ||||||||||| ||||||
Db     886 TCCAACTCTACATCCCGTCATGCATGCTAGTCATCGTATCCTGGGTTTCATTTTGGTTTG 945

Qy      66 AGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCA 125
           |   |    |    || || ||   | | || ||  |||||  |  | || || |||||
Db     946 ATCGAACTGCAATCCCGGCTCGTGTCACCCTCGGAGTCACCACGCTGCTTACAATGACAG 1005

Qy     126 CGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATT 185
           |       ||  |    |   | || |  || ||||||||||  ||  | |||
Db    1006 CTCAATCAGCCGGTATCAATTCACAACTACCTCCAGTTTCCTATATCAAGGCGATTGATG 1065

Qy     186 TCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCA 245
           |||  || |     ||  |    |||   ||||||||  ||||||||||||  || | |
Db    1066 TCTGGATTGGTGCATGTATGACATTCATTTTCTGCGCGTTGTTGGAGTTTGCATTGGTAA 1125

Qy     246 ACTTCCTGATCTACAACCAG 265
           |     |     |||| |||
Db    1126 ATCATATAGCTAACAAGCAG 1145


RESULT  10
PCT-US95-06556-1
; Sequence 1, Application PC/TUS9506556
;  GENERAL INFORMATION:
;    APPLICANT:  Cully, Doris F.
;    APPLICANT:  Arena, Joseph P.
;    APPLICANT:  Liu, Ken K.
;    APPLICANT:  Vassilatis, Demetrios
;    TITLE OF INVENTION:  DNA ENCODING GLUTAMATE GATED CHLORIDE
;    TITLE OF INVENTION:  CHANNELS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wallen, John W.
;      STREET:  126 E. Lincoln Ave., P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06556
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/249,112
;      FILING DATE:  25-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wallen, John W.
;      REGISTRATION NUMBER:  35,403
;      REFERENCE/DOCKET NUMBER:  19194
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-3905
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1542 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US95-06556-1


  Query Match             10.7%;  Score 72.8;  DB 6;  Length 1542;
  Best Local Similarity   55.0%;  Pred. No. 7.6e-13;
  Matches  143;  Conservative    0;  Mismatches  117;  Indels    0;  Gaps    0;

Qy       6 TTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCA 65
           | |||  |||  |||| || | | ||      ||  | ||||||||||| ||||||
Db     886 TCCAACTCTACATCCCGTCATGCATGCTAGTCATCGTATCCTGGGTTTCATTTTGGTTTG 945

Qy      66 AGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCA 125
           |   |    |    || || ||   | | || ||  |||||  |  | || || |||||
Db     946 ATCGAACTGCAATCCCGGCTCGTGTCACCCTCGGAGTCACCACGCTGCTTACAATGACAG 1005

Qy     126 CGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATT 185
           |       ||  |    |   | || |  || ||||||||||  ||  | |||
Db    1006 CTCAATCAGCCGGTATCAATTCACAACTACCTCCAGTTTCCTATATCAAGGCGATTGATG 1065

Qy     186 TCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCA 245
           |||  || |     ||  |    |||   ||||||||  ||||||||||||  || | |
Db    1066 TCTGGATTGGTGCATGTATGACATTCATTTTCTGCGCGTTGTTGGAGTTTGCATTGGTAA 1125

Qy     246 ACTTCCTGATCTACAACCAG 265
           |     |     |||| |||
Db    1126 ATCATATAGCTAACAAGCAG 1145


RESULT  11
US-08-554-659-1
; Sequence 1, Application US/08554659
; Patent No. 5767261
;  GENERAL INFORMATION:
;    APPLICANT:  Wingate, Vincent
;    APPLICANT:  Wolff, Mark
;    TITLE OF INVENTION:  LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
;    TITLE OF INVENTION:  AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/554,659
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  DiGiglio, Frank S
;       REGISTRATION NUMBER:  31,346
;       REFERENCE/DOCKET NUMBER:  9732
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (516) 742-4343
;       TELEFAX:  (516) 742-4366
;       TELEX:  230 901 SANS UR
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1657 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  115..1581
US-08-554-659-1


  Query Match             10.6%;  Score 72;  DB 2;  Length 1657;
  Best Local Similarity   55.6%;  Pred. No. 1.4e-12;
  Matches  138;  Conservative    0;  Mismatches  110;  Indels    0;  Gaps    0;

Qy       6 TTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCA 65
             |||| |  ||| | || |||  | | |      ||  | || ||||| || |||||| | |
Db     881 TTCAGATTTATATTCCGTCTGGCCTAATTGTCATTATATCTTGGGTATCATTTTGGTTGA 940

Qy      66 AGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCA 125
           |   | |  |  | || ||  ||   || |||||  ||||  ||||  |||| ||||| |
Db     941 ATCGAAATGCGACACCTGCAAGGGTATCACTAGGTGTCACAACTGTATTGACGATGACGA 1000

Qy     126 CGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATT 185
           || |     | |   |   |  | | ||     |||| ||| |||   || | |||
Db    1001 CGCTCATGTCGTCCACGAATGCGGCTCTGCCCAAGATCTCATATGTCAAGTCCATCGATG 1060

Qy     186 TCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCA 245
           ||||| | |  |  || |||||| |   |||| |  | | |  | || | |||   | |
Db    1061 TCTATCTGGGAACTTGTTTCGTCATGGTCTTCACCAGTTTACTAGAATATGCCACGGTTG 1120

Qy     246 ACTTCCTG 253
             ||   ||
Db    1121 GCTATATG 1128


RESULT  12
US-08-554-659-3
; Sequence 3, Application US/08554659
; Patent No. 5767261
;  GENERAL INFORMATION:
;    APPLICANT:  Wingate, Vincent
;    APPLICANT:  Wolff, Mark
;    TITLE OF INVENTION:  LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
;    TITLE OF INVENTION:  AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/554,659
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9732
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1657 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  115..1581
US-08-554-659-3


  Query Match             10.4%;  Score 70.4;  DB 2;  Length 1657;
  Best Local Similarity   55.2%;  Pred. No. 4.2e-12;
  Matches  137;  Conservative    0;  Mismatches  111;  Indels    0;  Gaps    0;

Qy       6 TTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCA 65
             |||| |  ||| | || |||  | | |      ||  | || ||||| || |||||| | |
Db     881 TTCAGATTTATATTCCGTCTGGCCTAATTGTCATTATATCTTGGGTATCATTTTGGTTGA 940

Qy      66 AGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCA 125
           |   | |  |  | || ||  ||   | |||||  ||||  ||||  |||| ||||| |
Db     941 ATCGAAATGCGACACCTGCAAGGGTAGCACTAGGTGTCACAACTGTATTGACGATGACGA 1000

Qy     126 CGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATT 185
           || |     | |   |   |  | | ||     |||| ||| |||   || | |||
Db    1001 CGCTCATGTCGTCCACGAATGCGGCTCTGCCCAAGATCTCATATGTCAAGTCCATCGATG 1060

Qy     186 TCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCA 245
           ||||| | |  |  || |||||| |   |||| |  | | |  | || | |||   | |
Db    1061 TCTATCTGGGAACTTGTTTCGTCATGGTCTTCACCAGTTTACTAGAATATGCCACGGTTG 1120

Qy     246 ACTTCCTG 253
             ||   ||
Db    1121 GCTATATG 1128


RESULT  13
US-08-072-064-3
; Sequence 3, Application US/08072064
; Patent No. 6008046
;  GENERAL INFORMATION:
;    APPLICANT:  FFRENCH-CONSTANT, RICHARD H.
;    APPLICANT:  JACKSON, MEYER B.
;    TITLE OF INVENTION:  DRUG AND PESTICIDE SCREENING
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER G. CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/072,064
;      FILING DATE:  19930602
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 770,881
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
```

```
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  OPHD-00574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2066 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
US-08-072-064-3


  Query Match             9.7%;  Score 65.6;  DB 5;  Length 2066;
  Best Local Similarity   54.0%;  Pred. No. 1.3e-10;
  Matches  134;  Conservative    0;  Mismatches  114;  Indels    0;  Gaps    0;

Qy      6 TTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCA 65
          | |||| ||| | || |||    ||| |    | | || ||||| || |||||| |||
Db    909 TACAAATCTACATACCCTCTGGACTGATCGTTGTTATATCATGGGTATCATTTTGGCTCA 968

Qy     66 AGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCA 125
          |    | |  | || || ||    || || ||  | ||  | ||  |||| |||||||
Db    969 ATCGCAATGCAACGCCGGCGCGTGTGTCGCTCGGTGTGACAACCGTGTTGACAATGACCA 1028

Qy    126 CGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATT 185
          | |||    | |   |   |       | ||     | || ||  ||| | |  | ||
Db   1029 CTTTGATGTCGTCAACAAATGCAGCGCTGCCAAAGATTTCGTACGTCAAATCGATTGACG 1088

Qy    186 TCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCA 245
          ||||| | |  |  |||||||  |   |||   |  |||  |||| |  ||   | ||
Db   1089 TCTATCTGGGAACATGCTTCGTTATGGTCTTTGCCAGTCTACTGGAATACGCCACGGTCG 1148

Qy    246 ACTTCCTG 253
            || | ||
Db   1149 GCTACATG 1156


RESULT  14
US-08-072-064-5
; Sequence 5, Application US/08072064
; Patent No. 6008046
;  GENERAL INFORMATION:
;    APPLICANT:  FFRENCH-CONSTANT, RICHARD H.
;    APPLICANT:  JACKSON, MEYER B.
;    TITLE OF INVENTION:  DRUG AND PESTICIDE SCREENING
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER G. CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/072,064
;      FILING DATE:  19930602
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 770,881
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  OPHD-00574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2066 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
US-08-072-064-5


  Query Match             9.7%;  Score 65.6;  DB 5;  Length 2066;
  Best Local Similarity   54.0%;  Pred. No. 1.3e-10;
  Matches  134;  Conservative    0;  Mismatches  114;  Indels    0;  Gaps    0;

Qy      6 TTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCA 65
          | |||| ||| | || |||    ||| |    | | || ||||| || |||||| |||
Db    909 TACAAATCTACATACCCTCTGGACTGATCGTTGTTATATCATGGGTATCATTTTGGCTCA 968

Qy     66 AGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCA 125
          |    | |  | || || ||    || || ||  | ||  | ||  |||| |||||||
Db    969 ATCGCAATGCAACGCCGGCGCGTGTGTCGCTCGGTGTGACAACCGTGTTGACAATGACCA 1028

Qy    126 CGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATT 185
          | |||    | |   |   |       | ||     | || ||  ||| | |  | ||
Db   1029 CTTTGATGTCGTCAACAAATGCAGCGCTGCCAAAGATTTCGTACGTCAAATCGATTGACG 1088

Qy    186 TCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCA 245
          ||||| | |  |  |||||||  |   |||   |  |||  |||| |  ||   | ||
Db   1089 TCTATCTGGGAACATGCTTCGTTATGGTCTTTGCCAGTCTACTGGAATACGCCACGGTCG 1148

Qy    246 ACTTCCTG 253
            || | ||
Db   1149 GCTACATG 1156


RESULT  15
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-Fls
US-08-232-463-14


  Query Match             9.5%;  Score 64.8;  DB 1;  Length 7218;
  Best Local Similarity   2.4%;  Pred. No. 4.3e-10;
  Matches    9;  Conservative  231;  Mismatches  138;  Indels    0;  Gaps    0;

Qy      13 CTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAGACAGA 72
           :: : :::::::::::: :  :: :  : ::::::::   :::::::::   ::    :
Db    1069 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1128

Qy      73 GTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACGTTGGG 132
            ::: ::::  :::   ::::::::      :: ::::: :::::  :: :  :: : ::
Db    1129 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1188

Qy     133 CACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATAT 192
           : :::::::::: :     :::::: : : :::::: : :: :  ::::   ::::: : :
Db    1189 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1248

Qy     193 CGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAACTTCCT 252
           : :: ::: :::: :::::: ::::: : :::: ::    ::: :: : :::  ::::::
Db    1249 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1308

Qy     253 GATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAG 312
             ::: :  ::   :     ::: : ::::::::   :::: :: ::::: : ::  :
Db    1309 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1368

Qy     313 CCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGC 372
           :: : ::: : ::: : ::: : : : :::::   ::: : ::: ::  : ::      :
Db    1369 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1428

Qy     373 TTTTGTGTGCCAGATTGT 390
           :::: :|| ||| ||| |
Db    1429 YYYYYYGTACCAAATTCT 1446


Search completed: March  9, 2000, 13:40:14
Job time: 962 sec
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2000, 22:45:20 ; Search time 235.59 Seconds
(without alignments)
721.085 Million cell updates/sec

Title: US-09-030-832-41_COPY_880_1558
Perfect score: 679
Sequence: 1 TGCCTTTCAAAACTATGTCC.....GGCTTGTTTGCCTTAACTTG 679

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	679	100.0	3123	1	V11776	GABA-A receptor ep
2	679	100.0	3026	1	V11777	Variant of GABA-A
3	677.4	99.8	1552	1	V36319	Human GABA recepto
4	379.8	55.9	10697	1	V11778	GABA-A receptor ep
5	112	16.5	1565	1	T02334	GABA-A receptor ga
6	106.6	15.7	1408	1	Q33130	GABA-A receptor al
7	106.6	15.7	1408	1	Q69142	Human GABA recepto
8	99.6	14.7	1707	1	T28988	Human GABA-A recep
9	95.2	14.0	2310	1	Q33129	GABA-A receptor al
10	95.2	14.0	2310	1	Q69141	Human GABA recepto
11	91.6	13.5	1638	1	Q33128	GABA-A receptor al
12	91.6	13.5	1638	1	Q69140	Human GABA recepto
13	90.8	13.4	1866	1	Q33131	GABA-A receptor be
14	90.8	13.4	1866	1	Q69143	Human GABA recepto
15	90.2	13.3	1884	1	V83111	Human GABA-A recep
16	90.2	13.3	1884	1	V83112	Human GABA-A recep
17	89.6	13.2	1491	1	Q99330	GABA receptor subu
18	89.6	13.2	1491	1	V84685	Insect GABA recept
19	85.6	12.6	2189	1	Q33127	GABA-A receptor al
20	85.6	12.6	2189	1	Q69139	Human GABA recepto
21	83	12.2	1555	1	T28989	Human GABA-A recep
22	81	11.9	2635	1	V84686	Insect GABA recept
23	72.8	10.7	1542	1	T09695	Caenorhabditis ele
24	72.2	10.6	1368	1	X24372	Cat flea glutamate
25	72.2	10.6	1297	1	X24373	Cat flea glutamate
26	72	10.6	1657	1	V55007	GABA gated chlorid
27	72	10.6	1844	1	V64372	GABA-gated chlorid
28	70.4	10.4	1657	1	V55008	GABA gated chlorid
29	67.2	9.9	1519	1	V64373	GABA-gated chlorid
30	67.2	9.9	669	1	V64374	GABA-gated chlorid
31	64.6	9.5	1650	1	T10500	Human GABA-A recep
32	64.6	9.5	1650	1	T84630	Human GABA-A recep
33	64	9.4	2059	1	Q40045	Sequence of cDNA N
34	62.4	9.2	1823	1	X16065	DNA sequence of Lu
35	62.2	9.2	3958	1	T43596	Glutamate-gated ch
36	56	8.2	1479	1	T09696	Caenorhabditis ele
37	45	6.6	45	1	V36324	Human GABA recepto
38	43.4	6.4	45	1	V36325	Human GABA recepto
39	39.2	5.8	152	1	T43599	Glutamate-gated ch
40	36.4	5.4	575	1	V55016	Fragment of GABA g
c 41	36.2	5.3	3252	1	Q54375	Human BDNF vector.
c 42	36.2	5.3	1353	1	Q54374	Human BDNF cDNA. E
43	36	5.3	1323	1	Q87844	Cladosporium herba
c 44	34.4	5.1	607	1	V87463	EST clone BP833. N
c 45	34.2	5.0	2744	1	V84799	Nucleotide sequenc

ALIGNMENTS

RESULT 1
V11776
ID V11776 standard; cDNA; 3123 BP.
AC V11776;
DT 25-SEP-1998 (first entry)
DE GABA-A receptor epsilon sub-unit related gene.
KW ss; GABA-A receptor; diagnosis; therapy; drug screening.
OS Mammalia.
FH Key Location/Qualifiers
FT CDS 55. .1573
FT /*tag= a
FT /product= "GABA-A receptor epsilon sub-unit related
FT protein"
PN DE19644501-A1.
PD 30-APR-1998.
PF 25-OCT-1996; 044501.
PR 25-OCT-1996; DE-044501.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR WPI; 98-252096/23.
DR P-PSDB; W59048.
PT Protein related to GABA-A receptor sub-unit epsilon - useful for
PT diagnosis, therapy or drug screening
PS Example 1; Fig 1; 12pp; German.
CC The GABA-A receptor sub-unit epsilon related protein is used for the
CC diagnosis and/or therapy of related disorders. It can also be used to
CC screen for substances that modulate the activity of the protein.
SQ Sequence 3123 BP; 710 A; 877 C; 686 G; 849 T;

Query Match 100.0%; Score 679; DB 1; Length 3123;
Best Local Similarity 100.0%; Pred. No. 1.2e-186;
Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     894 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 953

Qy      61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     954 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 1013

Qy     121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1014 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 1073

Qy     181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1074 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 1133

Qy     241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1134 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 1193

Qy     301 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1194 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 1253

Qy     361 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1254 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 1313
```

```
Qy    421 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1314 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 1373

Qy    481 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1374 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 1433

Qy    541 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1434 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 1493

Qy    601 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1494 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 1553

Qy    661 GCTTGTTTGCCTTAACTTG 679
          ||||||||||||||||||||
Db   1554 GCTTGTTTGCCTTAACTTG 1572
```

RESULT 2
V11777
ID V11777 standard; DNA; 3026 BP.
AC V11777;
DT 25-SEP-1998 (first entry)
DE Variant of GABA-A receptor epsilon sub-unit related gene.
KW ss; GABA-A receptor; diagnosis; therapy; drug screening.
OS Mammalia.
FH Key Location/Qualifiers
FT CDS 55. .1479
FT /*tag= a
FT /product= "Variant of GABA-A receptor epsilon sub-unit
FT related protein"
PN DE19644501-A1.
PD 30-APR-1998.
PF 25-OCT-1996; 044501.
PR 25-OCT-1996; DE-044501.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR WPI; 98-252096/23.
DR P-PSDB; W59048.
PT Protein related to GABA-A receptor sub-unit epsilon - useful for
PT diagnosis, therapy or drug screening
PS Disclosure; Fig 2; 12pp; German.
CC The GABA-A receptor sub-unit epsilon related protein is used for the
CC diagnosis and/or therapy of related disorders. It can also be used to
CC screen for substances that modulate the activity of the protein.
SQ Sequence 3026 BP; 689 A; 853 C; 663 G; 821 T;

Query Match 100.0%; Score 679; DB 1; Length 3026;
Best Local Similarity 100.0%; Pred. No. 1.2e-186;
Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    798 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 857

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    858 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 917

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    918 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 977

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    978 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 1037

Qy    241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1038 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 1097

Qy    301 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1098 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 1157

Qy    361 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1158 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 1217

Qy    421 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1218 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 1277

Qy    481 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1278 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 1337

Qy    541 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 1397

Qy    601 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1398 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 1457

Qy    661 GCTTGTTTGCCTTAACTTG 679
          ||||||||||||||||||||
Db   1458 GCTTGTTTGCCTTAACTTG 1476
```

RESULT 3
V36319
ID V36319 standard; cDNA; 1552 BP.
AC V36319;
DT 12-OCT-1998 (first entry)
DE Human GABA receptor epsilon subunit cDNA.
KW GABA receptor; gamma-amino butyric acid receptor; human;
KW appetite; cognition; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 18. .1538
FT /*tag= a
PN WO9823742-A1.
PD 04-JUN-1998.
PF 18-NOV-1997; G03159.
PR 03-OCT-1997; GB-020995.
PR 25-NOV-1996; GB-024442.
PA (MERI) MERCK SHARP & DOHME LTD.
PI Whiting PJ;
DR WPI; 98-322722/28.
DR P-PSDB; W61045.
PT New isolated GABA receptor subunit, epsilon - used to develop
PT products for the screening and design of drugs, e.g. for modulating
PT appetite behaviours, hormonal interactions and cognition
PS Claim 5; Fig 1; 37pp; English.
CC This cDNA sequence codes for a novel class of subunit (see W61045),
CC classified as epsilon, within the human GABA receptor gene family.
CC It was generated from human brain cDNA by PCR using primers (see
CC V36322-23) derived from the 5' untranslated region (UTR) of an
CC anchored PCR product (see V36320-21) and from the 3'UTR of EST
CC R49718 (obtained from an EST database search using a GABA-A
CC receptor polypeptide). A stably co-transfected eukaryotic cell
CC line capable of expressing the GABA epsilon receptor subunit, at
CC least one alpha receptor subunit and at least one beta receptor
CC subunit is claimed. A recombinant expression vector, and protein
CC and membrane preparations of the GABA receptor obtained from the
CC co-transfected cells are also claimed. The new GABA-A receptor
CC epsilon subunit and products can be used in the screening and
CC design of drugs which act upon the GABA receptor. The ligands or
CC drug candidates identified may be used as therapeutic agents, e.g.
CC for the modulation of appetite behaviours, hormonal interactions
CC and cognition. They can also be used for the study of structure,

```
CC   pharmacology and function of the various GABA receptor subtypes.
SQ   Sequence   1552 BP;    344 A;    443 C;    349 G;    416 T;


  Query Match             99.8%;  Score 677.4;  DB 1;  Length 1552;
  Best Local Similarity   99.9%;  Pred. No. 2.7e-186;
  Matches  678;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     857 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 916

Qy      61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     917 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 976

Qy     121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     977 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 1036

Qy     181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1037 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 1096

Qy     241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1097 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTTCTCCTAAACTCCGCCATCC 1156

Qy     301 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1157 TCGTATCAATAGCCGTGCCCATGCCCGTACCCGTGCACGTTCCCGAGCCTGTGCCCGCCA 1216

Qy     361 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1217 ACATCAGGAAGCTTTTGTGTGCCAGATTGTCACCACTGAGGGAAGTGATGGAGAGGAGCG 1276

Qy     421 CCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 480
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    1277 CCCGTCTTGCTCTGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCT 1336

Qy     481 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1337 CTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGT 1396

Qy     541 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1397 CCCCGATTGTGAGGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCT 1456

Qy     601 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1457 GGATAACTACTCGAGAGTTGTTTTCCCAGTGACTTTCTTCTTCTTCAATGTGCTCTACTG 1516

Qy     661 GCTTGTTTGCCTTAACTTG 679
          ||||||||||||||||||||
Db    1517 GCTTGTTTGCCTTAACTTG 1535


RESULT   4
V11778
ID   V11778 standard; DNA; 10697 BP.
AC   V11778;
DT   25-SEP-1998  (first entry)
DE   GABA-A receptor epsilon sub-unit related genomic sequence.
KW   ss; GABA-A receptor; diagnosis; therapy; drug screening.
OS   Mammalia.
FH   Key             Location/Qualifiers
FT   exon            1. .110
FT                   /*tag= a
FT                   /number= 1
FT   intron          111. .1217
FT                   /*tag= b
FT                   /number= 1
FT   exon            1218. .1435
FT                   /*tag= c
FT                   /number= 2
FT   intron          1436. .1883
FT                   /*tag= d
FT                   /number= 2
FT   exon            1884. .2172
FT                   /*tag= e
FT                   /number= 3
FT   intron          2173. .3169
FT                   /*tag= f
FT                   /number= 3
FT   exon            3170. .3252
FT                   /*tag= g
FT                   /number= 4
FT   intron          3253. .4559
FT                   /*tag= h
FT                   /number= 4
FT   exon            4560. .4697
FT                   /*tag= i
FT                   /number= 5
FT   intron          4698. .7962
FT                   /*tag= j
FT                   /number= 5
FT   exon            7963. .8115
FT                   /*tag= k
FT                   /number= 6
FT   intron          8116. .8255
FT                   /*tag= l
FT                   /number= 6
FT   exon            8256. .8455
FT                   /*tag= m
FT                   /number= 7
FT   intron          8456. .8738
FT                   /*tag= n
FT                   /number= 7
FT   exon            8739. .10697
FT                   /*tag= o
FT                   /number= 8
PN   DE19644501-A1.
PD   30-APR-1998.
PF   25-OCT-1996; 044501.
PR   25-OCT-1996; DE-044501.
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI   Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR   WPI; 98-252096/23.
PT   Protein related to GABA-A receptor sub-unit epsilon - useful for
PT   diagnosis, therapy or drug screening
PS   Disclosure; Fig 3; 12pp; German.
CC   The GABA-A receptor sub-unit epsilon related protein is used for the
CC   diagnosis and/or therapy of related disorders.  It can also be used to
CC   screen for substances that modulate the activity of the protein.
SQ   Sequence   10697 BP;    2524 A;    2704 C;    2471 G;    2991 T;


  Query Match             55.9%;  Score 379.8;  DB 1;  Length 10697;
  Best Local Similarity   95.8%;  Pred. No. 5.2e-100;
  Matches  390;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy     273 CCCATGCTTCTCCTAAACTCCGCCATCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 332
           ||||    | ||||   |      | ||||||||||||||||||||||||||||||||||
Db    8713 CCCACTTCTTTCCTTGTCCATTTTAGCCTCGTATCAATAGCCGTGCCCATGCCCGTACCC 8772

Qy     333 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8773 GTGCACGTTCCCGAGCCTGTGCCCGCCAACATCAGGAAGCTTTTGTGTGCCAGATTGTCA 8832

Qy     393 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 452
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8833 CCACTGAGGGAAGTGATGGAGAGGAGCGCCCGTCTTGCTCAGCCCAGCAGCCCCCTAGCC 8892

Qy     453 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 512
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8893 CAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCTGGCCTGCTGTGAGTGGTGCA 8952
```

```
Qy     513 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 572
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8953 AGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGAGGGCAGTACCTGGCAGCAGG 9012

Qy     573 GCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 632
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    9013 CCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTACTCGAGAGTTGTTTTCCCAGTGA 9072

Qy     633 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTGTTTGCCTTAACTTG 679
           ||||||||||||||||||||||||||||| ||||||||||||||
Db    9073 CTTTCTTCTTCTTCAATGTGCTCTACTGGCTTTTTTGCCTTAACTTG 9119


RESULT   5
T02334
ID   T02334 standard; cDNA; 1565 BP.
AC   T02334;
DT   02-FEB-1996  (first entry)
DE   GABA-A receptor gamma-3 subunit cDNA.
KW   GABA-A receptor; gamma-aminobutyric acid receptor; gamma-3 subunit;
KW   ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             33. .1436
FT                   /*tag=  a
PN   WO9529234-A1.
PD   02-NOV-1995.
PF   12-APR-1995; G00834.
PR   22-APR-1994; GB-008064.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Whiting PJ;
DR   WPI; 95-382983/49.
DR   P-PSDB; R83968.
PT   New cell line expressing human GABA-A receptor sub-units - useful in
PT   drug screening and design
PS   Claim 5; Page 18-20; 30pp; English.
CC   A rat GABA-A receptor gamma-3 subunit cDNA probe was used to screen
CC   a human foetal brain cDNA library.  The single isolated clone
CC   lacked the 5' and 3' ends of the gamma-3 subunit coding region.
CC   These were obtd. by further PCR using primers based on the
CC   truncated sequence, giving a complete cDNA sequence (T02334).
CC   This can be used to express gamma-3 in transfected eukaryotic
CC   (pref. rodent fibroblast) cell lines for prodn. of hybrid GABA-A
CC   receptors having novel subunit compositions.
SQ   Sequence   1565 BP;    430 A;    397 C;    339 G;    399 T;


  Query Match             16.5%;  Score 112;  DB 1;  Length 1565;
  Best Local Similarity   65.7%;  Pred. No. 5.2e-23;
  Matches  163;  Conservative    0;  Mismatches   85;  Indels    0;  Gaps    0;

Qy       3 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 62
           || |||| |  ||  | || | |    ||||   | |  | |||||||| || |||||||
Db     802 CCATTCAGACATACATTCCCTGTATACTGACTGTGGTTTTATCCTGGGTGTCATTTTGGA 861

Qy      63 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 122
           |||| | |||  || | |||||  | ||  |  |||| |||||| | || ||||||||||
Db     862 TCAAAAAAGATGCTACGCCAGCAAGAACAGCATTAGGCATCACCACGGTGCTGACCATGA 921

Qy     123 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGG 182
           ||||  || ||||| |  |  | |||   || || || || |||||  | || ||| |||
Db     922 CCACCCTGAGCACCATCGCCAGGAAGTCCTTGCCACGCGTGTCCTACGTGACCGCCATGG 981

Qy     183 ATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGC 242
           |  | | | |  |  | ||||||| | ||   ||||  ||| ||| ||||||| |||    |
Db     982 ACCTTTTTGTGACTGTGTGCTTCCTGTTTGTCTTCGCCGCGCTGATGGAGTATGCCACCC 1041

Qy     243 TCAACTTC 250
           |||||| |
Db    1042 TCAACTAC 1049
```

```
RESULT   6
Q33130
ID   Q33130 standard; DNA; 1408 BP.
AC   Q33130;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-6 subunit gene.
KW   Primer; human; alpha-6; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             27. .1388
FT                   /*tag=  a
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   P-PSDB; R31187.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Claim 8; Fig 5; 43pp; English.
CC   The sequence given encodes the human alpha-6 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Rat alpha-6 cDNA was used as a probe
CC   and a human alpha-6 cDNA clone was isolated from a cerebellum cDNA
CC   library.  No full length cDNA's were isolated. To obtain a full length
CC   cDNA 3 clones were joined together using convenient restriction sites.
CC   GABA-A receptor comprises a multimeric protein of molecular size
CC   230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   1408 BP;    392 A;    321 C;    300 G;    395 T;


  Query Match             15.7%;  Score 106.6;  DB 1;  Length 1408;
  Best Local Similarity   62.6%;  Pred. No. 1.8e-21;
  Matches  166;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy       6 TTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCA 65
           | || |  ||    ||||      ||||    || || |||  ||| || || |||||  |
Db     760 TACAGATATACACTCCTTGCATTATGACAGTCATTCTTTCCCAGGTGTCTTTCTGGATTA 819

Qy      66 AGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCA 125
           | |  |||||  |  |||||  | ||   ||| |||||||||| ||||| | || |||||||
Db     820 ATAAGGAGTCCGTCCCAGCAAGAACTGTTCTTGGGATCACCACTGTTTTAACTATGACCA 879

Qy     126 CGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATT 185
           | ||| ||| |  | | | ||  |   ||| ||   || || |||  ||| ||| ||||||
Db     880 CTTTGAGCATCAGTGCCCGGCACTCTTTGCCAAAAGTGTCATATGCCACTGCCATGGATT 939

Qy     186 TCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCA 245
           |  || ||  | ||||| |  |||  |||||  |||||  | ||||| || |   |||
Db     940 GGTTCATAGCTGTTTGCTTTGCATTCGTCTTCTCTGCTCTTATCGAGTTCGCAGCTGTCA 999

Qy     246 ACTTCCTGATCTACAACCAGACAAA 270
           ||| | | | | |    |||||| |
Db    1000 ACTACTTTACCAATCTTCAGACACA 1024


RESULT   7
```

```
Q69142
ID   Q69142 standard; DNA; 1408 BP.
AC   Q69142;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha6 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             27. .1388
FT                   /*tag=  a
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   P-PSDB; R59865.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.5; 79pp; English.
CC   This receptor DNA may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   1408 BP;    392 A;    321 C;    300 G;    395 T;


  Query Match             15.7%;  Score 106.6;  DB 1;  Length 1408;
  Best Local Similarity   62.6%;  Pred. No. 1.8e-21;
  Matches  166;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy       6 TTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCA 65
           | || |  ||    ||||      ||||    || || |||  ||| || || ||||| |
Db     760 TACAGATATACACTCCTTGCATTATGACAGTCATTCTTTCCCAGGTGTCTTTCTGGATTA 819

Qy      66 AGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCA 125
           | |  ||||| |  |||||  | ||   ||| |||||||||| ||||| | || |||||||
Db     820 ATAAGGAGTCCGTCCCAGCAAGAACTGTTCTTGGGATCACCACTGTTTTAACTATGACCA 879

Qy     126 CGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATT 185
           | ||| ||| |  | | ||  |   ||| ||    || || |||  ||| ||| ||||||
Db     880 CTTTGAGCATCAGTGCCCGGCACTCTTTGCCAAAAGTGTCATATGCCACTGCCATGGATT 939

Qy     186 TCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCA 245
             |  || ||  | ||||| |  |||  |||||  |||||  | ||||| || |   |||
Db     940 GGTTCATAGCTGTTTGCTTTGCATTCGTCTTCTCTGCTCTTATCGAGTTCGCAGCTGTCA 999

Qy     246 ACTTCCTGATCTACAACCAGACAAA 270
           |||  | | | | |    |||||| |
Db    1000 ACTACTTTACCAATCTTCAGACACA 1024


RESULT   8
T28988
ID   T28988 standard; cDNA; 1707 BP.
AC   T28988;
DT   06-JAN-1997  (first entry)
DE   Human GABA-A receptor alpha 4 subunit cDNA.
KW   GABA-A receptor; gamma-aminobutyric acid; alpha-4 subunit; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             39. .1703
FT                   /*tag=  a
PN   WO9610637-A1.
PD   11-APR-1996.
PF   29-SEP-1995; G02323.
PR   01-OCT-1994; GB-020010.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Le Bourdelles B,  Whiting PJ;
DR   WPI; 96-209359/21.
DR   P-PSDB; R97298.
PT   DNA encoding alpha-4 and delta subunit(s) of the human GABAa
PT   receptor  - also stably co-transfected eukaryotic cells expressing
PT   receptors contg. these subunit(s), used for screening and designing
PT   drugs
PS   Claim 9; Fig 2; 45pp; English.
CC   A cDNA clone (T28988) codes for the alpha-4 subunit (R97298) of the
CC   human GABA-A receptor.  It was isolated from human brain thalamus
CC   cDNA using primers (see also T28994-95) based on the 5' and 3'
CC   untranslated regions of a partial cDNA clone.  The cDNA can be
CC   incorporated into a vector and used to direct expression of the
CC   alpha-4 subunit in transfected cells, partic. rodent fibroblasts.
CC   Co-transfected host cells capable of expressing the alpha-4, delta
CC   (see also R97299) and beta subunits can be used to screen or design
CC   drugs that act on GABA-A receptors.
SQ   Sequence   1707 BP;    490 A;    373 C;    368 G;    476 T;


  Query Match             14.7%;  Score 99.6;  DB 1;  Length 1707;
  Best Local Similarity   60.9%;  Pred. No. 2.1e-19;
  Matches  162;  Conservative    0;  Mismatches  104;  Indels    0;  Gaps    0;

Qy       6 TTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCA 65
           |||| | |||| | || |      ||||   ||| || ||    ||||| |||||||| |
Db     820 TTCAGACCTATATTCCGTGCATTATGACAGTGATTCTTTCTCAAGTTTCATTTTGGATAA 879

Qy      66 AGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCA 125
           | | ||| || | ||| ||  |||||    | || || ||   |||| || ||||||||||
Db     880 ATAAAGAATCAGTTCCCGCTAGGACCGTATTTGGAATAACAACTGTCCTCACCATGACCA 939

Qy     126 CGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATT 185
           |  | ||| |  | | ||  |   ||| ||    || ||||||   || ||| |||| |
Db     940 CACTAAGCATCAGTGCACGACATTCTTTGCCCAAAGTGTCCTATGCTACCGCCATGGACT 999

Qy     186 TCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCA 245
             |  || ||  ||||||| |  ||    || |  || ||  | ||||||||   |||
Db    1000 GGTTCATAGCTGTCTGCTTTGCTTTTGTATTTTCGGCCCTTATCGAGTTTGCTGCTGTCA 1059

Qy     246 ACTTCCTGATCTACAACCAGACAAAA 271
           |||  | | | | |  || |   ||
Db    1060 ACTATTTCACCAATATTCAAATGGAA 1085


RESULT   9
Q33129
ID   Q33129 standard; DNA; 2310 BP.
AC   Q33129;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-5 subunit gene.
KW   Primer; human; alpha-5; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             298. .1686
FT                   /*tag=  a
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   P-PSDB; R31186.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Claim 7; Fig 4; 43pp; English.
CC   The sequence given encodes the human alpha-5 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Rat alpha-5 cDNA was used as a probe
CC   and a human alpha-5 cDNA clone was isolated from a hippocampal cDNA
```

```
CC   library.  GABA-A receptor comprises a multimeric protein of molecular
CC   size 230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   2310 BP;    655 A;    582 C;    512 G;    561 T;


  Query Match             14.0%;  Score 95.2;  DB 1;  Length 2310;
  Best Local Similarity   60.4%;  Pred. No. 4.3e-18;
  Matches  157;  Conservative    0;  Mismatches  103;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          || | | || | |||  | || |      |||||  |||  | ||   ||| ||||||||
Db   1077 TGTCATCCAGACCTACCTTCCCTGCATAATGACCGTGATCTTATCACAGGTGTCCTTTTG 1136

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          | | ||    || || |  |||||| ||||   | | ||| ||||| | || ||||||||
Db   1137 GCTGAACCGGGAATCAGTCCCAGCCAGGACAGTTTTTGGGGTCACCACGGTGCTGACCAT 1196

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||| ||  |  ||| |    |  | ||   | | ||    ||  ||||   ||| ||| |
Db   1197 GACGACCCTCAGCATCAGCGCCAGGAACTCTCTGCCCAAAGTGGCCTACGCCACCGCCAT 1256

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||| |  |  || ||  | ||||  | ||||  |||||  || ||| | ||||||||
Db   1257 GGACTGGTTCATAGCTGTGTGCTATGCCTTCGTCTTCTCGGCGCTGATAGAGTTTGCCAC 1316

Qy    241 GCTCAACTTCCTGATCTACA 260
          | |||| | | | | | | |
Db   1317 GGTCAATTACTTTACCAAGA 1336


RESULT  10
Q69141
ID   Q69141 standard; DNA; 2310 BP.
AC   Q69141;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha5 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             298. .1687
FT                   /*tag=  a
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   P-PSDB; R59864.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.4; 79pp; English.
CC   This receptor DNA may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   2310 BP;    654 A;    583 C;    513 G;    560 T;


  Query Match             14.0%;  Score 95.2;  DB 1;  Length 2310;
  Best Local Similarity   60.4%;  Pred. No. 4.3e-18;
  Matches  157;  Conservative    0;  Mismatches  103;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          || | | || | |||  | || |      |||||  |||  | ||   ||| ||||||||
Db   1077 TGTCATCCAGACCTACCTTCCCTGCATAATGACCGTGATCTTATCACAGGTGTCCTTTTG 1136

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          | | ||    || || |  |||||| ||||   | | ||| ||||| | || ||||||||
Db   1137 GCTGAACCGGGAATCAGTCCCAGCCAGGACAGTTTTTGGGGTCACCACGGTGCTGACCAT 1196

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||| ||  |  ||| |    |  | ||   | | ||    ||  ||||   ||| ||| |
Db   1197 GACGACCCTCAGCATCAGCGCCAGGAACTCTCTGCCCAAAGTGGCCTACGCCACCGCCAT 1256

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||| |  |  || ||  | ||||  | ||||  |||||  || ||| | ||||||||
Db   1257 GGACTGGTTCATAGCTGTGTGCTATGCCTTCGTCTTCTCGGCGCTGATAGAGTTTGCCAC 1316

Qy    241 GCTCAACTTCCTGATCTACA 260
          | |||| | | | | | | |
Db   1317 GGTCAATTACTTTACCAAGA 1336


RESULT  11
Q33128
ID   Q33128 standard; DNA; 1638 BP.
AC   Q33128;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-3 subunit gene.
KW   Primer; human; alpha-3; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             87. .1565
FT                   /*tag=  a
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   P-PSDB; R31185.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Claim 6; Fig 3; 43pp; English.
CC   The sequence given encodes the human alpha-3 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Bovine alpha-3 cDNA was used as a
CC   probe and an alpha-3 cDNA clone was isolated from a human foetal
CC   brain cDNA library, which was missing approx. 100 bp of the 5' end.
CC   This missing fragment was isolated by PCR.  The two fragments were
CC   ligated together to give a full length alpha-3 cDNA.    GABA-A
CC   receptor comprises a multimeric protein of molecular size 230-370 kD
CC   with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   1638 BP;    430 A;    436 C;    365 G;    407 T;
```

```
  Query Match             13.5%;  Score 91.6;  DB 1;  Length 1638;
  Best Local Similarity   59.7%;  Pred. No. 4.1e-17;
  Matches  154;  Conservative    0;  Mismatches  104;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||   | || | |||  | || | |  | ||||    || || ||    || || || ||
Db    920 TGTGATCCAGACCTACTTGCCATGTATCATGACTGTCATTCTGTCACAAGTGTCGTTCTG 979

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          | |||| | |||||||| ||| ||||| ||      | ||  ||||| |||| || |||||
Db    980 GCTCAACAGAGAGTCTGTTCCTGCCCGTACAGTCTTTGGTGTCACCACTGTGCTTACCAT 1039

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          |||||| ||| | | |  | |  | ||    || ||    ||  | |||   || ||| |
Db   1040 GACCACCTTGAGTATCAGTGCCAGAAATTCCTTACCTAAAGTGGCATATGCGACGGCCAT 1099

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||| |  |  || ||| |||| |  | |||    || |  || ||| | || |||||
Db   1100 GGACTGGTTCATAGCCGTCTGTTATGCCTTTGTATTTTCTGCACTGATTGAATTTGCCAC 1159

Qy    241 GCTCAACTTCCTGATCTA 258
          ||||||   | | | |
Db   1160 TGTCAACTATTTCACCAA 1177


RESULT  12
Q69140
ID   Q69140 standard; DNA; 1638 BP.
AC   Q69140;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha3 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             87. .1562
FT                   /*tag=  a
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   P-PSDB; R59863.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.3; 79pp; English.
CC   This receptor DNA may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   1638 BP;    430 A;    437 C;    364 G;    407 T;


  Query Match             13.5%;  Score 91.6;  DB 1;  Length 1638;
  Best Local Similarity   59.7%;  Pred. No. 4.1e-17;
  Matches  154;  Conservative    0;  Mismatches  104;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          ||   | || | |||  | || | |  | ||||    || || ||    || || || ||
Db    920 TGTGATCCAGACCTACTTGCCATGTATCATGACTGTCATTCTGTCACAAGTGTCGTTCTG 979

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          | |||| | |||||||| ||| ||||| ||      | ||  ||||| |||| || |||||
Db    980 GCTCAACAGAGAGTCTGTTCCTGCCCGTACAGTCTTTGGTGTCACCACTGTGCTTACCAT 1039

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          |||||| ||| | | |  | |  | ||    || ||    ||  | |||   || ||| |
Db   1040 GACCACCTTGAGTATCAGTGCCAGAAATTCCTTACCTAAAGTGGCATATGCGACGGCCAT 1099

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||| |  |  || ||| |||| |  | |||    || |  || ||| | || |||||
Db   1100 GGACTGGTTCATAGCCGTCTGTTATGCCTTTGTATTTTCTGCACTGATTGAATTTGCCAC 1159

Qy    241 GCTCAACTTCCTGATCTA 258
          ||||||   | | | |
Db   1160 TGTCAACTATTTCACCAA 1177


RESULT  13
Q33131
ID   Q33131 standard; DNA; 1866 BP.
AC   Q33131;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor beta-2 subunit gene.
KW   Primer; human; beta-2; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             225. .1649
FT                   /*tag=  a
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   P-PSDB; R31188.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Claim 9; Fig 6; 43pp; English.
CC   The sequence given encodes the human beta-2 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Short human beta-2 cDNA was used as
CC   a probe and a human beta-2 cDNA clone was isolated from a hippocampal
CC   cDNA library.  The largest cDNA clone isolated lacked the 5' 500 bp of
CC   the beta-2 coding sequence.  This missing fragment was isolated by PCR.
CC   The two fragments were ligated together to give a full length beta-2
CC   cDNA.  GABA-A receptor comprises a multimeric protein of molecular size
CC   230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   1866 BP;    505 A;    452 C;    436 G;    473 T;


  Query Match             13.4%;  Score 90.8;  DB 1;  Length 1866;
  Best Local Similarity   59.8%;  Pred. No. 7.4e-17;
  Matches  152;  Conservative    0;  Mismatches  102;  Indels    0;  Gaps    0;

Qy      4 CTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGAT 63
          | | ||||  ||  | |||||  | |||  || || ||||||||||| ||||| |||||
Db    962 CCTGCAAACATACATGCCTTCCATCCTGATTACCATCCTCTCCTGGGTCTCCTTCTGGAT 1021

Qy     64 CAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGAC 123
            ||    ||  || |  | ||  ||    |  |||| |||||  |||| || || |||||
Db   1022 TAATTACGATGCTTCAGCTGCAAGGGTGGCATTAGGAATCACAACTGTCCTCACAATGAC 1081

Qy    124 CACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGA 183
          |||  |   ||||      ||  | | | ||||     || ||||| | |  ||| | ||
Db   1082 CACAATCAACACCCACCTCCGGGAAACTCTCCCTAAAATCCCCTATGTGAAGGCCATTGA 1141
```

```
Qy    184 TTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCT 243
          | ||  |       |||||  ||||||   |||   || ||  ||||  | |||  |  |
Db   1142 CATGTACCTGATGGGGTGCTTTGTCTTCGTTTTCATGGCCCTTCTGGAATATGCCCTAGT 1201

Qy    244 CAACTTCCTGATCT 257
          |||||  |  |  |||
Db   1202 CAACTACATCTTCT 1215
```

RESULT 14
Q69143
ID Q69143 standard; DNA; 1866 BP.
AC Q69143;
DT 20-MAR-1995 (first entry)
DE Human GABA receptor beta2 subunit DNA.
KW GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW central nervous system; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 225. .1650
FT /*tag= a
PN WO9413799-A.
PD 23-JUN-1994.
PF 07-DEC-1993; G02506.
PR 10-DEC-1992; GB-025776.
PR 07-SEP-1993; GB-018528.
PA (MERI) MERCK SHARP & DOHME LTD.
PI Hadingham KL, Whiting PJ;
DR WPI; 94-234213/28.
DR P-PSDB; R59866.
PT Cell lines expressing GABA-A receptors - used for screening for
PT and designing medicaments which act on the GABA-A receptors
PS Disclosure; Fig.6; 79pp; English.
CC This receptor DNA may be expressed in mammal cell lines which may be
CC used for screening for and designing medicaments which act on the
CC human GABAA receptor. The cells expressing this subunit are ideal
CC systems for the study of the structure, pharmacology and function
CC of the receptor subtype.
SQ Sequence 1866 BP; 504 A; 452 C; 437 G; 473 T;

Query Match 13.4%; Score 90.8; DB 1; Length 1866;
Best Local Similarity 59.8%; Pred. No. 7.4e-17;
Matches 152; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

```
Qy      4 CTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGAT 63
          | | ||||  ||  | |||||   | |||  || || ||||||||||| ||||| |||||
Db    962 CCTGCAAACATACATGCCTTCCATCCTGATTACCATCCTCTCCTGGGTCTCCTTCTGGAT 1021

Qy     64 CAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGAC 123
           ||    ||  || |  | ||  ||    |  |||| |||||  |||| || || |||||
Db   1022 TAATTACGATGCTTCAGCTGCAAGGGTGGCATTAGGAATCACAACTGTCCTCACAATGAC 1081

Qy    124 CACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGA 183
           |||  |   ||||      ||  | | | ||||     || ||||| | |  ||| | ||
Db   1082 CACAATCAACACCCACCTCCGGGAAACTCTCCCTAAAATCCCCTATGTGAAGGCCATTGA 1141

Qy    184 TTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCT 243
          | ||  |       |||||  ||||||   |||   || ||  ||||  | |||  |  |
Db   1142 CATGTACCTGATGGGGTGCTTTGTCTTCGTTTTCATGGCCCTTCTGGAATATGCCCTAGT 1201

Qy    244 CAACTTCCTGATCT 257
          |||||  |  |  |||
Db   1202 CAACTACATCTTCT 1215
```

RESULT 15
V83111
ID V83111 standard; cDNA; 1884 BP.
AC V83111;
DT 02-MAR-1999 (first entry)
DE Human GABA-A receptor theta subunit coding sequence.
KW GABA; Gamma-amino butyric acid; CNS; central nervous system;
KW synapse; alpha; beta; gamma; delta; theta; receptor; subunit;
KW epsilon; emotion; pain perception; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1. .1884
FT /*tag= a
FT /product= GABA-A_theta_subunit
PN WO9849293-A1.
PD 05-NOV-1998.
PF 24-APR-1998; G01206.
PR 25-APR-1997; GB-008479.
PA (MERI) MERCK SHARP & DOHME LTD.
PI Bonnert TP, Whiting PJ;
DR WPI; 99-024057/02.
DR P-PSDB; W85596.
PT New DNA encoding the theta subunit of the gamma-aminobutyric acid
PT receptor - related vectors and cells that express receptors
PT including this subunit, used to screen for specific modulators,
PT potentially useful for treating emotional disorders
PS Claim 13; Figure 1; 50pp; English.
CC The GABA (gamma-aminobutyric acid) receptor (A) has been found to
CC comprise a new subunit designated the theta subunit. Stable
CC transfected cells that express the GABA-A receptor comprising the
CC theta subunit and at least one alpha subunit and optionally at
CC least one beta , gamma , delta or epsilon subunit can be used to
CC screen or design agents that act (as agonists, antagonists or
CC allosteric modulators) on GABA-A receptors containing a theta subunit
CC (claimed), i.e. agents potentially useful for modulating emotions
CC such as anger or fear, sexual or appetite behaviour, or pain
CC perception. They may also be used to determine efficacy and affinity
CC of known drugs. Also the theta subunit may be used to raise
CC antibodies and these used to identify other GABA receptor subunits.
CC The cells also allow the design of drugs that act on receptors
CC containing theta subunits and receptors having a specific
CC combination of subunits. An alternative theta subunit coding
CC sequence is described in V83112.
SQ Sequence 1884 BP; 441 A; 513 C; 462 G; 468 T;

Query Match 13.3%; Score 90.2; DB 1; Length 1884;
Best Local Similarity 59.6%; Pred. No. 1.1e-16;
Matches 152; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

```
Qy      6 TTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCA 65
          | |||  |||    ||| ||  | | |||||  ||   ||| ||| | || ||||||||| |
Db    794 TGCAAGTCTACTGGCCTACTGTCCTCACCACTATTACCTCTTGGATATCGTTTTGGATGA 853

Qy     66 AGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCA 125
          |    || ||  || ||||| ||    |  | ||  | || ||  | || | | ||||||
Db    854 ACTATGATTCCTCTGCAGCCAGGGTGACAATTGGCTTAACTTCAATGCTCATCCTGACCA 913

Qy    126 CGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATT 185
          | | | |   |  ||  | ||  ||||     | |||| |||||  ||| | |||
Db    914 CCATCGACTCACATCTGCGGGATAAGCTCCCCAACATTTCCTGTATCAAGGCCATTGATA 973

Qy    186 TCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCA 245
          ||||||||  | | |||||  ||||    |||    |  || ||||||  ||      |||
Db    974 TCTATATCCTCGTGTGCTTGTTCTTTGTGTTCCTGTCCTTGCTGGAGTATGTCTACATCA 1033

Qy    246 ACTTCCTGATCTACA 260
          |||  ||  ||||||
Db   1034 ACTATCTTTTCTACA 1048
```

Search completed: March 9, 2000, 22:45:35
Job time: 634 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2000, 02:00:34 ; Search time 3156.82 Seconds
(without alignments)
812.107 Million cell updates/sec

Title: US-09-030-832-41_COPY_880_1558
Perfect score: 679
Sequence: 1 TGCCTTTCAAAACTATGTCC.....GGCTTGTTTGCCTTAACTTG 679

Scoring table: IDENTITY_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

Number of hits that pass the threshold : 9077268

1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*
44: gb_est25:*
45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_gss1:*
80: gb_gss2:*
81: gb_gss3:*
82: gb_gss4:*
83: em_gss1:*
84: em_gss2:*
85: em_gss3:*
86: em_gss4:*
87: gb_gss5:*
88: gb_gss6:*
89: gb_gss7:*
90: gb_gss8:*
91: gb_gss9:*
92: em_gss5:*
93: em_gss6:*
94: em_gss7:*
95: em_gss8:*
96: em_gss9:*
97: em_gss10:*
98: em_gss11:*
99: gb_gss10:*
100: gb_gss11:*
101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	235.6	34.7	317	21	R07883	R07883 yf16g04.s1
c	2	171	25.2	177	32	AA347289	AA347289 EST53562
	3	120.2	17.7	491	21	T75122	T75122 yc87e11.r1
	4	116.8	17.2	308	21	F13483	F13483 HSC3DG111 n
	5	116	17.1	450	21	R13309	R13309 yf75d07.r1
	6	111.4	16.4	269	21	F12738	F12738 HSC3DF111 n
	7	104.6	15.4	623	64	AW077068	AW077068 fj04d06.y

8	102.6	15.1	641	26	W22429	W22429 67C11 Human
9	96.8	14.3	944	64	AL119253	AL119253 DKFZp761I
10	95.2	14.0	349	21	F06915	F06915 HSC1OG061 n
c 11	93.4	13.8	382	61	AI839865	AI839865 UI-M-AH0-
12	90.6	13.3	383	64	AW048575	AW048575 UI-M-BH1-
13	81.6	12.0	334	64	AL118953	AL118953 DKFZp761D
c 14	75.6	11.1	373	43	AI228492	AI228492 EST225187
15	72	10.6	290	21	F07441	F07441 HSC25G051 n
16	70.8	10.4	289	21	F07440	F07440 HSC25G041 n
17	70.4	10.4	522	22	R49718	R49718 yg71c11.r1
c 18	70.4	10.4	408	23	H41122	H41122 yn88g01.s1
19	68.2	10.0	307	20	T29443	T29443 EST79973 Hu
20	67.2	9.9	559	64	AL120988	AL120988 DKFZp762J
c 21	65.2	9.6	609	79	FR0021371	AL014246 F.rubripe
22	58.8	8.7	323	32	AA332108	AA332108 EST36019
23	58.4	8.6	223	20	T27015	T27015 NIBT136C07R
24	56	8.2	392	21	R15435	R15435 ya48h12.r1
25	56	8.2	258	32	AA332100	AA332100 EST36258
26	51.6	7.6	400	31	AA294204	AA294204 SWOv3MCA1
27	48.6	7.2	538	105	AQ601729	AQ601729 HS_2111_A
28	48.4	7.1	324	44	AI324390	AI324390 mb50h05.y
c 29	45.2	6.7	249	61	AI841413	AI841413 UI-M-AH0-
30	44.2	6.5	498	34	AA464024	AA464024 zx86a10.r
31	44.2	6.5	576	51	AI734165	AI734165 zx86a10.y
32	44	6.5	540	22	R35346	R35346 yg65e01.r1
33	43.4	6.4	272	31	AA324114	AA324114 EST26984
34	43.2	6.4	102	21	R20186	R20186 yg33e05.r1
35	43.2	6.4	417	69	AW114729	AW114729 rs53h11.y
36	43	6.3	450	21	R12710	R12710 yf58a04.r1
37	43	6.3	997	79	CNS005TE	AL060767 Drosophil
c 38	42.8	6.3	1101	79	CNS0037Q	AL064465 Drosophil
39	41.2	6.1	393	42	AI133799	AI133799 BSBmMFSZ4
40	41	6.0	708	79	CNS00Z1Q	AL097112 Drosophil
41	40.8	6.0	599	30	AA206715	AA206715 zq56e12.r
c 42	40	5.9	839	79	CNS004NB	AL054280 Drosophil
43	40	5.9	925	79	CNS0091P	AL053013 Drosophil
c 44	39.8	5.9	307	43	AU032919	AU032919 AU032919
c 45	39.6	5.8	1101	80	CNS0181N	AL108773 Drosophil

ALIGNMENTS

RESULT 1
R07883/c
LOCUS R07883 317 bp mRNA EST 05-APR-1995
DEFINITION yf16g04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127062 3' similar to SP:GAC4_CHICK P34904 GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4 SUBUNIT PRECURSOR ;, mRNA sequence.
ACCESSION R07883
VERSION R07883.1 GI:759806
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 317)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 681
High qality sequence stops: 241 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 681 Std Error: 0.00
Seq primer: -21m13
High quality sequence stop: 241.
FEATURES Location/Qualifiers
source 1. .317
/organism="Homo sapiens"
/db_xref="GDB:479223"
/db_xref="taxon:9606"
/clone="IMAGE:127062"
/clone_lib="Soares fetal liver spleen 1NFLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 98 a 64 c 91 g 57 t 7 others
ORIGIN

Query Match 34.7%; Score 235.6; DB 21; Length 317;
Best Local Similarity 96.3%; Pred. No. 2e-55;
Matches 261; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

```
Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGA-CCACGATGCTCTCCTGGGTTTCC--TT 57
          |||||||||||||||||||| |||||||||| ||||||||||||||  || || |  ||
Db    272 TGCCTTTCAAAACTATGTCCCNTCTTCCGTGACCCACGATGCTCTCCCTGGGTTTCCTTT 213

Qy     58 TTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGAC 117
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    212 TNGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGAC 153

Qy    118 CATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGC 177
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    152 CATGACCACGTTGGGNACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGC 93

Qy    178 CTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGC 237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     92 CTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGC 33

Qy    238 TGTGCTCAACTTCCTGATCTACAACCAGACA 268
          |||||||||||||||||||||||||||||||
Db     32 TGTGCTCAACTTCCTGATCTACAACCAGACA 2
```

RESULT 2
AA347289/c
LOCUS AA347289 177 bp mRNA EST 21-APR-1997
DEFINITION EST53562 Fetal heart II Homo sapiens cDNA 3' end, mRNA sequence.
ACCESSION AA347289
VERSION AA347289.1 GI:1999526
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 177)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

```
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., ,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   12140200
COMMENT     On Sep 12, 1996 this sequence version replaced gi:1288680.
            Other_ESTs: EST53563
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13-21.
FEATURES             Location/Qualifiers
     source          1. .177
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):148569"
                     /db_xref="taxon:9606"
                     /clone_lib="Fetal heart II"
                     /dev_stage="fetus"
                     /note="Organ: heart; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI"
BASE COUNT       37 a     48 c     56 g     30 t      6 others
ORIGIN


  Query Match             25.2%;  Score 171;  DB 32;  Length 177;
  Best Local Similarity   96.6%;  Pred. No. 1.5e-37;
  Matches  171;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    433 AGCCCAGCAGCCCCCTAGCCCAGGTAGCCCTGAGGGTCCCCGCAGCCTCTGCTCCAAGCT 492
          ||||||||||||||||| |||||||||||||||||||||||| |||||||||||||||||
Db    177 AGCCCAGCAGCCCCCTANCCCAGGTAGCCCTGAGGGTCCCCGNAGCCTCTGCTCCAAGCT 118

Qy    493 GGCCTGCTGTGAGTGGTGCAAGCGTTTTAAGAAGTACTTCTGCATGGTCCCCGATTGTGA 552
          |||||||||||||||||||| |||||||||||| |||||||||||||||||||||||||
Db    117 GGCCTGCTGTGAGTGGTGCAANCGTTTTAAGAAGTNCTTCTGCATGGTCCCCGATTGTGA 58

Qy    553 GGGCAGTACCTGGCAGCAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTA 609
          ||||||| |||||||| ||||||||||||||||||||||||||||||||||||||||
Db     57 GGGCAGTNCCTGGCAGNAGGGCCGCCTCTGCATCCATGTCTACCGCCTGGATAACTA 1


RESULT   3
T75122
LOCUS       T75122         491 bp    mRNA            EST       03-MAR-1995
DEFINITION  yc87e11.r1 Soares infant brain 1NIB Homo sapiens cDNA clone
            IMAGE:22770 5' similar to gb:X15376 GAMMA-AMINOBUTYRIC-ACID
            RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   T75122
VERSION     T75122.1  GI:691884
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 422
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: M13RP1
            High quality sequence stop: 422.
FEATURES             Location/Qualifiers
     source          1. .491
                     /organism="Homo sapiens"
                     /db_xref="GDB:395117"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:22770"
                     /clone_lib="Soares infant brain 1NIB"
                     /sex="female"
                     /dev_stage="73 days post natal"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
                     I; Site_2: Hind III; 1st strand cDNA was primed with a Not
                     I - oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3']
                     double-stranded cDNA was ligated to Hind III adaptors
                     (Pharmacia), digested with Not I and directionally cloned
                     into the Not I and Hind III sites of the Lafmid BA vector.
                     Library went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      123 a    119 c    111 g    130 t      8 others
ORIGIN


  Query Match             17.7%;  Score 120.2;  DB 21;  Length 491;
  Best Local Similarity   64.4%;  Pred. No. 3.3e-23;
  Matches  179;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
            | || | || | |||| |||| |   |  | |      | || ||||||| || || ||
Db      6 TNCCATCCAGACCTATATCCCCTGCACACTCATTGTCGTCCTATCCTGGGTGTCTTTCTG 65

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          |||||| |  ||  ||| ||||||| | || ||| |||| |||||| |||| ||||| ||
Db     66 GATCAATAAGGATGCTGTTCCAGCCAGAACATCTTTAGGTATCACCACTGTCCTGACAAT 125

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||  |  ||||| || | || ||     ||||    |||||||| |||||||  |
Db    126 GACCACCCTCAGCACCATTGCCCGGAAATCGCTCCCCAAGGTCTCCTATGTCACAGCGAT 185

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          |||| ||| | |  |  | || ||| |||   |||||  |||||| |||||| ||
Db    186 GGATCTCTTTGTATCTGTTTGTTTCATCTTTGTCTTCTCTGCTCTGGTGGAGTATGGCAC 245

Qy    241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATG 278
            | | |   |  ||  ||||| || |  |  | | |
Db    246 CTTGCATTATTTTGTCAGCAACCGGAAACCAAGCAAGG 283


RESULT   4
F13483
LOCUS       F13483         308 bp    mRNA            EST       15-MAR-1995
DEFINITION  HSC3DG111 normalized infant brain cDNA Homo sapiens cDNA clone
            c-3dg11, mRNA sequence.
ACCESSION   F13483
VERSION     F13483.1  GI:710128
KEYWORDS    EST.
SOURCE      human.
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 308)
  AUTHORS   Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
            Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
            Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
            Sebastiani-Kabaktchis,C. and Tessier,A.
  TITLE     IMAGE: molecular integration of the analysis of the human genome
            and its expression
  JOURNAL   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
  MEDLINE   95277534
COMMENT     Contact: Genethon
            Genexpress-Genethon
            Genethon Centre de recherche sur le Genome Humain
            1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
            Tel: 33169472800
            Fax: 33160778698
            Email: genexpress@genethon.fr
            Single read.
            Genexpress_library_idt: C; Genexpress_sequence_idt: y2c-3dg11
            Insert Length: 1966   Std Error: 0.00
            Seq primer: (-21)M13_universal
            High quality sequence stop: 328.
FEATURES             Location/Qualifiers
     source          1. .308
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="c-3dg11"
                     /clone_lib="normalized infant brain cDNA"
                     /sex="Female"
                     /tissue_type="total brain"
                     /dev_stage="3 months old"
                     /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
                     Site_2: NotI; sex=Female; dev_stage=3 months old;
                     isolate=muscular atrophy patient;  tissue_type=total
                     brain;  total mRNA was oligo-(dT) primed and directionally
                     cloned 5' -> 3' into the  HindIII -> NotI sites of the
                     lafmid BA vector. Clone library from B.Soares,  Psychiatry
                     Dept. Columbia University, USA.  Normalization_method:
                     Bento Soares, P.N.A.S in press"
BASE COUNT       69 a     81 c     60 g     94 t      4 others
ORIGIN


  Query Match             17.2%;  Score 116.8;  DB 21;  Length 308;
  Best Local Similarity   64.2%;  Pred. No. 2.4e-22;
  Matches  172;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy       1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
           | || | || | |||| |||| |   |  | |       | || |||||||| || || ||
Db      36 TACCATCCAGACCTATATCCCCTGCACACTCATTGTCGTCCTATCCTGGGTGTCTTTCTG 95

Qy      61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
           |||||| |  ||  ||| |||||||| | || ||| |||| |||||| |||| ||||| ||
Db      96 GATCAATAAGGATGCTGTTCCAGCCAGAACATCTTTAGGTATCACCACTGTCCTGACAAT 155

Qy     121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
           ||||||  |  ||||| ||   || ||     ||||  |||||||| |||||||  |
Db     156 GACCACCNTCAGCACCATTGNCCGGAAATCGNTCCCCAAGGTCTCCTATGTCACAGCGAT 215

Qy     181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
           |||| ||| | |  |  | || ||| |||    |||||  ||| || ||||||  ||
Db     216 GGATCTCTTTGTATCTGTTTGTTTCATCTNTGTCTTCTCTGCTATGGTGGAGTATGGCAC 275

Qy     241 GCTCAACTTCCTGATCTACAACCAGACA 268
           |  | |   |  ||  ||||| || |
Db     276 CTTGCATTATTTTGTCAGCAACCGGAAA 303


RESULT   5
R13309
LOCUS       R13309        450 bp    mRNA            EST       12-APR-1995
DEFINITION  yf75d07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone
            IMAGE:28218 5' similar to gb:X15376 GAMMA-AMINOBUTYRIC-ACID
            RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   R13309
VERSION     R13309.1  GI:766385
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 450)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 333
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: M13RP1
            High quality sequence stop: 333.
FEATURES             Location/Qualifiers
     source          1. .450
                     /organism="Homo sapiens"
                     /db_xref="GDB:400565"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:28218"
                     /clone_lib="Soares infant brain 1NIB"
                     /sex="female"
                     /dev_stage="73 days post natal"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
                     I; Site_2: Hind III; 1st strand cDNA was primed with a Not
                     I - oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'];
                     double-stranded cDNA was ligated to Hind III adaptors
                     (Pharmacia), digested with Not I and directionally cloned
                     into the Not I and Hind III sites of the Lafmid BA vector.
                     Library went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      112 a    112 c    101 g    123 t      2 others
ORIGIN


  Query Match             17.1%;  Score 116;  DB 21;  Length 450;
  Best Local Similarity   68.2%;  Pred. No. 4.7e-22;
  Matches  161;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy       1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
           | || | || | |||| |||| |   |  | |       | || |||||||| || || ||
Db      35 TACCATCCAGACCTATATCCCCTGCACACTCATTGTCGTCCTATCCTGGGTGTCTTTCTG 94

Qy      61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
           |||||| |  ||  ||| ||||||| | || ||| |||| |||||| |||| ||||| ||
Db      95 GATCAATAAGGATGCTGTTCCAGCCAGAACATCTTTAGGTATCACCACTGTCCTGACAAT 154

Qy     121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
           ||||||  |  ||||| || | || ||     ||||    |||||||| |||||||  |
Db     155 GACCACCCTCAGCACCATTGCCCGGAAATCGCTCCCCAAGGTCTCCTATGTCACAGCGAT 214

Qy     181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTG 236
           |||| ||| | |  |  | || ||| ||||   |||||  |||||| |||||| ||
Db     215 GGATCTCTTTGTATCTGTTTGTTTCATCTTTGTCTTCTCTGCTCTGGTGGAGTATG 270
```

```
RESULT   6
F12738
LOCUS       F12738        269 bp    mRNA            EST       14-MAR-1995
DEFINITION  HSC3DF111 normalized infant brain cDNA Homo sapiens cDNA clone
            c-3df11, mRNA sequence.
ACCESSION   F12738
VERSION     F12738.1  GI:708744
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 269)
  AUTHORS   Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
            Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
            Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
            Sebastiani-Kabaktchis,C. and Tessier,A.
  TITLE     IMAGE: molecular integration of the analysis of the human genome
            and its expression
  JOURNAL   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
  MEDLINE   95277534
COMMENT     Contact: Genethon
            Genexpress-Genethon
            Genethon Centre de recherche sur le Genome Humain
            1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
            Tel: 33169472800
            Fax: 33160778698
            Email: genexpress@genethon.fr
            Single read.
            Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-3df11
            Insert Length: 1273   Std Error: 0.00
            Seq primer: (-21)M13_universal
            High quality sequence stop: 283.
FEATURES             Location/Qualifiers
     source          1. .269
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="c-3df11"
                     /clone_lib="normalized infant brain cDNA"
                     /sex="Female"
                     /tissue_type="total brain"
                     /dev_stage="3 months old"
                     /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
                     Site_2: NotI; sex=Female; dev_stage=3 months old;
                     isolate=muscular atrophy patient;  tissue_type=total
                     brain;  total mRNA was oligo-(dT) primed and directionally
                     cloned 5' -> 3' into the  HindIII -> NotI sites of the
                     lafmid BA vector. Clone library from B.Soares,  Psychiatry
                     Dept. Columbia University, USA.  Normalization_method:
                     Bento Soares, P.N.A.S in press"
BASE COUNT       57 a     73 c     52 g     87 t
ORIGIN
```

```
  Query Match           16.4%;  Score 111.4;  DB 21;  Length 269;
  Best Local Similarity  67.4%;  Pred. No. 7.1e-21;
  Matches  157;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          | || | || | |||| |||| |   |  | |      | || |||||||| || || ||
Db     36 TACCATCCAGACCTATATCCCCTGCACACTCATTGTCGTCCTATCCTGGGTGTCTTTCTG 95

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          |||||| |  ||  ||| ||||||| | || ||| |||| |||||| |||| ||||| ||
Db     96 GATCAATAAGGATGCTGTTCCAGCCAGAACATCTTTAGGTATCACCACTGTCCTGACAAT 155

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||||||  |  ||||| || | || ||     | ||    ||||||||| |||||||  |
Db    156 GACCACCCTCAGCACCATTGCCCGGAAATCGCTTCCCAAGGTCTCCTATGTCACAGCGAT 215

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGT 233
          |||| ||| | |  |  | || ||| ||||   |||||  ||| || ||||||
```

```
Db    216 GGATCTCTTTGTATCTGTTTGTTTCATCTTTGTCTTCTCTGCTTTGGTGGAGT 268
```

```
RESULT   7
AW077068
LOCUS       AW077068      623 bp    mRNA            EST       14-OCT-1999
DEFINITION  fj04d06.y1 Zebrafish adult olfactory Danio rerio cDNA 5' similar to
            gb:X15376 GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT
            PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AW077068
VERSION     AW077068.1  GI:6032220
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
            Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
            Cyprinoidea; Cyprinidae; Rasborinae; Danio.
REFERENCE   1  (bases 1 to 623)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     On Dec 20, 1995 this sequence version replaced gi:1135328.
            Other_ESTs: fj04d06.x1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Seq primer: T3 ET from Amersham
            High quality sequence stop: 483.
FEATURES             Location/Qualifiers
     source          1. .623
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone_lib="Zebrafish adult olfactory"
                     /sex="mixed"
                     /tissue_type="Olfactory rosettes"
                     /dev_stage="adult"
                     /lab_host="D10Hb (Gibco BRL)"
                     /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; This
                     is a directionally cloned cDNA library from adult
                     Zebrafish olfactory epithelium."
BASE COUNT      145 a    151 c    146 g    179 t      2 others
ORIGIN
```

```
  Query Match           15.4%;  Score 104.6;  DB 64;  Length 623;
  Best Local Similarity  65.2%;  Pred. No. 8.1e-19;
  Matches  152;  Conservative    0;  Mismatches   81;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          | || | || |  ||| |||| | | |  ||| |    | || ||||||||||| || ||
Db    390 TACCATCCAGACATATATCCCCTGTACTCTGATCGTTGTCCTGTCCTGGGTTTCATTCTG 449

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          |||||| |  ||  | |  |||||||| |||||  |  | |||||  | || || |||||
Db    450 GATCAACAAGGATGCAGTGCCAGCCCGAACCTCCTTGNGAATCACAACGGTGCTTACCAT 509

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
```

```
Db    510 GACCACTTTGAGTACCATTGCCAGGAAGTCTTTACCGAAAGTGTCGTATGTCACGGCTAT 569

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGT 233
Db    570 GGACCTCTTCGTGTCTGTGTGCTTCATNCTTGTTTTCGCCGCTCTGATCGAGT 622


RESULT   8
W22429
LOCUS       W22429         641 bp    mRNA            EST       06-MAY-1996
DEFINITION  67C11 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens
            cDNA not directional, mRNA sequence.
ACCESSION   W22429
VERSION     W22429.1  GI:1299262
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 641)
  AUTHORS   Macke, J., Smallwood, P. and Nathans, J.
  TITLE     Adult Human Retina cDNA
  JOURNAL   Unpublished (1996)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:837599.
            Contact: Dr. Jeremy Nathans
            Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
            Johns Hopkins School of Medicine
            725 North Wolfe Street, Baltimore, MD 21205
            Tel: 410 955 4678
            Fax: 410 614 0827
            Email: jeremy_nathans@qmail.bs.jhu.edu
            Clones from this library are NOT available.
            PCR PRimers
            FORWARD: CTTTTGAGCAAGTTCAGCCTGGTTAAGT
            BACKWARD: GAGGTGGCTTATGAGTATTTCTTCCAGGGTAA
            Seq primer: GGGTAAAAAGCAAAAGAATT.
FEATURES             Location/Qualifiers
     source          1. .641
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Human retina cDNA Tsp509I-cleaved sublibrary"
                     /sex="mixed (males and females)"
                     /tissue_type="retina"
                     /dev_stage="adult"
                     /lab_host="E. coli strain K802"
                     /note="Organ: eye; Vector: lambda gt10; Site_1: EcoRI;
                     Site_2: EcoRI; The library used for sequencing was a
                     sublibrary derived from a human retina cDNA library.
                     Inserts from retina cDNA library DNA were isolated,
                     cleaved with Tsp509I, size selected, and cloned into lamda
                     gt10.  Individual plaques were arrayed and used as
                     templates for PCR amplification and these PCR products
                     were used for sequencing."
BASE COUNT      157 a    156 c    150 g    143 t     35 others
ORIGIN


  Query Match             15.1%;  Score 102.6;  DB 26;  Length 641;
  Best Local Similarity   59.4%;  Pred. No. 2.9e-18;
  Matches  165;  Conservative    0;  Mismatches  113;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
Db    105 TACCATCCAGACCTATATCCCCTGAACACTCATTGTCGTCCTATCCTGGGTGTCTAGCTG 164

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
Db    165 GATCAATAAGGATGCTGTCCCAGCCAGAACATCTGTAGGTATCACCACTGNCCTGACAAT 224

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
Db    225 GACCACCCTCAGCACCATTGGCCGGAAATCGCTCCCCAAGGNCTCCTATGTCACAGCGAT 284

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
Db    285 GGATCTCTTNGTATCTGNNGGTTTCATCTNNGTCTCCTCTGCTCTGGGGGAGTATGGCAC 344

Qy    241 GCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATG 278
Db    345 CTGGNATCATTTGGTCAGCANCCGGAAACCAAGCAAGG 382


RESULT   9
AL119253
LOCUS       AL119253       944 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp761I1713_r1 761 (synonym: hamy2) Homo sapiens cDNA clone
            DKFZp761I1713 5', mRNA sequence.
ACCESSION   AL119253
VERSION     AL119253.1  GI:5925152
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 944)
  AUTHORS   Ansorge,W., Benes,V., Krieger,S., Mewes,H.W., Gassenhuber,J. and
            Wiemann,S.
  TITLE     EST (Ansorge, Benes, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 5, 1998 this sequence version replaced gi:3189703.
            Contact: Ansorge W
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by EMBL within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .944
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp761I1713"
                     /clone_lib="761 (synonym: hamy2)"
                     /tissue_type="amygdala"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      285 a    236 c    195 g    228 t
ORIGIN


  Query Match             14.3%;  Score 96.8;  DB 64;  Length 944;
  Best Local Similarity   60.8%;  Pred. No. 1.4e-16;
  Matches  158;  Conservative    0;  Mismatches  102;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
Db     40 TGTCATCCAGACCTACCTTCCCTGCATAATGACCGTGATCTTATCACAGGTGTCCTTTTG 99

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
Db    100 GCTGAACCGGGAATCAGTCCCAGCCAGGACAGTTTTTGGGGTCACCACGGTGCTGACCAT 159

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
Db    160 GACGACCCTCAGCATCAGCGCCAGGAACTCTCTGCCCAAAGTGGCCTACGCCACCGCCAT 219

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
Db    220 GGACTGGTTCATAGCCGTGTGCTATGCCTTCGTCTTCTCGGCGCTGATAGAGTTTGCCAC 279
```

```
Qy    241 GCTCAACTTCCTGATCTACA 260
          | |||| | | | | | | |
Db    280 GGTCAATTACTTTACCAAGA 299


RESULT  10
F06915
LOCUS       F06915         349 bp    mRNA            EST       20-FEB-1995
DEFINITION  HSC1OG061 normalized infant brain cDNA Homo sapiens cDNA clone
            c-1og06, mRNA sequence.
ACCESSION   F06915
VERSION     F06915.1  GI:672549
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 349)
  AUTHORS   Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
            Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
            Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
            Sebastiani-Kabaktchis,C. and Tessier,A.
  TITLE     IMAGE: molecular integration of the analysis of the human genome
            and its expression
  JOURNAL   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
  MEDLINE   95277534
COMMENT     Contact: Genethon
            Genexpress-Genethon
            Genethon Centre de recherche sur le Genome Humain
            1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
            Tel: 33169472800
            Fax: 33160778698
            Email: genexpress@genethon.fr
            Single read.
            Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-1og06
            Insert Length: 1122   Std Error: 0.00
            Seq primer: (-21)M13_universal
            High quality sequence stop: 264.
FEATURES             Location/Qualifiers
     source          1. .349
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="c-1og06"
                     /clone_lib="normalized infant brain cDNA"
                     /sex="Female"
                     /tissue_type="total brain"
                     /dev_stage="3 months old"
                     /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
                     Site_2: NotI; sex=Female; dev_stage=3 months old;
                     isolate=muscular atrophy patient;  tissue_type=total
                     brain;  total mRNA was oligo-(dT) primed and directionally
                     cloned 5' -> 3' into the  HindIII -> NotI sites of the
                     lafmid BA vector. Clone library from B.Soares,  Psychiatry
                     Dept. Columbia University, USA.  Normalization_method:
                     Bento Soares, P.N.A.S in press"
BASE COUNT       83 a    103 c     82 g     81 t
ORIGIN


  Query Match             14.0%;  Score 95.2;  DB 21;  Length 349;
  Best Local Similarity   60.4%;  Pred. No. 2.6e-16;
  Matches  157;  Conservative    0;  Mismatches  103;  Indels    0;  Gaps    0;

Qy      1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
          || | | || | |||  | || |      |||||  |||  | ||   ||| ||||||||
Db     89 TGTCATCCAGACCTACCTTCCCTGCATAATGACCGTGATCTTATCACAGGTGTCCTTTTG 148

Qy     61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
          | | ||    || || |  |||||| ||||   | | ||| ||||| | || ||||||||
Db    149 GCTGAACCGGGAATCAGTCCCAGCCAGGACAGTTTTTGGGGTCACCACGGTGCTGACCAT 208

Qy    121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
          ||| ||  |  ||| |    |  | ||   | | ||    ||  ||||   ||| ||| |
Db    209 GACGACCCTCAGCATCAGCGCCAGGAACTCTCTGCCCAAAGTGGCCTACGCCACCGCCAT 268

Qy    181 GGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGT 240
          ||| |  |  || ||  | ||||  | ||||  |||||  || ||| | ||||||||
Db    269 GGACTGGTTCATAGCTGTGTGCTATGCCTTCGTCTTCTCGGCGCTGATAGAGTTTGCCAC 328

Qy    241 GCTCAACTTCCTGATCTACA 260
          | |||| | | | | | | |
Db    329 GGTCAATTACTTTACCAAGA 348


RESULT  11
AI839865/c
LOCUS       AI839865       382 bp    mRNA            EST       14-JUL-1999
DEFINITION  UI-M-AH0-acw-a-01-0-UI.s1 NIH_BMAP_MCE Mus musculus cDNA clone
            UI-M-AH0-acw-a-01-0-UI 3', mRNA sequence.
ACCESSION   AI839865
VERSION     AI839865.1  GI:5474078
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 382)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     On Feb 22, 1999 this sequence version replaced gi:4283805.
            Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to verify it as a clone from the
            non-normalized cerebellum library cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
            available by the means that is soon to be determined. When NIH
            determines the means for distribution of the BMAP cDNA clones, this
            record will be updated accordingly when that means is determined.
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .382
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-AH0-acw-a-01-0-UI"
                     /clone_lib="NIH_BMAP_MCE"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_MCE library is a non-normalized library
                     constructed from  mouse cerebellum. The tag is a string of
                     5 nucleotides present  between the Not I site and the
                     oligo-dT track.  The library was  constructed as described
                     by Bonaldo, Lennon and Soares,  Genome Research 6:
                     791-806, 1996. Tissue provided by Ms. Annie Novakovich,
                     Zivic-Miller Laboratories.
                     TAG_LIB=NIH_BMAP_MCE
                     TAG_TISSUE=cerebellum
                     TAG_SEQ=AATCC"
BASE COUNT       98 a     71 c    105 g    108 t
ORIGIN
```

```
  Query Match             13.8%;  Score 93.4;  DB 61;  Length 382;
  Best Local Similarity   59.7%;  Pred. No. 8.6e-16;
  Matches  157;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy       8 CAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATCAAG 67
           ||  |  ||    || |    | ||||    || || ||    || || || ||||| ||
Db     381 CAGATATACACTCCGTGCATCATGACAGTCATTCTTTCTCAAGTGTCTTTCTGGATTAAT 322

Qy      68 ACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACCACG 127
           |  ||||| |  ||||| | ||     | || |||||| ||||| | ||||||||||
Db     321 AAGGAGTCAGTCCCAGCAAGAACTGTCTTTGGAATCACCACTGTTTTAACCATGACCACC 262

Qy     128 TTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTC 187
           ||  ||| |  | ||||  |   | | ||    || ||||||   || ||| ||||||
Db     261 TTAAGCATCAGTGCTCGGCACTCTCTACCCAAAGTGTCCTATGCAACCGCCATGGATTGG 202

Qy     188 TATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGCTGTGCTCAAC 247
           |  || ||  | ||||| |  ||   ||| |  |||||  | || || || |   |||||
Db     201 TTCATAGCTGTATGCTTTGCTTTTGTCTTTTCTGCTCTCATTGAATTCGCAGCTGTCAAC 142

Qy     248 TTCCTGATCTACAACCAGACAAA 270
           | | | | | |   |||| || |
Db     141 TACTTCACCAATCTCCAGTCACA 119


RESULT  12
AW048575
LOCUS       AW048575      383 bp    mRNA            EST       18-SEP-1999
DEFINITION  UI-M-BH1-alx-f-07-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone
            UI-M-BH1-alx-f-07-0-UI 3', mRNA sequence.
ACCESSION   AW048575
VERSION     AW048575.1  GI:5909104
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 383)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     On Feb 17, 1998 this sequence version replaced gi:2889728.
            Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to identify it as a clone from the
            normalized corpus striatum library cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
            available by the means that is soon to be determined. When NIH
            determines the means for distribution of the BMAP cDNA clones, this
            record will be updated accordingly when that means is determined.
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .383
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-BH1-alx-f-07-0-UI"
                     /clone_lib="NIH_BMAP_M_S2"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_M_S2 library is a subtracted library derived from
                     NIH_BMAP_M_S1, which in turn is a subtracted library
                     derived from a mixture of normalized libraries from ten
                     regions of the mouse brain (cerebellum, brain stems,
                     olfactory bulbs, hypothalamus, cortex, amygdala, basal
                     ganglia, pineal gland, striatum, hipoccampus). The driver
                     used for subtraction consisted of a pool of 5,000 clones
                     from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
                     obtained from non-normalized and normalized mouse brain
                     spinal cord libraries.
                     TAG_LIB=NIH_BMAP_M_S2
                     TAG_TISSUE=corpus-striatum
                     TAG_SEQ=ACGGC"
BASE COUNT      106 a     90 c     69 g    118 t
ORIGIN


  Query Match             13.3%;  Score 90.6;  DB 64;  Length 383;
  Best Local Similarity   63.6%;  Pred. No. 5.2e-15;
  Matches  138;  Conservative    0;  Mismatches   79;  Indels    0;  Gaps    0;

Qy      50 GTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCT 109
           |||||||| ||||| || |  |||||| ||||||  | ||     | || || ||| |
Db      21 GTTTCCTTCTGGATAAACAAGGAGTCTGTTCCAGCTAGAACTGTATTTGGAATAACCACA 80

Qy     110 GTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTAT 169
           || || || ||||||||  |  ||| |  | ||||  |   ||| ||    || ||||||
Db      81 GTCCTCACGATGACCACCCTAAGCATCAGTGCTCGGCATTCTTTGCCCAAAGTGTCCTAT 140

Qy     170 ATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTG 229
             || ||| ||||||  |  || ||  |||| || |  ||    || |  |||||  |
Db     141 GCGACTGCCATGGATTGGTTCATAGCTGTCTGTTTTGCTTTTGTATTTTCGGCTCTTATT 200

Qy     230 GAGTTTGCTGTGCTCAACTTCCTGATCTACAACCAGA 266
           ||||||||||   ||||||   | | | |||  || |
Db     201 GAGTTTGCTGCTGTCAACTATTTCACCAACATTCAAA 237


RESULT  13
AL118953
LOCUS       AL118953      334 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp761D17121_r1 761 (synonym: hamy2) Homo sapiens cDNA clone
            DKFZp761D17121 5', mRNA sequence.
ACCESSION   AL118953
VERSION     AL118953.1  GI:5924852
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 334)
  AUTHORS   Poustka,A., Klein,M., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Poustka, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 5, 1998 this sequence version replaced gi:3189399.
            Contact: Poustka A.J.
            Department Lehrach
            Max-Planck-Institute for Molecular Genetics
            Ihnestrasse 73, 14195 Berlin, Germany
            Tel: +49-30-84131623
            Fax: +49-30-84131128
            Email: poustka@mpimg-berlin-dahlem.mpg.de
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by DKFZ within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
```

```
           Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .334
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp761D17121"
                     /clone_lib="761 (synonym: hamy2)"
                     /tissue_type="amygdala"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT       83 a     93 c     56 g     99 t      3 others
ORIGIN


  Query Match             12.0%;  Score 81.6;  DB 64;  Length 334;
  Best Local Similarity   59.0%;  Pred. No. 1.6e-12;
  Matches  138;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy       4 CTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGAT 63
           | | ||||  ||  | |||||   | |||  || || ||||||||||| ||||| |||||
Db     100 CCTGCAAACATACATGCCTTCCATCCTGATTACCATCCTCTCCTGGGTCTCCTTCTGGAT 159

Qy      64 CAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGAC 123
             ||     |  || |  | ||  ||     |  |||| ||| |  |||| || || |||||
Db     160 TAATTACNATGCTTCAGCTGCAAGGGTGGCATTAGGAATCNCAACTGTCCTCACAATGAC 219

Qy     124 CACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGA 183
           |||  |   ||||      ||  | | | ||||     || ||||| | |  ||| | ||
Db     220 CACAATCAACACCCACCTCCGGGAAACTCTCCCTAAAATCCCCTATGTGAAGGCCATTGA 279

Qy     184 TTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCGCTCTGTTGGAGTTTGC 237
             | ||  |       ||||| ||||||   |||   || ||  |||| | |||
Db     280 CATGTACCTGATGGGGTGCTTTGTCTTCGTTTTCATGGCCCTTCTGGAATATGC 333


RESULT  14
AI228492/c
LOCUS       AI228492       373 bp    mRNA            EST       30-OCT-1998
DEFINITION  EST225187 Normalized rat brain, Bento Soares Rattus sp. cDNA clone
            RBRCV61 3' end, mRNA sequence.
ACCESSION   AI228492
VERSION     AI228492.1  GI:3812379
KEYWORDS    EST.
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
            Kerlavage,A.R. and Adams,M.D.
  TITLE     Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
            Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Lee, NH
            ATCC
            The Institute for Genomic Research
            9712, Medical Center Drive, Rockville, MD 20850, USA
            Tel: (301)-838-3529
            Fax: (301)-838-0208
            Email: nhlee@tigr.org
            Seq primer: M13-21.
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Rattus sp."
                     /db_xref="taxon:10118"
                     /clone="RBRCV61"
                     /clone_lib="Normalized rat brain, Bento Soares"
                     /note="Organ: brain; Vector: pT7T3Pac; Site_1: EcoRI;
                     Site_2: NotI"
BASE COUNT      114 a     87 c    103 g     69 t
ORIGIN


  Query Match             11.1%;  Score 75.6;  DB 43;  Length 373;
  Best Local Similarity   57.0%;  Pred. No. 7.7e-11;
  Matches  138;  Conservative    0;  Mismatches  104;  Indels    0;  Gaps    0;

Qy      42 TCTCCTGGGTTTCCTTTTGGATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGA 101
           | |||||||| |||||||||| |    |    | |  || |||      ||| |||| |
Db     276 TGTCCTGGGTCTCCTTTTGGATTAGCCAACCAGCAGTGCCTGCCAAAGTATCTTTAGGCA 217

Qy     102 TCACCTCTGTTCTGACCATGACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTG 161
           ||||| |||| ||||| |||||| |  |          | | ||          ||||||| |
Db     216 TCACCCCTGTGCTGACAATGACCCCACTCATGGTTAGTGCCCGCTCCTCCCTCCCGCGGG 157

Qy     162 TCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTCGTCTTCTGCTTCTGCG 221
             |    |||||  ||  ||||| | ||| |    || ||||  || ||    ||    |
Db     156 GTTTTGCTATCAAGGCTCTGGATGTGTATTTTTGGATTTGCTATGTTTTTGTGTTTGCTG 97

Qy     222 CTCTGTTGGAGTTTGCTGTGCTCAACTTCCTGATCTACAACCAGACAAAAGCCCATGCTT 281
           | ||| |||||| |||  |   | |||||       || ||  || ||||    | || |
Db      96 CCCTGGTGGAGTATGCATTTGCCCACTTCAATGCTGACTACAGGAAAAAACGGAAAGCCT 37

Qy     282 CT 283
           ||
Db      36 CT 35


RESULT  15
F07441
LOCUS       F07441         290 bp    mRNA            EST       20-FEB-1995
DEFINITION  HSC25G051 normalized infant brain cDNA Homo sapiens cDNA clone
            c-25g05, mRNA sequence.
ACCESSION   F07441
VERSION     F07441.1  GI:673101
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 290)
  AUTHORS   Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
            Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
            Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
            Sebastiani-Kabaktchis,C. and Tessier,A.
  TITLE     IMAGE: molecular integration of the analysis of the human genome
            and its expression
  JOURNAL   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
  MEDLINE   95277534
COMMENT     On Sep 21, 1992 this sequence version replaced gi:276107.
            Contact: Genethon
            Genexpress-Genethon
            Genethon Centre de recherche sur le Genome Humain
            1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
            Tel: 33169472800
            Fax: 33160778698
            Email: genexpress@genethon.fr
            Single read.
            Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-25g05
            Insert Length: 929   Std Error: 0.00
            Seq primer: (-21)M13_universal
            High quality sequence stop: 300.
FEATURES             Location/Qualifiers
     source          1. .290
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="c-25g05"
                     /clone_lib="normalized infant brain cDNA"
                     /sex="Female"
                     /tissue_type="total brain"
                     /dev_stage="3 months old"
                     /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
                     Site_2: NotI; sex=Female; dev_stage=3 months old;
                     isolate=muscular atrophy patient;  tissue_type=total
                     brain;  total mRNA was oligo-(dT) primed and directionally
```

cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press"
BASE COUNT 72 a 88 c 67 g 63 t
ORIGIN

Query Match 10.6%; Score 72; DB 21; Length 290;
Best Local Similarity 59.1%; Pred. No. 6.9e-10;
Matches 123; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

```
Qy       1 TGCCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTG 60
           || | | || | |||  | || |      |||||  |||  | ||   ||| ||||||||
Db      83 TGTCATCCAGACCTACCTTCCCTGCATAATGACCGTGATCTTATCACAGGTGTCCTTTTG 142

Qy      61 GATCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCAT 120
           | | ||    || || |  ||||||| ||||   | | ||| ||||| | || ||||||||
Db     143 GCTGAACCGGGAATCAGTCCCAGCCAGGACAGTTTTTGGGGTCACCACGGTGCTGACCAT 202

Qy     121 GACCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCCTT 180
           ||| ||  |  ||| |    |  | ||   | | ||    ||  ||||   ||| ||| |
Db     203 GACGACCCTCAGCATCAGCGCCAGGAACTCTCTGCCCAAAGTGGCCTACGGCACCGCCAT 262

Qy     181 GGATTTCTATATCGCCATCTGCTTCGTC 208
           ||| |  |  || ||  | ||||  | |
Db     263 GGACTGGTTCATAGCTGTGTGCTATGCC 290
```

Search completed: March 11, 2000, 02:00:39
Job time: 3227 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2000, 08:51:51 ; Search time 47.6 Seconds
(without alignments)
251.789 Million cell updates/sec

Title: US-09-030-832-42
Perfect score: 2691
Sequence: 1 MLSKVLPVLLGILLILQSRV.....VFPVTFFFFNVLYWLVCLNL 506

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database : A_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 188963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2688	99.9	506	1	W59048	GABA-A receptor ep
2	2688	99.9	506	1	W61045	Human GABA recepto
3	2486	92.4	474	1	W59049	Variant of GABA-A
4	1073.5	39.9	467	1	R83968	GABA-A receptor ga
5	855	31.8	453	1	R31187	GABA-A receptor al
6	855	31.8	453	1	R59865	Human GABA recepto
7	842	31.3	554	1	R97298	Human GABA-A recep
8	813	30.2	462	1	R31186	GABA-A receptor al
9	813	30.2	462	1	R59864	Human GABA recepto
10	798.5	29.7	492	1	R31185	GABA-A receptor al
11	798.5	29.7	492	1	R59863	Human GABA recepto
12	781	29.0	451	1	R31184	GABA-A receptor al
13	781	29.0	451	1	R59862	Human GABA recepto
14	667	24.8	474	1	R31188	GABA-A receptor be
15	667	24.8	474	1	R59866	Human GABA recepto
16	662.5	24.6	686	1	W86162	Insect GABA recept
17	652	24.2	452	1	R97299	Human GABA-A recep
18	632.5	23.5	496	1	R89336	GABA receptor subu
19	632.5	23.5	496	1	W86161	Insect GABA recept
20	610.5	22.7	496	1	W81633	GABA-gated chlorid
21	610.5	22.7	467	1	W81634	GABA-gated chlorid
22	607.5	22.6	627	1	W85597	Human GABA-A recep
23	601.5	22.4	627	1	W85596	Human GABA-A recep
24	598.5	22.2	488	1	W69285	GABA gated chlorid
25	597	22.2	561	1	W97413	Lucilia cuprina GA
26	595.5	22.1	488	1	W69286	GABA gated chlorid
27	595.5	22.1	481	1	W81635	GABA-gated chlorid
28	595.5	22.1	459	1	W81636	GABA-gated chlorid
29	579.5	21.5	637	1	R34035	Sequence of a GABA
30	561	20.8	510	1	R88360	Caenorhabditis ele
31	559	20.8	440	1	R93118	Human GABA-A recep
32	559	20.8	440	1	W26464	Human GABA-A recep
33	555.5	20.6	456	1	W05246	Drosophila glutama
34	555.5	20.6	455	1	W97860	Cat flea glutamate
35	549.5	20.4	487	1	R88361	Caenorhabditis ele
36	394	14.6	222	1	W81637	GABA-gated chlorid
37	183	6.8	522	1	R06265	Fish acetylcholine
38	180	6.7	479	1	R89358	Alpha-9 nicotinic
39	174.5	6.5	498	1	W09027	Neuronal nicotinic
40	173.5	6.4	498	1	W44154	Human neuronal nic
41	172.5	6.4	502	1	W09026	Neuronal nicotinic
42	172.5	6.4	502	1	W44157	Human neuronal nic
43	164.5	6.1	495	1	R07143	Neuronal nicotinic
44	159.5	5.9	511	1	W12369	Neuronal alpha-bun
45	159	5.9	494	1	W09018	Neuronal nicotinic

ALIGNMENTS

RESULT 1
W59048
ID W59048 standard; Protein; 506 AA.
AC W59048;
DT 25-SEP-1998 (first entry)
DE GABA-A receptor epsilon sub-unit related protein.
KW GABA-A receptor; diagnosis; therapy; drug screening.
OS Mammalia.
PN DE19644501-A1.
PD 30-APR-1998.
PF 25-OCT-1996; 044501.
PR 25-OCT-1996; DE-044501.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR WPI; 98-252096/23.
DR N-PSDB; V11776.
PT Protein related to GABA-A receptor sub-unit epsilon - useful for
PT diagnosis, therapy or drug screening
PS Example 1; Fig 1; 12pp; German.
CC The GABA-A receptor sub-unit epsilon related protein is used for the
CC diagnosis and/or therapy of related disorders. It can also be used to
CC screen for substances that modulate the activity of the protein.
SQ Sequence 506 AA;

Query Match 99.9%; Score 2688; DB 1; Length 506;
Best Local Similarity 99.8%; Pred. No. 2.7e-246;
Matches 505; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60

Qy      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
           ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEISVNSLGPLSILDMEYTIDI 120

Qy     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180

Qy     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240

Qy     241 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300

Qy     301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360

Qy     361 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 420

Qy     421 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 480

Qy     481 DNYSRVVFPVTFFFFNVLYWLVCLNL 506
```

```
                    ||||||||||||||||||||||||||
Db    481 DNYSRVVFPVTFFFFNVLYWLVCLNL 506


RESULT   2
W61045
ID   W61045 standard; Protein; 506 AA.
AC   W61045;
DT   12-OCT-1998  (first entry)
DE   Human GABA receptor epsilon subunit.
KW   GABA receptor; gamma-amino butyric acid receptor; human;
KW   appetite; cognition.
OS   Homo sapiens.
PN   WO9823742-A1.
PD   04-JUN-1998.
PF   18-NOV-1997; G03159.
PR   03-OCT-1997; GB-020995.
PR   25-NOV-1996; GB-024442.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Whiting PJ;
DR   WPI; 98-322722/28.
DR   N-PSDB; V36319.
PT   New isolated GABA receptor subunit, epsilon - used to develop
PT   products for the screening and design of drugs, e.g. for modulating
PT   appetite behaviours, hormonal interactions and cognition
PS   Claim 15; Fig 1; 37pp; English.
CC   This polypeptide comprises a novel class of subunit, classified as
CC   as epsilon, within the human GABA receptor gene family.  Its amino
CC   acid sequence was deduced from a cDNA clone (see V36319) isolated
CC   from a human brain cDNA library.  A stably co-transfected eukaryotic
CC   cell line capable of expressing the GABA epsilon receptor subunit,
CC   at least one alpha receptor subunit and at least one beta receptor
CC   subunit is claimed.  A recombinant expression vector, and protein
CC   and membrane preparations of the GABA receptor obtained from the
CC   co-transfected cells are also claimed.  The new GABA-A receptor
CC   epsilon subunit and products can be used in the screening and
CC   design of drugs which act upon the GABA receptor.  The ligands or
CC   drug candidates identified may be used as therapeutic agents, e.g.
CC   for the modulation of appetite behaviours, hormonal interactions
CC   and cognition.  They can also be used for the study of structure,
CC   pharmacology and function of the various GABA receptor subtypes.
SQ   Sequence   506 AA;


  Query Match             99.9%;  Score 2688;  DB 1;  Length 506;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-246;
  Matches  505;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60

Qy      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
           ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEISVNSLGPLSILDMEYTIDI 120

Qy     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180

Qy     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240

Qy     241 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300

Qy     301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360

Qy     361 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 420

Qy     421 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 480

Qy     481 DNYSRVVFPVTFFFFNVLYWLVCLNL 506
           ||||||||||||||||||||||||||
Db     481 DNYSRVVFPVTFFFFNVLYWLVCLNL 506


RESULT   3
W59049
ID   W59049 standard; Protein; 474 AA.
AC   W59049;
DT   25-SEP-1998  (first entry)
DE   Variant of GABA-A receptor epsilon sub-unit related protein.
KW   GABA-A receptor; diagnosis; therapy; drug screening.
OS   Mammalia.
PN   DE19644501-A1.
PD   30-APR-1998.
PF   25-OCT-1996; 044501.
PR   25-OCT-1996; DE-044501.
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI   Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR   WPI; 98-252096/23.
DR   N-PSDB; V11777.
PT   Protein related to GABA-A receptor sub-unit epsilon - useful for
PT   diagnosis, therapy or drug screening
PS   Disclosure; Fig 2; 12pp; German.
CC   The GABA-A receptor sub-unit epsilon related protein is used for the
CC   diagnosis and/or therapy of related disorders.  It can also be used to
CC   screen for substances that modulate the activity of the protein.
SQ   Sequence   474 AA;


  Query Match             92.4%;  Score 2486;  DB 1;  Length 474;
  Best Local Similarity   93.5%;  Pred. No. 3.3e-227;
  Matches  473;  Conservative    1;  Mismatches    0;  Indels   32;  Gaps    1;

Qy       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60

Qy      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
           ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEISVNSLGPLSILDMEYTIDI 120

Qy     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
           ||||||                                ||||||||||||||||||||
Db     121 IFSQTW--------------------------------NSKRTHEHEITMPNQMVRIYKD 148

Qy     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     149 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 208

Qy     241 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     209 KLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFW 268

Qy     301 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     269 IKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAV 328

Qy     361 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     329 LNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEER 388

Qy     421 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     389 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 448
```

```
Qy    481 DNYSRVVFPVTFFFFNVLYWLVCLNL 506
          |||||||||||||||||||||||||||
Db    449 DNYSRVVFPVTFFFFNVLYWLVCLNL 474
```

```
RESULT   4
R83968
ID   R83968 standard; Protein; 467 AA.
AC   R83968;
DT   02-FEB-1996  (first entry)
DE   GABA-A receptor gamma-3 subunit.
KW   GABA-A receptor; gamma-aminobutyric acid receptor; gamma-3 subunit.
OS   Homo sapiens.
PN   WO9529234-A1.
PD   02-NOV-1995.
PF   12-APR-1995; G00834.
PR   22-APR-1994; GB-008064.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Whiting PJ;
DR   WPI; 95-382983/49.
DR   N-PSDB; T02334.
PT   New cell line expressing human GABA-A receptor sub-units - useful in
PT   drug screening and design
PS   Disclosure; Page 21-23; 30pp; English.
CC   A cDNA clone isolated from a human foetal brain cDNA library
CC   encoded the GABA-A receptor gamma-3 subunit (R83968).
CC   The cDNA can be expressed in eukaryotic (pref. rodent fibroblast)
CC   cell lines to produce recombinant gamma-3 subunit or hybrid
CC   GABA-A receptors having novel subunit compositions.
SQ   Sequence   467 AA;
```

```
  Query Match           39.9%;  Score 1073.5;  DB 1;  Length 467;
  Best Local Similarity   42.5%;  Pred. No. 2e-93;
  Matches  220;  Conservative   82;  Mismatches  145;  Indels   71;  Gaps    9;

Qy      7 PVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETETGSRVG 66
          | || :|| | | :          | || |          ||      || :|
Db      3 PKLL-LLLCLFSGL---------HARSRKVEEDEYEDSSSNQKWVLAPKSQDT------- 46

Qy     67 KLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTW 126
             : : ||| :|  || |||| || ||||: |:| |||:||:| ::||| ||| |:|||
Db     46 ---DVTLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSINMEYQIDIFFAQTW 102

Qy    127 YDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYT 186
           | || :| | : | || |:|  :||||| |||||     | || |||::||: |||:|||
Db    103 TDSRLRFNSTMKILTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQLLRIWNDGKILYT 162

Qy    187 IRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFD 246
          :|:||:| | | :  |||| ||||| |||: ||: :|||:|    ::  :: ||:|:|||
Db    163 LRLTINAECQLQLHNFPMDEHSCPLIFSSYGYPKEQMIYRWRKNSVQAADQKSWRLYQFD 222

Qy    247 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 306
          | |: | |||:||  ||::|||||:| :| | ||   | |:|  :| :|||||||||| ::
Db    223 FMGLRNTTEIVTTSAGDYVVMTIYFELSTRMGYFTIQTYIPCILTVVLSWVSFWIKKDAT 282

Qy    307 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 366
          ||||:||||:|||||| | :||: |||||:||:| :: :||:| | ||:|:| ||:  |
Db    283 PARTALGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEYATLNY--Y 340

Qy    367 NQTKAHASPK----LRHP--------RINSRAHARTRARSRACARQHQEAFVCQIVTTEG 414
          :  :   : |     | ||         ||: :| :
Db    341 SSCRKPTTTKKTTSLLHPDSSRWIPERISLQAPSNY---------------------- 377

Qy    415 SDGEERPSCSAQQPPSPGSPEGPRSLC---SKLACCEWC---KRFKKYFCMVPDCEGSTW 468
                |   :|| |       |:     :  |   |   | : :||   :|:  :|
Db    377 -------SLLDMRPPPPAMITLNNSVYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSW 429

Qy    469 QQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
          ::||: | :  ||:|||| || :|  ||::||:  | |
Db    430 RKGRIHIDILELDSYSRVFFPTSFLLFNLVYWVGYLYL 467
```

```
RESULT   5
R31187
ID   R31187 standard; Protein; 453 AA.
AC   R31187;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-6 subunit.
KW   Primer; human; alpha-6; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta.
OS   Homo sapiens.
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   N-PSDB; Q33130.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Disclosure; Fig 5; 43pp; English.
CC   This sequence represents the human alpha-6 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Rat alpha-6 cDNA was used as a probe
CC   and a human alpha-6 cDNA clone was isolated from a cerebellum cDNA
CC   library.  No full length cDNA's were isolated. To obtain a full length
CC   cDNA 3 clones were joined together using convenient restriction sites.
CC   GABA-A receptor comprises a multimeric protein of molecular size
CC   230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   453 AA;
```

```
  Query Match           31.8%;  Score 855;  DB 1;  Length 453;
  Best Local Similarity   38.1%;  Pred. No. 9.2e-73;
  Matches  180;  Conservative   86;  Mismatches  127;  Indels   80;  Gaps   10;

Qy     65 VGKL--------PEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEY 116
          :|||           ||||: :|  ||::|||| |   | |  :| | | ||:| ::|||
Db     18 LGKLEVEGNFYSENVSRILDNLLEGYDNRLRPGFGGAVTEVKTDIYVTSFGPVSDVEMEY 77

Qy    117 TIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVR 176
             |:|: | ||| |||| :    | | ||  :||::| |||||||  |::  | :| ||:: |
Db     78 TMDVFFRQTWTDERLKFGGPTEILSLNNLMVSKIWTPDTFFRNGKKSIAHNMTTPNKLFR 137

Qy    177 IYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLE 233
          | ::| :|||:|:||:| | : :: |||| |:||| | |::||::|:|| |:    : :|
Db    138 IMQNGTILYTMRLTINADCPMRLVNFPMDGHACPLKFGSYAYPKSEIIYTWKKGPLYSVE 197

Qy    234 INEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTM 293
          : |::|  | |:|  | :  :| | :  |::::||::|:: |: ||   | | |  :| :
Db    198 VPEESS-SLLQYDLIGQTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVI 256

Qy    294 LSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFC 353
          || |||||  || |||| ||||:|||||||   :| : |:||| ||:|::||:|| | |
Db    257 LSQVSFWINKESVPARTVLGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFS 316

Qy    354 ALLEFAVLNFLIYNQTK------AHASPK--------------LRHPRINSRAHARTRA 392
          ||:||| :|:    ||:         |:|                : ||  :|: | : |
Db    317 ALIEFAAVNYFTNLQTQKAKRKAQFAAPPTVTISKATEPLEAEIVLHP--DSKYHLKKRI 374

Qy    393 RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKR 452
```

```
Db    375 TSLS----------LPIVSS-----SEANKVLTRAPILQSTPVTPPPL------------ 408

Qy    453 FKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
Db    408 --------PPAFGGT----------SKIDQYSRILFPVAFAGFNLVYWVVYLS 442


RESULT   6
R59865
ID   R59865 standard; Protein; 453 AA.
AC   R59865;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha6 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   N-PSDB; Q69142.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.5; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   453 AA;


  Query Match             31.8%;  Score 855;  DB 1;  Length 453;
  Best Local Similarity   38.1%;  Pred. No. 9.2e-73;
  Matches  180;  Conservative   86;  Mismatches  127;  Indels   80;  Gaps   10;

Qy     65 VGKL--------PEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEY 116
Db     18 LGKLEVEGNFYSENVSRILDNLLEGYDNRLRPGFGGAVTEVKTDIYVTSFGPVSDVEMEY 77

Qy    117 TIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVR 176
Db     78 TMDVFFRQTWTDERLKFGGPTEILSLNNLMVSKIWTPDTFFRNGKKSIAHNMTTPNKLFR 137

Qy    177 IYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLE 233
Db    138 IMQNGTILYTMRLTINADCPMRLVNFPMDGHACPLKFGSYAYPKSEIIYTWKKGPLYSVE 197

Qy    234 INEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTM 293
Db    198 VPEESS-SLLQYDLIGQTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVI 256

Qy    294 LSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFC 353
Db    257 LSQVSFWINKESVPARTVLGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFS 316

Qy    354 ALLEFAVLNFLIYNQTK------AHASPK---------------LRHPRINSRAHARTRA 392
Db    317 ALIEFAAVNYFTNLQTQKAKRKAQFAAPPTVTISKATEPLEAEIVLHP--DSKYHLKKRI 374

Qy    393 RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKR 452
Db    375 TSLS----------LPIVSS-----SEANKVLTRAPILQSTPVTPPPL------------ 408

Qy    453 FKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
Db    408 --------PPAFGGT----------SKIDQYSRILFPVAFAGFNLVYWVVYLS 442


RESULT   7
R97298
ID   R97298 standard; Protein; 554 AA.
AC   R97298;
DT   06-JAN-1997  (first entry)
DE   Human GABA-A receptor alpha 4 subunit.
KW   GABA-A receptor; gamma-aminobutyric acid; alpha-4 subunit.
OS   Homo sapiens.
PN   WO9610637-A1.
PD   11-APR-1996.
PF   29-SEP-1995; G02323.
PR   01-OCT-1994; GB-020010.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Le Bourdelles B,  Whiting PJ;
DR   WPI; 96-209359/21.
DR   N-PSDB; T28988.
PT   DNA encoding alpha-4 and delta subunit(s) of the human GABAa
PT   receptor  - also stably co-transfected eukaryotic cells expressing
PT   receptors contg. these subunit(s), used for screening and designing
PT   drugs
PS   Example 1; Fig 2; 45pp; English.
CC   The amino acid sequence (R97298) of the alpha-4 subunit of the
CC   human GABA-A receptor was deduced from a cDNA clone (T28988)
CC   isolated from a human brain thalamus cDNA library.  The alpha-4
CC   subunit can be produced in transfected host cells, partic. rodent
CC   fibroblasts.  Co-transfected host cells capable of expressing the
CC   alpha-4, delta (see also R97299) and beta subunits can be used to
CC   screen or design drugs that act on GABA-A receptors, e.g.
CC   benzodiazepines, barbiturates, beta-carbolines and neurosteroids.
CC   Construction of recombinant receptors contg. the alpha-4 and
CC   delta subunits becomes possible for the first time.
SQ   Sequence   554 AA;


  Query Match             31.3%;  Score 842;  DB 1;  Length 554;
  Best Local Similarity   36.0%;  Pred. No. 2.1e-71;
  Matches  194;  Conservative   89;  Mismatches  150;  Indels  106;  Gaps   15;

Qy     44 PLENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAV 103
Db     34 PGQNQ--KEEKLCTENFT----------RILDSLLDGYDNRLRPGFGGPVTEVKTDIYV 80

Qy    104 NSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRT 163
Db     81 TSFGPVSDVEVEYTMDVFFRQTWIDKRLKYDGPIEILRLNNMMVTKVWTPDTFFRNGKKS 140

Qy    164 HEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEM 223
Db    141 VSHNMTAPNKLFRIMRNGTILYTMRLTISAECPMRLVDFPMDGHACPVKFGSYAYPKSEM 200

Qy    224 IYKW---ENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYV 280
Db    201 IYTWTKGPEKSVEV-PKESSSLVQYDLIGQTVSSETIKSITGEYIVMTVYFHLRRKMGYF 259

Qy    281 AFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITAL 340
Db    260 MIQTYIPCIMTVILSQVSFWINKESVPARTVFGITTVLTMTTLSISARHSLPKVSYATAM 319

Qy    341 DFYIAICFVFCFCALLEFAVLNFLIYNQ-----------TKAHASP--KLRHPRI---N 383
Db    320 DWFIAVCFAFVFSALIEFAAVNYFTNIQMEKAKRKTSKPPQEVPAAPVQREKHPEAPLQN 379

Qy    384 SRAHARTRARSRACARQHQEAFV-----------CQIVTTEGSDGEER----------- 421
Db    380 TNANLNMRKRTNALV--HSESDVGNRTEVGNHSSKSSTVVQESSKGTPRSYLASSPNPFS 437

Qy    421 -------------PSCS--------AQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFC 458
Db    438 RANAAETISAARALPSASPTSIRTGYMPRKASVGSASTRHVFGSRL------QRIKTTVN 491

Qy    459 MVPDCEGSTWQQGRLCI----------HVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
```

```
Db    492 TI----GAT---GKLSATPPPSAPPPSGSGTSKIDKYARILFPVTFGAFNMVYWVVYLS 543


RESULT   8
R31186
ID   R31186 standard; Protein; 462 AA.
AC   R31186;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-5 subunit.
KW   Primer; human; alpha-5; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta.
OS   Homo sapiens.
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   N-PSDB; Q33129.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Disclosure; Fig 4; 43pp; English.
CC   This sequence represents the human alpha-5 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Rat alpha-5 cDNA was used as a probe
CC   and a human alpha-5 cDNA clone was isolated from a hippocampal cDNA
CC   library.  GABA-A receptor comprises a multimeric protein of molecular
CC   size 230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   462 AA;

  Query Match             30.2%;  Score 813;  DB 1;  Length 462;
  Best Local Similarity   36.1%;  Pred. No. 9e-69;
  Matches  167;  Conservative   89;  Mismatches  150;  Indels   56;  Gaps    7;

Qy      54 TKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILD 113
           | | : ||   :      :|||: :|  ||::||||:||: | |  :| | | ||:|  :
Db      35 TSSVKDETNDNITIF---TRILDGLLDGYDNRLRPGLGERITQVRTDIYVTSFGPVSDTE 91

Qy     114 MEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
           ||||||: | |:| |||| :    : | ||  : |::| ||||| | |::  | :| ||:
Db      92 MEYTIDVFFRQSWKDERLRFKGPMQRLPLNNLLASKIWTPDTFFHNGKKSIAHNMTTPNK 151

Qy     174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN--FK 231
           ::|:  || :|||:|:|| | | : :  ||||:|:||| | |::|| :|:::| | |   |
Db     152 LLRLEDDGTLLYTMRLTISAECPMQLEDFPMDAHACPLKFGSYAYPNSEVVYVWTNGSTK 211

Qy     232 LEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVT 291
             :  ::  :| |:   | :  || |:|  |:: :||  |:: |: ||   | |:|  :|
Db     212 SVVVAEDGSRLNQYHLMGQTVGTENISTSTGEYTIMTAHFHLKRKIGYFVIQTYLPCIMT 271

Qy     292 TMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFC 351
            :|| ||||:  || ||||  |:|:|||||||   :| : |:|:| ||:|:::||:|: |
Db     272 VILSQVSFWLNRESVPARTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFV 331

Qy     352 FCALLEFAVLNFL-----IYNQTKAHASPKLRHPR---INSRAHARTRARSRACARQHQE 403
           | ||:||| :|:       ::  ||  : |::  |   :|   :| | :
Db     332 FSALIEFATVNYFTKRGWAWDGKKALEAAKIKKKREVILNKSTNAFTTGKM--------- 383
```

```
Qy     404 AFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDC 463
                           |:  :|     :| |  :  |                    |
Db     383 -------------SHPPNIPKEQ-----TPAGTSNTTS--------------VSVKPS 408

Qy     464 EGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
           | | :  :    : ::|  ||:|||| |  ||::||   ||
Db     409 EEKTSESKKTYNSISKIDKMSRIVFPVLFGTFNLVYWATYLN 450


RESULT   9
R59864
ID   R59864 standard; Protein; 462 AA.
AC   R59864;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha5 subunit.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   N-PSDB; Q69141.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.4; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   462 AA;

  Query Match             30.2%;  Score 813;  DB 1;  Length 462;
  Best Local Similarity   36.1%;  Pred. No. 9e-69;
  Matches  167;  Conservative   89;  Mismatches  150;  Indels   56;  Gaps    7;

Qy      54 TKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILD 113
           | | : ||   :      :|||: :|  ||::||||:||: | |  :| | | ||:|  :
Db      35 TSSVKDETNDNITIF---TRILDGLLDGYDNRLRPGLGERITQVRTDIYVTSFGPVSDTE 91

Qy     114 MEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
           ||||||: | |:| |||| :    : | ||  : |::| ||||| | |::  | :| ||:
Db      92 MEYTIDVFFRQSWKDERLRFKGPMQRLPLNNLLASKIWTPDTFFHNGKKSIAHNMTTPNK 151

Qy     174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN--FK 231
           ::|:  || :|||:|:|| | | : :  ||||:|:||| | |::|| :|:::| | |   |
Db     152 LLRLEDDGTLLYTMRLTISAECPMQLEDFPMDAHACPLKFGSYAYPNSEVVYVWTNGSTK 211

Qy     232 LEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFENVSRRFGYVAFQNYVPSSVT 291
             :  ::  :| |:   | :  || |:|  |:: :||  |:: |: ||   | |:|  :|
Db     212 SVVVAEDGSRLNQYHLMGQTVGTENISTSTGEYTIMTAHFHLKRKIGYFVIQTYLPCIMT 271

Qy     292 TMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFC 351
            :|| ||||:  || ||||  |:|:|||||||   :| : |:|:| ||:|:::||:|: |
Db     272 VILSQVSFWLNRESVPARTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFV 331

Qy     352 FCALLEFAVLNFL-----IYNQTKAHASPKLRHPR---INSRAHARTRARSRACARQHQE 403
           | ||:||| :|:       ::  ||  : |::  |   :|   :| | :
Db     332 FSALIEFATVNYFTKRGWAWDGKKALEAAKIKKKREVILNKSTNAFTTGKM--------- 383

Qy     404 AFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDC 463
                           |:  :|     :| |  :  |                    |
Db     383 -------------SHPPNIPKEQ-----TPAGTSNTTS--------------VSVKPS 408

Qy     464 EGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
           | | :  :    : ::|  ||:|||| |  ||::||   ||
Db     409 EEKTSESKKTYNSISKIDKMSRIVFPVLFGTFNLVYWATYLN 450
```

```
RESULT  10
R31185
ID   R31185 standard; Protein; 492 AA.
AC   R31185;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-3 subunit.
KW   Primer; human; alpha-3; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta.
OS   Homo sapiens.
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   N-PSDB; Q33128.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Disclosure; Fig 3; 43pp; English.
CC   This sequence represents the human alpha-3 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Bovine alpha-3 cDNA was used as a
CC   probe and an alpha-3 cDNA clone was isolated from a human foetal
CC   brain cDNA library, which was missing approx. 100 bp of the 5' end.
CC   This missing fragment was isolated by PCR.  The two fragments were
CC   ligated together to give a full length alpha-3 cDNA.    GABA-A
CC   receptor comprises a multimeric protein of molecular size 230-370 kD
CC   with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   492 AA;

  Query Match           29.7%;  Score 798.5;  DB 1;  Length 492;
  Best Local Similarity  35.8%;  Pred. No. 2.3e-67;
  Matches  166;  Conservative   83;  Mismatches  134;  Indels   81;  Gaps    7;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           :|||: :|  ||::||||:|:  | |  :| | | ||:|  |||||||: | |||:||||
Db      68 TRILDRLLDGYDNRLRPGLGDAVTEVKTDIYVTSFGPVSDTDMEYTIDVFFRQTWHDERL 127

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
            ::   : | ||  : |::| |||||  | |::  | :| ||:::|:  :| :|||:|:||
Db     128 KFDGPMKILPLNNLLASKIWTPDTFFHNGKKSVAHNMTTPNKLLRLVDNGTLLYTMRLTI 187

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEINEKNSWKLFQFDFT 248
           | | :|:  |||| |:||| | |::|   |::| |   :|  :|: :  | :| |:|
Db     188 HAECPMHLEDFPMDVHACPLKFGSYAYTTAEVVYSWTLGKNKSVEVAQDGS-RLNQYDLL 246

Qy     249 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 308
           |    |||| :  |:::|||  |:: |: ||   | |:|  :| :|| |||| :  || ||
Db     247 GHVVGTEIIRSSTGEYVVMTTHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPA 306

Qy     309 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 368
           ||  |:|:|||||||   :| : |:|:| ||:|:::|:|: | | ||:||| :|:
Db     307 RTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYF---- 363

Qy     369 TKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQP 428
           ||                      || |                   :|:: |     :
Db     363 TK----------------------RSWAW------------------EGKKVPEALEMKK 382

Qy     429 PSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQG---------------- 472
           :| :|    |    :    :     |      | | ||  :|
Db     383 KTPAAPAKKTSTTFNIVGTTYPINLAK------DTEFSTISKGAAPSASSTPTIIASPKA 436

Qy     472 ----------RLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
                    :    | ::|  ||::||| |  ||::||   :|
Db     437 TYVQDSPTETKTYNSVSKVDKISRIIFPVLFAIFNLVYWATYVN 480


RESULT  11
R59863
ID   R59863 standard; Protein; 492 AA.
AC   R59863;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha3 subunit.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   N-PSDB; Q69140.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.3; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   492 AA;

  Query Match           29.7%;  Score 798.5;  DB 1;  Length 492;
  Best Local Similarity  35.8%;  Pred. No. 2.3e-67;
  Matches  166;  Conservative   83;  Mismatches  134;  Indels   81;  Gaps    7;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           :|||: :|  ||::||||:|:  | |  :| | | ||:|  |||||||: | |||:||||
Db      68 TRILDRLLDGYDNRLRPGLGDAVTEVKTDIYVTSFGPVSDTDMEYTIDVFFRQTWHDERL 127

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
            ::   : | ||  : |::| |||||  | |::  | :| ||:::|:  :| :|||:|:||
Db     128 KFDGPMKILPLNNLLASKIWTPDTFFHNGKKSVAHNMTTPNKLLRLVDNGTLLYTMRLTI 187

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEINEKNSWKLFQFDFT 248
           | | :|:  |||| |:||| | |::|   |::| |   :|  :|: :  | :| |:|
Db     188 HAECPIHLEDFPMDVHACPLKFGSYAYTTAEVVYSWTLGKNKSVEVAQDGS-RLNQYDLL 246

Qy     249 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 308
           |    |||| :  |:::|||  |:: |: ||   | |:|  :| :|| |||| :  || ||
Db     247 GHVVGTEIIRSSTGEYVVMTTHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPA 306

Qy     309 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 368
           ||  |:|:|||||||   :| : |:|:| ||:|:::|:|: | | ||:||| :|:
Db     307 RTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYF---- 363

Qy     369 TKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQP 428
           ||                      || |                   :|:: |     :
Db     363 TK----------------------RSWAW------------------EGKKVPEALEMKK 382

Qy     429 PSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQG---------------- 472
           :| :|    |    :    :     |      | | ||  :|
Db     383 KTPAAPAKKTSTTFNIVGTTYPINLAK------DTEFSTISKGAAPSASSTPTIIASPKA 436

Qy     472 ----------RLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
```

Db 437 TYVQDSPTETKTYNSVSKVDKISRIIFPVLFAIFNLVYWATYVN 480

RESULT 12
R31184
ID R31184 standard; Protein; 451 AA.
AC R31184;
DT 10-MAY-1993 (first entry)
DE GABA-A receptor alpha-2 subunit.
KW Primer; human; alpha-3; subunit; gamma-amino butyric acid; GABA; -A;
KW receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW ligand; alpha; beta; gamma; delta.
OS Homo sapiens.
PN WO9222652-A.
PD 23-DEC-1992.
PF 09-JUN-1992; G01031.
PR 11-JUN-1991; GB-012504.
PA (MERI) MERCK SHARP & DOHME LTD.
PI Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR WPI; 93-018138/02.
DR N-PSDB; Q33127.
PT Stably transfected eukaryotic cell line - expresses human GABA-A
PT receptor comprising alpha, beta and gamma sub-units, useful for
PT medicament prepn.
PS Disclosure; Fig 2; 43pp; English.
CC This sequence represents the human alpha-2 subunit of gamma-amino
CC butyric acid (GABA)-A receptor. Bovine alpha-2 cDNA was used as a
CC probe and an alpha-2 cDNA clone was isolated from a human foetal
CC brain cDNA library. GABA-A receptor comprises a multimeric protein
CC of molecular size 230-270 kD with specific binding sites for various
CC drugs including benzodiazepines, barbiturates, and beta-carbolines,
CC in addition to the agonist ligand GABA. The receptor is composed of
CC several distinct types of subunit, which are divided into four classes
CC (alpha, beta, gamma and delta) based on sequence homology. To date
CC six types of alpha, three types of beta, two types of gamma and one
CC type of delta subunit have been identified. It has been found that
CC in addition to an alpha and a beta subunit, either gamma-1 or gamma-2
CC is also required to confer benzodiazipine sensitivity. The benzo-
CC diazepine pharmacology of the receptor is largely dependent on the
CC identity of the alpha and gamma subunits present. Receptors
CC containing a delta subunit do not appear to bind benzodiazepines.
SQ Sequence 451 AA;

Query Match 29.0%; Score 781; DB 1; Length 451;
Best Local Similarity 37.4%; Pred. No. 9.3e-66;
Matches 165; Conservative 77; Mismatches 151; Indels 48; Gaps 7;

Qy 72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
Db 43 TRILDRLLDGYDNRLRPGLGDSITEVFTNIYVTSFGPVSDTDMEYTIDVFFRQKWKDERL 102

Qy 132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
Db 103 KFKGPMNILRLNNLMASKIWTPDTFFHNGKKSVAHNMTMPNKLLRIQDDGTLLYTMRLTV 162

Qy 192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEINEKNSWKLFQFDFT 248
Db 163 QAECPMHLEDFPMDAHSCPLKFGSYAYTTSEVTYIWTYNASDSVQVAPDGS-RLNQYDLL 221

Qy 249 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 308
Db 222 GQSIGKETIKSSTGEYTVMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPA 281

Qy 309 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 368
Db 282 RTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYF---- 338

Qy 369 TKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEE----RPSCS 424
Db 338 TK-------RGWTWDGKSVVNDKKKEKASVMIQNNAYAVAVANYAPNLSKDPVLSTISKS 390

Qy 425 AQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYS 484
Db 391 ATTPEPNKKPENKPA--------EAKKTFNS--------------------VSKIDRMS 421

Qy 485 RVVFPVTFFFFNVLYWLVCLN 505
Db 422 RIVFPVLFGTFNLVYWATYLN 442

RESULT 13
R59862
ID R59862 standard; Protein; 451 AA.
AC R59862;
DT 20-MAR-1995 (first entry)
DE Human GABA receptor alpha2 subunit.
KW GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW central nervous system.
OS Homo sapiens.
PN WO9413799-A.
PD 23-JUN-1994.
PF 07-DEC-1993; G02506.
PR 10-DEC-1992; GB-025776.
PR 07-SEP-1993; GB-018528.
PA (MERI) MERCK SHARP & DOHME LTD.
PI Hadingham KL, Whiting PJ;
DR WPI; 94-234213/28.
DR N-PSDB; Q69139.
PT Cell lines expressing GABA-A receptors - used for screening for
PT and designing medicaments which act on the GABA-A receptors
PS Disclosure; Fig.2; 79pp; English.
CC This receptor may be expressed in mammal cell lines which may be
CC used for screening for and designing medicaments which act on the
CC human GABAA receptor. The cells expressing this subunit are ideal
CC systems for the study of the structure, pharmacology and function
CC of the receptor subtype.
SQ Sequence 451 AA;

Query Match 29.0%; Score 781; DB 1; Length 451;
Best Local Similarity 37.4%; Pred. No. 9.3e-66;
Matches 165; Conservative 77; Mismatches 151; Indels 48; Gaps 7;

Qy 72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
Db 43 TRILDRLLDGYDNRLRPGLGDSITEVFTNIYVTSFGPVSDTDMEYTIDVFFRQKWKDERL 102

Qy 132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
Db 103 KFKGPMNILRLNNLMASKIWTPDTFFHNGKKSVAHNMTMPNKLLRIQDDGTLLYTMRLTV 162

Qy 192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEINEKNSWKLFQFDFT 248
Db 163 QAECPMHLEDFPMDAHSCPLKFGSYAYTTSEVTYIWTYNASDSVQVAPDGS-RLNQYDLL 221

Qy 249 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 308
Db 222 GQSIGKETIKSSTGEYTVMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPA 281

Qy 309 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 368
Db 282 RTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYF---- 338

Qy 369 TKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEE----RPSCS 424
Db 338 TK-------RGWTWDGKSVVNDKKKEKASVMIQNNAYAVAVANYAPNLSKDPVLSTISKS 390

Qy 425 AQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYS 484
Db 391 ATTPEPNKKPENKPA--------EAKKTFNS--------------------VSKIDRMS 421

Qy 485 RVVFPVTFFFFNVLYWLVCLN 505

```
Db    422 RIVFPVLFGTFNLVYWATYLN 442


RESULT  14
R31188
ID   R31188 standard; Protein; 474 AA.
AC   R31188;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor beta-2 subunit.
KW   Primer; human; beta-2; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta.
OS   Homo sapiens.
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   N-PSDB; Q33131.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Disclosure; Fig 6; 43pp; English.
CC   This sequence represents the human beta-2 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Short human beta-2 cDNA was used as
CC   a probe and a human beta-2 cDNA clone was isolated from a hippocampal
CC   cDNA library.  The largest cDNA clone isolated lacked the 5' 500 bp of
CC   the beta-2 coding sequence.  This missing fragment was isolated by PCR.
CC   The two fragments were ligated together to give a full length beta-2
CC   cDNA.  GABA-A receptor comprises a multimeric protein of molecular size
CC   230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   474 AA;

  Query Match             24.8%;  Score 667;  DB 1;  Length 474;
  Best Local Similarity   31.0%;  Pred. No. 6.3e-55;
  Matches  142;  Conservative   90;  Mismatches  176;  Indels   50;  Gaps    7;

Qy      75 LNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERLCYN 134
           :: :|  || :|||  |  |  | : | : |:  :| ::|:||: : | | | |:|| ||
Db      40 VDRLLKGYDIRLRPDFGGPPVAVGMNIDIASIDMVSEVNMDYTLTMYFQQAWRDKRLSYN 99

Qy     135 DTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAG 194
             :| |:  |  |||:|||:| | |::  | :|: |:|:|:: || ||| :|:|  |
Db     100 VIPLNLTLDNRVADQLWVPDTYFLNDKKSFVHGVTVKNRMIRLHPDGTVLYGLRITTTAA 159

Qy     195 CSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKT 254
           | : : |:|:|  :| |   |: |  ::: : |      :  ||        |
Db     160 CMMDLRRYPLDEQNCTLEIESYGYTTDDIEFYWRGDDNAVTGVTKIELPQFSIVDYKLIT 219

Qy     255 EIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGI 314
           : :    | :  ::: | : |  ||   | |:|| : |:|||||||  ::: || :|||
Db     220 KKVVFSTGSYPRLSLSFKLKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALGI 279

Qy     315 TSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHAS 374
           |:|||||: |  |:  |:: |: |:| |:  |||| | ||||:|::|:: :
Db     280 TTVLTMTTINTHLRETLPKIPYVKAIDMYLMGCFVFVFMALLEYALVNYIFFG------- 333

Qy     375 PKLRHPRINSRAHARTRARSRACAR-------QHQEAFVC------QIVTTEGSDGEERP 421
           | |:   :|  :  : :    |         |:   :        :: |:|   |   |
Db     333 ---RGPQRQKKAAEKAASANNEKMRLDVNKMDPHENILLSTLEIKNEMATSEAVMGLGDP 389

Qy     422 -------SCSAQQPPSPGSPEG-------PRSLCSKLACCEWCKRFKKYFCMVPDCEGST 467
                 |: |    | |           | :  | :     :|  :    :||
Db     390 RSTMLAYDASSIQYRKAGLPRHSFGRNALERHVAQKKSRLR--RRASQLKITIPD----- 443

Qy     468 WQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
                 |  :| :||: ||| | |||::|||  :|
Db     443 ------LTDVNAIDRWSRIFFPVVFSFFNIVYWLYYVN 474


RESULT  15
R59866
ID   R59866 standard; Protein; 474 AA.
AC   R59866;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor beta2 subunit.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   Q-PSDB; Q69143.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.6; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   474 AA;

  Query Match             24.8%;  Score 667;  DB 1;  Length 474;
  Best Local Similarity   31.0%;  Pred. No. 6.3e-55;
  Matches  142;  Conservative   90;  Mismatches  176;  Indels   50;  Gaps    7;

Qy      75 LNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERLCYN 134
           :: :|  || :|||  |  |  | : | : |:  :| ::|:||: : | | | |:|| ||
Db      40 VDRLLKGYDIRLRPDFGGPPVAVGMNIDIASIDMVSEVNMDYTLTMYFQQAWRDKRLSYN 99

Qy     135 DTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAG 194
             :| |:  |  |||:|||:| | |::  | :|: |:|:|:: || ||| :|:|  |
Db     100 VIPLNLTLDNRVADQLWVPDTYFLNDKKSFVHGVTVKNRMIRLHPDGTVLYGLRITTTAA 159

Qy     195 CSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKT 254
           | : : |:|:|  :| |   |: |  ::: : |      :  ||        |
Db     160 CMMDLRRYPLDEQNCTLEIESYGYTTDDIEFYWRGDDNAVTGVTKIELPQFSIVDYKLIT 219

Qy     255 EIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGI 314
           : :    | :  ::: | : |  ||   | |:|| : |:|||||||  ::: || :|||
Db     220 KKVVFSTGSYPRLSLSFKLKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALGI 279

Qy     315 TSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHAS 374
           |:|||||: |  |:  |:: |: |:| |:  |||| | ||||:|::|:: :
Db     280 TTVLTMTTINTHLRETLPKIPYVKAIDMYLMGCFVFVFMALLEYALVNYIFFG------- 333

Qy     375 PKLRHPRINSRAHARTRARSRACAR-------QHQEAFVC------QIVTTEGSDGEERP 421
           | |:   :|  :  : :    |         |:   :        :: |:|   |   |
Db     333 ---RGPQRQKKAAEKAASANNEKMRLDVNKMDPHENILLSTLEIKNEMATSEAVMGLGDP 389

Qy     422 -------SCSAQQPPSPGSPEG-------PRSLCSKLACCEWCKRFKKYFCMVPDCEGST 467
                 |: |    | |           | :  | :     :|  :    :||
Db     390 RSTMLAYDASSIQYRKAGLPRHSFGRNALERHVAQKKSRLR--RRASQLKITIPD----- 443
```

```
Qy     468 WQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
                 |  :| :||: ||| | |||::|||  :|
Db     443 ------LTDVNAIDRWSRIFFPVVFSFFNIVYWLYYVN 474
```

Search completed: March 10, 2000, 08:51:54
Job time: 5287 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:01:22 ; Search time 34.6 Seconds
(without alignments)
194.467 Million cell updates/sec

Title: US-09-030-832-42
Perfect score: 2691
Sequence: 1 MLSKVLPVLLGILLILQSRV.....VFPVTFFFFNVLYWLVCLNL 506

Scoring table: BLOSUM62

Searched: 133990 seqs, 13297546 residues

Database : Issued_Patents_AA:*

Word size : 0

Number of hits that pass the threshold : 133990
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/PCTUS9_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1067	39.7	467	1	US-08-459-100A-3	Sequence 3, Appli
2	855	31.8	453	1	US-08-417-330A-18	Sequence 18, Appl
3	813	30.2	462	1	US-08-417-330A-16	Sequence 16, Appl
4	798.5	29.7	492	1	US-08-417-330A-14	Sequence 14, Appl
5	781	29.0	451	1	US-08-417-330A-12	Sequence 12, Appl
6	677.5	25.2	474	1	US-08-459-100A-4	Sequence 4, Appli
7	667	24.8	474	1	US-08-417-330A-20	Sequence 20, Appl
8	662.5	24.6	686	2	US-08-768-301-4	Sequence 4, Appli
9	632.5	23.5	496	1	US-08-137-614A-2	Sequence 2, Appli
10	632.5	23.5	496	2	US-08-768-301-2	Sequence 2, Appli
11	611.5	22.7	617	1	US-08-137-614A-25	Sequence 25, Appl
12	609.5	22.6	617	1	US-08-137-614A-24	Sequence 24, Appl
13	598.5	22.2	488	1	US-08-554-659-2	Sequence 2, Appli
14	595.5	22.1	488	1	US-08-554-659-4	Sequence 4, Appli
15	590.5	21.9	637	3	US-08-072-064-4	Sequence 4, Appli
16	590.5	21.9	637	3	US-08-072-064-6	Sequence 6, Appli
17	587.5	21.8	637	3	US-08-072-064-1	Sequence 1, Appli
18	587.5	21.8	637	4	PCT-US92-08558-1	Sequence 1, Appli
19	586.5	21.8	637	3	US-08-072-064-8	Sequence 8, Appli
20	578	21.5	617	1	US-08-137-614A-26	Sequence 26, Appl
21	561	20.8	510	1	US-08-249-112-3	Sequence 3, Appli
22	561	20.8	510	4	PCT-US95-06556-3	Sequence 3, Appli
23	559	20.8	440	1	US-08-459-100A-2	Sequence 2, Appli
24	559	20.8	440	4	PCT-US94-09589-2	Sequence 2, Appli
25	555.5	20.6	456	1	US-08-435-933-6	Sequence 6, Appli
26	555.5	20.6	456	4	PCT-US96-06035-6	Sequence 6, Appli
27	549.5	20.4	487	1	US-08-249-112-4	Sequence 4, Appli
28	549.5	20.4	487	4	PCT-US95-06556-4	Sequence 4, Appli
29	198	7.4	57	1	US-08-137-614A-21	Sequence 21, Appl
30	180	6.7	479	1	US-08-278-635B-2	Sequence 2, Appli
31	174	6.5	57	1	US-08-137-614A-19	Sequence 19, Appl
32	172.5	6.4	502	1	US-08-496-855A-4	Sequence 4, Appli
33	172.5	6.4	498	1	US-08-496-855A-6	Sequence 6, Appli
34	172.5	6.4	502	2	US-08-466-589-10	Sequence 10, Appl
35	172.5	6.4	498	2	US-08-466-589-12	Sequence 12, Appl
36	172.5	6.4	502	2	US-08-700-636-10	Sequence 10, Appl
37	172.5	6.4	498	2	US-08-700-636-12	Sequence 12, Appl
38	171	6.4	57	1	US-08-137-614A-17	Sequence 17, Appl
39	167	6.2	57	1	US-08-137-614A-23	Sequence 23, Appl
40	167	6.2	56	4	PCT-US92-08558-7	Sequence 7, Appli
41	166	6.2	57	1	US-08-137-614A-18	Sequence 18, Appl
42	164	6.1	449	5	5468481-1	Patent No. 5468481
43	161	6.0	57	1	US-08-137-614A-22	Sequence 22, Appl
44	159.5	5.9	511	1	US-08-278-635B-8	Sequence 8, Appli
45	159.5	5.9	528	2	US-08-466-589-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-459-100A-3
; Sequence 3, Application US/08459100A
; Patent No. 5654172
; GENERAL INFORMATION:
; APPLICANT: Li, ET AL.
; TITLE OF INVENTION: GABAA Receptor Epsilon Subunit
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,100A
; FILING DATE: June 2, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09589
; FILING DATE: 26 AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-325
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-459-100A-3

Query Match 39.7%; Score 1067; DB 1; Length 467;
Best Local Similarity 42.6%; Pred. No. 8.2e-96;
Matches 191; Conservative 94; Mismatches 115; Indels 48; Gaps 6;

```
Qy      67 KLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
           |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|||||||| |:|
Db      60 KVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFAQ 119

Qy     125 TWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVL 184
           ||| || :| | : | || |:| ::|||||||||||:   | || ||:|:||: ||:||
Db     120 MWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVL 179
```

```
Qy     185 YTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQ 244
           |::|:|||| | | :  |||| ||||| |||: ||  |::|:|:   :|: :  ||:|:|
Db     180 YSLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQ 239

Qy     245 FDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTE 304
           | | |: | ||:: |  ||::||:::|::||| ||   | |:| ::  :|||||||  :
Db     240 FSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKD 299

Qy     305 SAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL 364
           : |||||||||:|||||| | :||: |:|||:||:| ::::||:| | ||:|:  |::
Db     300 AVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYF 359

Qy     365 IYNQTKAHASPKLRH---PRINSRAHARTRARSRAC--ARQHQEAFVCQIVTTEGSDGE 418
           : |:  :    | :    | |: |  : |   : |     |  :  : |        ||:
Db     360 VSNRKPSKDKDKKKKNPAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGK 412

Qy     419 ERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVY 478
           :   |::                          :||   ||    |: ||: | :
Db     413 D---CAS-----------------------------FFCCFEDCRTGAWRHGRIHIRIA 439

Qy     479 RLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
           ::|:|:|: ||  |  ||::||:  | |
Db     440 KMDSYARIFFPTAFCLFNLVYWVSYLYL 467
```

```
RESULT   2
US-08-417-330A-18
; Sequence 18, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  453 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
```

US-08-417-330A-18

```
  Query Match             31.8%;  Score 855;  DB 1;  Length 453;
  Best Local Similarity   38.1%;  Pred. No. 3.7e-75;
  Matches  180;  Conservative   86;  Mismatches  127;  Indels   80;  Gaps   10;

Qy      65 VGKL--------PEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEY 116
           :|||          ||||: :|  ||::|||| |   | |  :| | | ||:| ::|||
Db      18 LGKLEVEGNFYSENVSRILDNLLEGYDNRLRPGFGGAVTEVKTDIYVTSFGPVSDVEMEY 77

Qy     117 TIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVR 176
           |:|: | ||| |||| :    | | ||  :||::| |||||||  |::  | :| ||:: |
Db      78 TMDVFFRQTWTDERLKFGGPTEILSLNNLMVSKIWTPDTFFRNGKKSIAHNMTTPNKLFR 137

Qy     177 IYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLE 233
           | ::| :|||:|:||:| | : :: |||| |:||| | |::||::|:|| |:    : :|
Db     138 IMQNGTILYTMRLTINADCPMRLVNFPMDGHACPLKFGSYAYPKSEIIYTWKKGPLYSVE 197

Qy     234 INEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTM 293
           : |::|  | |:|  | :  :| | :  |::::||::|:: |: ||   | | |  :| :
Db     198 VPEESS-SLLQYDLIGQTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVI 256

Qy     294 LSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFC 353
           || |||||  || |||| ||||:|||||||   :| : |:||| ||:|::||:|| | |
Db     257 LSQVSFWINKESVPARTVLGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFS 316

Qy     354 ALLEFAVLNFLIYNQTK------AHASPK--------------LRHPRINSRAHARTRA 392
           ||:||| :|:    ||:        |:|                : ||  :|: | : |
Db     317 ALIEFAAVNYFTNLQTQKAKRKAQFAAPPTVTISKATEPLEAEIVLHP--DSKYHLKKRI 374

Qy     393 RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKR 452
            | :           ||::      |      : |    :|  |  |
Db     375 TSLS----------LPIVSS-----SEANKVLTRAPILQSTPVTPPPL------------ 408

Qy     453 FKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
                 |   | |          ::| |||::||| |  ||::||:| |:
Db     408 --------PPAFGGT----------SKIDQYSRILFPVAFAGFNLVYWVVYLS 442
```

```
RESULT   3
US-08-417-330A-16
; Sequence 16, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
```

```
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  462 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-16


  Query Match             30.2%;  Score 813;  DB 1;  Length 462;
  Best Local Similarity   36.1%;  Pred. No. 4.7e-71;
  Matches  167;  Conservative   89;  Mismatches  150;  Indels   56;  Gaps    7;

Qy      54 TKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILD 113
           | | : ||   :      :|||: :|  ||::||||:||: | |  :| | | ||:|  :
Db      35 TSSVKDETNDNITIF---TRILDGLLDGYDNRLRPGLGERITQVRTDIYVTSFGPVSDTE 91

Qy     114 MEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
           ||||||: | |:| |||| :    : | ||  : |::| ||||| | |::  | :| ||:
Db      92 MEYTIDVFFRQSWKDERLRFKGPMQRLPLNNLLASKIWTPDTFFHNGKKSIAHNMTTPNK 151

Qy     174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN--FK 231
           ::|:  || :|||:|:|| | | : :  ||||:|:||| | |::|| :|::| | |   |
Db     152 LLRLEDDGTLLYTMRLTISAECPMQLEDFPMDAHACPLKFGSYAYPNSEVVYVWTNGSTK 211

Qy     232 LEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVT 291
             :  ::  :| |:   | :  || |:|  |:: :||  |:: |: ||    | |:|  :|
Db     212 SVVVAEDGSRLNQYHLMGQTVGTENISTSTGEYTIMTAHFHLKRKIGYFVIQTYLPCIMT 271

Qy     292 TMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFC 351
           :|| ||||:  || ||||  |:|:|||||||   :| : |:|:| ||:|::||:|: |
Db     272 VILSQVSFWLNRESVPARTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFV 331

Qy     352 FCALLEFAVLNFL-----IYNQTKAHASPKLRHPR---INSRAHARTRARSRACARQHQE 403
           | ||:||| :|:       ::  ||  : |::  |   :|   :| | :
Db     332 FSALIEFATVNYFTKRGWAWDGKKALEAAKIKKKREVILNKSTNAFTTGKM--------- 383

Qy     404 AFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDC 463
                       |:   :|     :| | :  |                 |
Db     383 --------------SHPPNIPKEQ-----TPAGTSNTTS--------------VSVKPS 408

Qy     464 EGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
           |  | :  :    : ::|  ||:|||| |  ||:::||   ||
Db     409 EEKTSESKKTYNSISKIDKMSRIVFPVLFGTFNLVYWATYLN 450


RESULT   4
US-08-417-330A-14
; Sequence 14, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  492 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-14


  Query Match             29.7%;  Score 798.5;  DB 1;  Length 492;
  Best Local Similarity   35.8%;  Pred. No. 1.3e-69;
  Matches  166;  Conservative   83;  Mismatches  134;  Indels   81;  Gaps    7;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           :|||: :|  ||::||||:|:  | |  :| | | ||:|  |||||||: | |||:||||
Db      68 TRILDRLLDGYDNRLRPGLGDAVTEVKTDIYVTSFGPVSDTDMEYTIDVFFRQTWHDERL 127

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
             ::   : | ||  : |::| |||| | |::  | :| ||:::|:  :| :|||:|:||
Db     128 KFDGPMKILPLNNLLASKIWTPDTFFHNGKKSVAHNMTTPNKLLRLVDNGTLLYTMRLTI 187

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEINEKNSWKLFQFDFT 248
           | | :|:  ||||  |:||| | |::|   |::| |   :|  :|: :  | :| |:|
Db     188 HAECPMHLEDFPMDVHACPLKFGSYAYTTAEVVYSWTLGKNKSVEVAQDGS-RLNQYDLL 246

Qy     249 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 308
           |    |||| :  |:::|||  |:: |: ||   | |:|  :| :|| |||:  || ||
Db     247 GHVVGTEIIRSSTGEYVVMTTHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPA 306

Qy     309 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 368
           ||  |:|:|||||||   :| : |:|:| ||:|::||:|: | | ||:||| :|:
Db     307 RTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYF---- 363

Qy     369 TKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQP 428
           ||                        || |                  :|:: |     :
Db     363 TK----------------------RSWAW-----------------EGKKVPEALEMKK 382

Qy     429 PSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQG---------------- 472
             :| :|    |    :    :     |      | | ||  :|
Db     383 KTPAAPAKKTSTTFNIVGTTYPINLAK------DTEFSTISKGAAPSASSTPTIIASPKA 436

Qy     472 ----------RLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
                      :    | ::|  ||::||| |  ||::||   :|
Db     437 TYVQDSPTETKTYNSVSKVDKISRIIFPVLFAIFNLVYWATYVN 480


RESULT   5
US-08-417-330A-12
; Sequence 12, Application US/08417330A
```

```
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  451 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-12


  Query Match           29.0%;  Score 781;  DB 1;  Length 451;
  Best Local Similarity  37.4%;  Pred. No. 5.9e-68;
  Matches  165;  Conservative   77;  Mismatches  151;  Indels   48;  Gaps    7;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           :|||: :|  ||::||||:|:  | |   | | | ||:|  |||||||: | | | ||||
Db      43 TRILDRLLDGYDNRLRPGLGDSITEVFTNIYVTSFGPVSDTDMEYTIDVFFRQKWKDERL 102

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
           :      | ||  : |::| ||||| | |::  | :||||:::|| || :|||:|:|:
Db     103 KFKGPMNILRLNNLMASKIWTPDTFFHNGKKSVAHNMTMPNKLLRIQDDGTLLYTMRLTV 162

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEINEKNSWKLFQFDFT 248
            | | :|:  ||||:||||| | |::|  :|: | |   :  :::    | :| |:|
Db     163 QAECPMHLEDFPMDAHSCPLKFGSYAYTTSEVTYIWTYNASDSVQVAPDGS-RLNQYDLL 221

Qy     249 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 308
           | |   | | :  |:: |||  |:: |: ||   | |:|  :| :|| ||||:  || ||
Db     222 GQSIGKETIKSSTGEYTVMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPA 281

Qy     309 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 368
           ||  |:|:|||||||   :| : |:|:| ||:|::||:|: | | ||:||| :|:
Db     282 RTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYF---- 338

Qy     369 TKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEE----RPSCS 424
           ||       |   : ::   : : :|      |:  :    :  ::     | |
Db     338 TK-------RGWTWDGKSVVNDKKKEKASVMIQNNAYAVAVANYAPNLSKDPVLSTISKS 390

Qy     425 AQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYS 484
           |  |     ||   :        |  | |                          | ::|  |
Db     391 ATTPEPNKKPENKPA--------EAKKTFNS--------------------VSKIDRMS 421

Qy     485 RVVFPVTFFFFNVLYWLVCLN 505
           |:|||| |  ||::||   ||
Db     422 RIVFPVLFGTFNLVYWATYLN 442


RESULT   6
US-08-459-100A-4
; Sequence 4, Application US/08459100A
; Patent No. 5654172
;  GENERAL INFORMATION:
;    APPLICANT:  Li, ET AL.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,100A
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09589
;      FILING DATE:  26 AUG 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-325
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  474 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-459-100A-4


  Query Match           25.2%;  Score 677.5;  DB 1;  Length 474;
  Best Local Similarity  32.1%;  Pred. No. 7.9e-58;
  Matches  148;  Conservative   88;  Mismatches  174;  Indels   51;  Gaps    7;

Qy      68 LPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWY 127
           :|     :: :|  || :|||  |  |  | : | | |:  :| ::|:||: : | |:|
Db      34 MPYVKETVDRLLKGYDIRLRPDFGGPPVDVGMRIDVASIDMVSEVNMDYTLTMYFQQSWK 93

Qy     128 DERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTI 187
           |:|| |:    :| |:  |  |||:|||:| | |::  | :|: |:|:|:: || ||| :
Db      94 DKRLSYSGIPLNLTLDNRVADQLWVPDTYFLNDKKSFVHGVTVKNRMIRLHPDGTVLYGL 153

Qy     188 RMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQF-- 246
           |:|  | | : : |:|:|  :| |   |: |  ::: : |   :  :   |  :| ||
Db     154 RITTTAACMMDLRRYPLDEQNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELPQFSI 213
```

```
Qy     246 -DFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTE 304
           |:  || | |   |   | :  ::: | : |  ||   | |:||:: |:||||||||  :
Db     214 VDYKMVSKKVEFTT---GAYPRLSLSFRLKRNIGYFILQTYMPSTLITILSWVSFWINYD 270

Qy     305 SAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL 364
           :: || :||||:|||||: |  |:  |:: |: |:| |:  |||| | ||||:| :|::
Db     271 ASAARVALGITTVLTMTTISTHLRETLPKIPYVKAIDIYLMGCFVFVFLALLEYAFVNYI 330

Qy     365 IYNQ----------TKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTE 413
           : :             |:   ||   ::   ||      :     :   : |   |:
Db     331 FFGKGPQKKGASKQDQSANEKNKLEMNKVQVDAHGNILLSTLEIRNETSGSEVLTSVSDP 390

Qy     414 GSDGEERPSCSAQ--QPPSP----------GSPEGPRSLCSKLACCEWCKRFKKYFCMV 460
           :      | | |  :| |           | |   |              :|  :   :
Db     391 KATMYSYDSASIQYRKPLSSREAYGRALDRHGVPSKGRIR----------RRASQLKVKI 440

Qy     461 PDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWL 501
           ||             |  :| :||: ||:||  |||:|||
Db     441 PD----------LTDVNSIDKWSRMFFPITFSLFNVVYWL 470


RESULT   7
US-08-417-330A-20
; Sequence 20, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  474 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-20


  Query Match             24.8%;  Score 667;  DB 1;  Length 474;
  Best Local Similarity   31.0%;  Pred. No. 8.3e-57;
  Matches  142;  Conservative   90;  Mismatches  176;  Indels   50;  Gaps    7;

Qy      75 LNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERLCYN 134
           :: :|  || :|||  |  |  | : | : |:  :| ::|:||: : | | | |:|| ||
Db      40 VDRLLKGYDIRLRPDFGGPPVAVGMNIDIASIDMVSEVNMDYTLTMYFQQAWRDKRLSYN 99

Qy     135 DTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAG 194
             :| |:  |  |||:|||:| | |::  | :|: |:|:|:: || ||| :|:|  |
Db     100 VIPLNLTLDNRVADQLWVPDTYFLNDKKSFVHGVTVKNRMIRLHPDGTVLYGLRITTTAA 159

Qy     195 CSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKT 254
           | : : |:|:|  :| | |  |: | ::: : |      :      :| ||        |
Db     160 CMMDLRRYPLDEQNCTLEIESYGYTTDDIEFYWRGDDNAVTGVTKIELPQFSIVDYKLIT 219

Qy     255 EIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGI 314
           : :    | :  ::: | : |  ||   | |:|| : |:|||||||  ::: || :|||
Db     220 KKVVFSTGSYPRLSLSFKLKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALGI 279

Qy     315 TSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHAS 374
           |:||||||: |  |:  |:: |: |:| |:  |||| | ||||:|::|:: :
Db     280 TTVLTMTTINTHLRETLPKIPYVKAIDMYLMGCFVFVFMALLEYALVNYIFFG------- 333

Qy     375 PKLRHPRINSRAHARTRARSRACAR-------QHQEAFVC------QIVTTEGSDGEERP 421
           | |:   :|  :  : :     |         |:   :        :: |:|   |   |
Db     333 ---RGPQRQKKAAEKAASANNEKMRLDVNKMDPHENILLSTLEIKNEMATSEAVMGLGDP 389

Qy     422 -------SCSAQQPPSPGSPEG-------PRSLCSKLACCEWCKRFKKYFCMVPDCEGST 467
                 |: |    | |           | :  | :     :|  :    :||
Db     390 RSTMLAYDASSIQYRKAGLPRHSFGRNALERHVAQKKSRLR--RRASQLKITIPD----- 443

Qy     468 WQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
                 |  :| :||: ||| | |||::|||  :|
Db     443 ------LTDVNAIDRWSRIFFPVVFSFFNIVYWLYYVN 474


RESULT   8
US-08-768-301-4
; Sequence 4, Application US/08768301
; Patent No. 5854002
;  GENERAL INFORMATION:
;    APPLICANT:  Tomalski, Michael D.
;    APPLICANT:  Gant, Daniel B.
;    TITLE OF INVENTION:  METHOD OF IDENTIFYING COMPOUNDS THAT BIND
;    TITLE OF INVENTION:  TO THE INSECT GABA RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brumbaugh, Graves, Donohue & Raymond
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  10112-0228
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/768,301
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacLeod, Janet M
;      REGISTRATION NUMBER:  35,263
;      REFERENCE/DOCKET NUMBER:  A30693
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-408-2500
;      TELEFAX:  212-765-2519
;      TELEX:
```

```
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  686 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
US-08-768-301-4


  Query Match             24.6%;  Score 662.5;  DB 2;  Length 686;
  Best Local Similarity   26.5%;  Pred. No. 4e-56;
  Matches  156;  Conservative   81;  Mismatches  161;  Indels  191;  Gaps    8;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           | :|: :|  ||: :||  |  |  : |:| | |:||:| :|| |::|  | |:| |:|| 
Db     110 SELLDNLLRGYDNSIRPDFGGPPATIEVDIMVRSMGPISEVDMTYSMDCYFRQSWVDKRL 169

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
            :   ::| |: ::::::| |||:| | |::: | || ||: ||||::|:|||: |:|| 
Db     170 AFEGAQDTLALSVSMLARIWKPDTYFYNGKQSYLHTITTPNKFVRIYQNGRVLYSSRLTI 229

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDF---- 248
           ||| :::  |||| |||  | || |  :::||:|   :  :      || ||| 
Db     230 KAGCPMNLADFPMDIQKCPLKFGSFGYTTSDVIYRWNKERPPVAIAEDMKLSQFDLVDCP 289

Qy     248 ------------------------------------------------------------ 248

Db     290 AGNLTDIVYKAAAPRPQRRPFNNKDPPRPTSKVMTTFAGPAAKNQHVRGTGLKLDKGAFG 349

Qy     248 ------------TGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLS 295
                       ||:|    : |    :: :: : |:: |  |    | | |  :  :|| 
Db     350 TGRDATGGSGSTTGLSGTITLETNHPSEYSMLMVNFHLQRHMGNFLIQVYGPCCLLVVLS 409

Qy     296 WVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCAL 355
           |||||:  |:   | |||||:|||| ||  :| : |:||| |||||:: : | | |  : 
Db     410 WVSFWLNREATADRVSLGITTVLTMTFLGLEARTDLPKVSYPTALDFFVFLSFGFIFATI 469

Qy     356 LEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGS 415
           |:|||:                        |  |: |  |       |: : : :|  
Db     470 LQFAVV------------------------HYYTKYGSGEC------YFIIEELDSESG 498

Qy     416 DGEERP--------------------SCSAQQPPSP-------GSPEGPRS------LCS 442
           : |  |                     |:   || |             ||:  
Db     499 ESETEPLTSDFRGSTESKIYEVIPLSMCAISMPPPPTRLGMLTSRNRRPRNRRHGLWSMK 558

Qy     443 KLACCEWCKRFKKYFCMVPDCEGSTWQQ----------------------------GR 472
             |   :| :| |       : |     |                            ||  
Db     559 LLGLFDWRRRRKPPRADSDEDEDDEQTQLRANEAPTTSAAAAAAQAAAQAARISPPTGGR 618

Qy     473 LCIHVYR--------------------LDNYSRVVFPVTFFFFNVLYW 500
             :  ||                     :|  ||:|||: |   || ||  
Db     619 RRMSYYRREEMEARRKGKRTPQYNSVSKIDRASRIVFPLLFILINVFYW 667


RESULT   9
US-08-137-614A-2
; Sequence 2, Application US/08137614A
; Patent No. 5487976
;  GENERAL INFORMATION:
;    APPLICANT:  Soderlund, David M.
;    APPLICANT:  Knipple, Douglas C.
;    APPLICANT:  Henderson, Joseph E.
;    TITLE OF INVENTION:  Gene Encoding An Insect
;    TITLE OF INVENTION:  Gamma-Aminobutyric Acid (GABA) Receptor Subunit
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,614A
;      FILING DATE:  15-OCT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716)263-1636
;      TELEFAX:  (716)263-1600
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  496 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-137-614A-2


  Query Match             23.5%;  Score 632.5;  DB 1;  Length 496;
  Best Local Similarity   30.1%;  Pred. No. 2.1e-53;
  Matches  144;  Conservative   90;  Mismatches  181;  Indels   63;  Gaps    9;

Qy      66 GKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQT 125
           |:|   :: :: ||  || :||| | :|  | ::: : |   :| ::|:||| :  :| 
Db      35 GRLENVTQTISNILQGYDIRLRPNFGGEPLHVGMDLTIASFDAISEVNMDYTITMYLNQY 94

Qy     126 WYDERLCYN-----------DTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
           | |||| :|               : | |:|:   ::|:||||| | | :  |::|  |: 
Db      95 WRDERLAFNIFGQYFDDENDDGISDVLTLSGDFAEKIWVPDTFFANDKNSFLHDVTERNK 154

Qy     174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLE 233
           :||:  || | | :| |    | : :  :|:|| :| :   |: |  :::  |: 
Db     155 LVRLGGDGAVTYGMRFTTTLACMMDLHYYPLDSQNCTVEIESYGYTVSDVVMYWK--PTP 212

Qy     234 INEKNSWKLFQFDFTG--VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVT 291
           :   :| ||   |   ::: | : |  | :  ::: | : |  ||  || |:|| : 
Db     213 VRGVEDAELPQFTIIGYETNDRKERLAT--GVYQRLSLSFKLQRNIGYFVFQTYLPSILI 270

Qy     292 TMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFC 351
           |||||||||  |:  || :||||:|||||: |  | : ||:||: |:| |: :|||| 
Db     271 VMLSWVSFWINHEATSARVALGITTVLTMTTISTGVRSSLPRISYVKAIDIYLVMCFVFV 330

Qy     352 FCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACA------------ 399
           | ||||:| :|:  : :    |  |::  :           ||  |: 
Db     331 FAALLEYAAVNYTYWGK---RAKKKIKKVKECCPGKIGKSERSETCSTTEDIIELQDVRM 387

Qy     399 -------RQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPE----GPRSLCSKLACC 447
                  |  : : | |   : |:  ||     :   |  :       | : :: 
Db     388 SPIPSLRRGTYNATLDSIGTETMNLGKFPPSFRITRNYGTGHSQLRRRAQRGISTRPRML 447

Qy     448 EWCKR----FKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWL 501
              ||     |     : |              |  :| |||::||::|  ||: ||| 
Db     448 HALKRGASAIKATIPKIKD-------------VNIIDKYSRMIFPISFLAFNLGYWL 491


RESULT  10
US-08-768-301-2
; Sequence 2, Application US/08768301
; Patent No. 5854002
;  GENERAL INFORMATION:
;    APPLICANT:  Tomalski, Michael D.
;    APPLICANT:  Gant, Daniel B.
```

```
;    TITLE OF INVENTION:  METHOD OF IDENTIFYING COMPOUNDS THAT BIND
;    TITLE OF INVENTION:  TO THE INSECT GABA RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brumbaugh, Graves, Donohue & Raymond
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  10112-0228
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/768,301
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacLeod, Janet M
;      REGISTRATION NUMBER:  35,263
;      REFERENCE/DOCKET NUMBER:  A30693
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-408-2500
;      TELEFAX:  212-765-2519
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  496 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
US-08-768-301-2


  Query Match            23.5%;  Score 632.5;  DB 2;  Length 496;
  Best Local Similarity  30.1%;  Pred. No. 2.1e-53;
  Matches  144;  Conservative   90;  Mismatches  181;  Indels   63;  Gaps    9;

Qy      66 GKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQT 125
           |:|   :: :: ||  || :|||  | :|  | ::: : |   :| ::|:|:|| :  :|
Db      35 GRLENVTQTISNILQGYDIRLRPNFGGEPLHVGMDLTIASFDAISEVNMDYTITMYLNQY 94

Qy     126 WYDERLCYN-----------DTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
           | |||| :|              : | |:|:   ::|:|||| | | :  |::|  |:
Db      95 WRDERLAFNIFGQYFDDENDDGISDVLTLSGDFAEKIWVPDTFFANDKNSFLHDVTERNK 154

Qy     174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLE 233
           :||:  || | | :| |    | : :  :|:|| :| :   |: |  :::  |:
Db     155 LVRLGGDGAVTYGMRFTTTLACMMDLHYYPLDSQNCTVEIESYGYTVSDVVMYWK--PTP 212

Qy     234 INEKNSWKLFQFDFTG--VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVT 291
           :      :| ||   |   ::: | : |  | :  ::: | : |  ||  || |:|| :
Db     213 VRGVEDAELPQFTIIGYETNDRKERLAT--GVYQRLSLSFKLQRNIGYFVFQTYLPSILI 270

Qy     292 TMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFC 351
           |||||||||  |:  || :||||:||||||: |  | : ||:||: |:| |: :||||
Db     271 VMLSWVSFWINHEATSARVALGITTVLTMTTISTGVRSSLPRISYVKAIDIYLVMCFVFV 330

Qy     352 FCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACA------------- 399
           | ||||:| :|:  : :   |  |::  :           ||  |:
Db     331 FAALLEYAAVNYTYWGK---RAKKKIKKVKECCPGKIGKSERSETCSTTEDIIELQDVRM 387

Qy     399 -------RQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPE----GPRSLCSKLACC 447
                  |   | :  | |   : |:  ||    :    |  :      | : ::
Db     388 SPIPSLRRGTYNATLDSIGTETMNLGKFPPSFRITRNYGTGHSQLRRRAQRGISTRPRML 447

Qy     448 EWCKR----FKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWL 501
           ||    |   : |                 |  :| |||::||::|  ||: |||
Db     448 HALKRGASAIKATIPKIKD-------------VNIIDKYSRMIFPISFLAFNLGYWL 491


RESULT  11
US-08-137-614A-25
; Sequence 25, Application US/08137614A
; Patent No. 5487976
;  GENERAL INFORMATION:
;    APPLICANT:  Soderlund, David M.
;    APPLICANT:  Knipple, Douglas C.
;    APPLICANT:  Henderson, Joseph E.
;    TITLE OF INVENTION:  Gene Encoding An Insect
;    TITLE OF INVENTION:  Gamma-Aminobutyric Acid (GABA) Receptor Subunit
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,614A
;      FILING DATE:  15-OCT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716)263-1636
;      TELEFAX:  (716)263-1600
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  617 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-137-614A-25


  Query Match            22.7%;  Score 611.5;  DB 1;  Length 617;
  Best Local Similarity  35.4%;  Pred. No. 3.2e-51;
  Matches  120;  Conservative   72;  Mismatches  118;  Indels   29;  Gaps    4;

Qy      75 LNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERLCYN 134
           :: :|  || :|||  |  |  | : | | |:  :| ::|:|:|: : | |:| |:|| |
Db      63 VDRLLKGYDIRLRPDFGGPPVDVGMRIDVASIDMVSEVNMDYTLTMYFQQSWKDKRLSYX 122

Qy     135 DTFE-----------SLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGK 182
                         :| |:  |  |||:|||:| | |::  | :|: |:|:|:: ||
Db     123 XXXXXXXXXXXSGIPLNLTLDNRVADQLWVPDTYFLNDKKSFVHGVTVKNRMIRLHPDGT 182

Qy     183 VLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKL 242
           ||| :|:|  | | : : |:|:|  :| |   |: |  ::: : |   :  :   |  :|
Db     183 VLYGLRITTTAACMMDLRRYPLDEQNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIEL 242

Qy     243 FQF---DFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSF 299
           ||   |:  || | | :|   | :  ::: | : |  ||   | |:||:: |:||||||
Db     243 PQFSIVDYKMVSKKVEFTT---GAYPRLSLSFRLKRNIGYFILQTYMPSTLITILSWVSF 299

Qy     300 WIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFA 359
           ||  ::: || :||||:||||||: |  |:  |:: |: |:| |:  ||||  | ||||:|
```

```
Db    300 WINYDASAARVALGITTVLTMTTISTHLRETLPKIPYVKAIDIYLMGCFVFVFLALLEYA 359

Qy    360 VLNFLIYNQ-----------TKAHASPKLRHPRINSRAH 387
Db    360 FVNYIFFGKGPQKKGASKQDQSANEKNKLEMNKVQVDAH 398


RESULT  12
US-08-137-614A-24
; Sequence 24, Application US/08137614A
; Patent No. 5487976
;  GENERAL INFORMATION:
;    APPLICANT:  Soderlund, David M.
;    APPLICANT:  Knipple, Douglas C.
;    APPLICANT:  Henderson, Joseph E.
;    TITLE OF INVENTION:  Gene Encoding An Insect
;    TITLE OF INVENTION:  Gamma-Aminobutyric Acid (GABA) Receptor Subunit
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,614A
;      FILING DATE:  15-OCT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716)263-1636
;      TELEFAX:  (716)263-1600
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  617 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-137-614A-24


  Query Match             22.6%;  Score 609.5;  DB 1;  Length 617;
  Best Local Similarity   36.1%;  Pred. No. 5e-51;
  Matches  123;  Conservative   67;  Mismatches  124;  Indels   27;  Gaps    7;

Qy     72 SRILNTI---LSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYD 128
Db     57 ANVTNTIDSLLKGYDIRLRPSFGGAPLEIGIEVILASFDSISEVDMDYTITMYLNQYWRD 116

Qy    129 ERL---CYNDTFE---------SLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVR 176
Db    117 ERLQFXIFNESLDLGENRSVTXTMTLTGAFAEKIWVPDTFLANDKNSFLHDITEKNKMVR 176

Qy    177 IYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINE 236
Db    177 LYGNGSLVYGMRFTTTLACMMDLHNYPLDHQECTVEIESYGYTMDDIVLYWLNDRGAVTG 236

Qy    237 KNSWKLFQFDFTGVS--NKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTML 294
Db    237 VEDVSLPQFSITNYATINKIEELST--GDYQRLSLIFQLQRNIGYFIFQTYLPSILIVML 294

Qy    295 SWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCA 354
Db    295 SWVSFWINHEATSARVALGITTVLTMTTISNGVRSSLPRISYVKAIDIYLVMCFVFVFAA 354

Qy    355 LLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSR 395
Db    355 LLEYAAVNYTYWG-----ARAKRKAKRLRERA---TSVRKR 387


RESULT  13
US-08-554-659-2
; Sequence 2, Application US/08554659
; Patent No. 5767261
;  GENERAL INFORMATION:
;    APPLICANT:  Wingate, Vincent
;    APPLICANT:  Wolff, Mark
;    TITLE OF INVENTION:  LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
;    TITLE OF INVENTION:  AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/554,659
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9732
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  488 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-554-659-2


  Query Match             22.2%;  Score 598.5;  DB 1;  Length 488;
  Best Local Similarity   29.7%;  Pred. No. 4.1e-50;
  Matches  138;  Conservative   81;  Mismatches  181;  Indels   65;  Gaps    8;

Qy     72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
Db     44 SAILDSLSVSYDKRVRPNYGGPPVDVGVNMYVLSISSLSEVKMDFTLDFYFRQFWTDPRL 103

Qy    132 CYNDT--FESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
Db    104 AYKKSTGVETLSVGSEFIRNIWVPDTFFVNEKQSYFHIATTSNEFIRIHHSGSITRSIRL 163

Qy    190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
Db    164 TITASCPMDLQYFPMDRQLCNIEIESFGYTMRDIRYKWNEGPNSVGVSSEVSLPQFKVLG 223

Qy    250 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 309
Db    224 HRQRAMEISLTTGNYSRLACEIQFVGSMGYYLIQIYIPSGLIVIISWVSFWLNRNATPAR 283

Qy    310 TSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQT 369
Db    284 VSLGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTCFVMVFTSLLEYATVGYMA---- 340
```

```
Qy    370 KAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPP 429
                 ||  |       : |  | |  :            ||   |  ||:  |
Db    340 ----------KRIQMR-------KQRFTAVQKMQI-----------DG---PPGSAEPIP 368

Qy    430 SPGSPEGPRSLCSKLACCEW----CKRFKKYFCMVPDCEGSTWQQGRL------------ 474
           | :    |   |:|:   :     | : |   :     |:  | |
Db    369 PPRTSTLSRPPPSRLSEVRFKVHDPKAYSKGGTLENTINGARGQPGPAPPADEEAGPPPH 428

Qy    474 CIHVYR------------LDNYSRVVFPVTFFFFNVLYWLVCLNL 506
            :| ::            :| |||:||||    ||::||:: |::
Db    429 LVHAFQGINKLLGTTPSDIDKYSRIVFPVCCVCFNLMYWIIYLHV 473


RESULT  14
US-08-554-659-4
; Sequence 4, Application US/08554659
; Patent No. 5767261
;  GENERAL INFORMATION:
;    APPLICANT:  Wingate, Vincent
;    APPLICANT:  Wolff, Mark
;    TITLE OF INVENTION:  LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
;    TITLE OF INVENTION:  AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/554,659
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9732
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  488 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-554-659-4


  Query Match             22.1%;  Score 595.5;  DB 1;  Length 488;
  Best Local Similarity   29.5%;  Pred. No. 8.1e-50;
  Matches  137;  Conservative   82;  Mismatches  181;  Indels   65;  Gaps    8;

Qy     72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
          | ||:::  :|| ::||  |  |  | | : | |:  || : |::|:|  | | | | ||
Db     44 SAILDSLSVSYDKRVRPNYGGPPVDVGVNMYVLSISSLSEVKMDFTLDFYFRQFWTDPRL 103

Qy    132 CYNDT--FESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
          |  :   |:| :    :  :|:|||| | |::: |  |  |: :||:  | :  :||:
Db    104 AYKKSTGVETLSVGSEFIRNIWVPDTFFVNEKQSYFHIATTSNEFIRIHHSGSITRSIRL 163

Qy    190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
          || | | : :  ||||   | :   || |   :: |||      :   :   | ||   |
Db    164 TITASCPMDLQYFPMDRQLCNIEIESFGYTMRDIRYKWNEGPNSVGVSSEVSLPQFKVLG 223

Qy    250 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 309
```

```
          :   |:   |::  :          ||   | |:|| :  ::||||||:   : |||
Db    224 HRQRAMEISLTTGNYSRLACEIQFVGSMGYYLIQIYIPSGLIVIISWVSFWLNRNATPAR 283

Qy    310 TSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQT 369
          :||:|:|||||| : :    |::||: ::| |:  |||  | :|||:| : ::
Db    284 VALGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTCFVMVFTSLLEYATVGYMA---- 340

Qy    370 KAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPP 429
                 ||  |       : |  | |  :            ||   |  ||:  |
Db    340 ----------KRIQMR-------KQRFTAVQKMQI-----------DG---PPGSAEPIP 368

Qy    430 SPGSPEGPRSLCSKLACCEW----CKRFKKYFCMVPDCEGSTWQQGRL------------ 474
           | :    |   |:|:   :     | : |   :     |:  | |
Db    369 PPRTSTLSRPPPSRLSEVRFKVHDPKAYSKGGTLENTINGARGQPGPAPPADEEAGPPPH 428

Qy    474 CIHVYR------------LDNYSRVVFPVTFFFFNVLYWLVCLNL 506
            :| ::            :| |||:||||    ||::||:: |::
Db    429 LVHAFQGINKLLGTTPSDIDKYSRIVFPVCCVCFNLMYWIIYLHV 473


RESULT  15
US-08-072-064-4
; Sequence 4, Application US/08072064
; Patent No. 6008046
;  GENERAL INFORMATION:
;    APPLICANT:  FFRENCH-CONSTANT, RICHARD H.
;    APPLICANT:  JACKSON, MEYER B.
;    TITLE OF INVENTION:  DRUG AND PESTICIDE SCREENING
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER G. CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/072,064
;      FILING DATE:  19930602
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 770,881
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  OPHD-00574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  637 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-072-064-4


  Query Match             21.9%;  Score 590.5;  DB 3;  Length 637;
  Best Local Similarity   24.6%;  Pred. No. 3.7e-49;
  Matches  153;  Conservative   93;  Mismatches  216;  Indels  159;  Gaps   14;

Qy     23 PQTESKNEASSR-DVVYGPQPQP----------LENQLLSEETKSTETET-------GSR 64
          |:| |   : |: | :    | |          :   |:::||      |       ||
Db     25 PKTHSTTMSDSKMDKLARMAPLPRTPLLTIWLAINMALIAQETGHKRIHTVQAATGGGSM 84

Qy     65 VGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
```

```
          :| :   | ||::   :|| ::||  |  |  | | : | |:  :| : |::|:|  | |
Db     85 LGDV-NISAILDSFSVSYDKRVRPNYGGPPVEVGVTMYVLSISSVSEVLMDFTLDFYFRQ 143

Qy    125 TWYDERLCYNDT--FESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGK 182
          | | || |      |:| :   :  :|:||||| | |::: |  |  |: :|::  |
Db    144 FWTDPRLAYRKRPGVETLSVGSEFIKNIWVPDTFFVNEKQSYFHIATTSNEFIRVHHSGS 203

Qy    183 VLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKL 242
          :  :||:|| | | :::  |||   | :   || |   :: | | :    :   :  :|
Db    204 ITRSIRLTITASCPMNLQYFPMDRQLCHIEIESFGYTMRDIRYFWRDGLSSVGMSSEVEL 263

Qy    243 FQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIK 302
           ||   |   :   |    |::  :       |  ||   | |:|| :  ::||||||:
Db    264 PQFRVLGHRQRATEINLTTGNYSRLACEIQFVRSMGYYLIQIYIPSGLIVVISWVSFWLN 323

Qy    303 TESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLN 362
          : ||| |||:|:|||||| : :    |::||: ::| |:  |||  | :|||:| :
Db    324 RNATPARVSLGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTCFVMVFASLLEYATVG 383

Qy    363 FLI-------------------------YNQTKAHASPKL------------------ 378
          ::                          || :|: :|
Db    384 YMAKRIQMRKQRFMAIQKIAEQKKQQLDGANQQQANPNPNANVGGPGGVGVGPGGPGGPG 443

Qy    378 --------------------RHPRINSRAHA---------------RTRARSRACA---- 399
                               |   :  ||               :    :| |:
Db    444 GGVNVGVGMGMGPEHGHGHGHHAHSHGHPHAPKQTVSNRPIGFSNIQQNVGTRGCSIVGP 503

Qy    399 ------------RQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSP-----------GSPE 435
                     : | :   :   |  | :   :   |   |                | ||
Db    504 LFQEVRFKVHDPKAHSKGGTLENTVNGGRGGPQSHGPGPGQGGGPPGGGGGGGGGGGPPE 563

Qy    436 G--------PRSLC--SKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSR 485
          |       |  |    |:      |   |   : |                 :| |||
Db    564 GGGDPEAAVPAHLLHPGKVK-----KDINKLLGITPS---------------DIDKYSR 602

Qy    486 VVFPVTFFFFNVLYWLVCLNL 506
          :|||| |  ||::||:: |::
Db    603 IVFPVCFVCFNLMYWIIYLHV 623
```

Search completed: March 11, 2000, 06:01:24
Job time: 1113 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:06:25 ; Search time 52.39 Seconds
(without alignments)
455.577 Million cell updates/sec

Title: US-09-030-832-42
Perfect score: 2691
Sequence: 1 MLSKVLPVLLGILLILQSRV.....VFPVTFFFFNVLYWLVCLNL 506

Scoring table: BLOSUM62

Searched: 142080 seqs, 47169319 residues

Database : PIR_62:*

Word size : 0

Number of hits that pass the threshold : 142080
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1202.5	44.7	457	2	S38296	gamma-aminobutyric
2	1097.5	40.8	467	2	S16915	gamma-aminobutyric
3	1087	40.4	474	2	S13086	gamma-aminobutyric
4	1083.5	40.3	467	2	S19317	gamma-aminobutyric
5	1081	40.2	474	2	JH0317	gamma-aminobutyric
6	1080	40.1	466	2	JH0316	gamma-aminobutyric
7	1077	40.0	466	2	JQ0077	gamma-aminobutyric
8	1074	39.9	475	2	B39272	gamma-aminobutyric
9	1067	39.7	467	2	S03905	gamma-aminobutyric
10	1054	39.2	465	2	S12056	gamma-aminobutyric
11	1051.5	39.1	464	2	JH0824	gamma-aminobutyric
12	858	31.9	453	2	S11087	gamma-aminobutyric
13	855.5	31.8	552	2	S17551	gamma-aminobutyric
14	850	31.6	554	2	G01928	gamma-aminobutyric
15	842	31.3	556	2	S06838	gamma-aminobutyric
16	813	30.2	462	2	A48933	gamma-aminobutyric
17	809	30.1	464	2	B34130	gamma-aminobutyric
18	803	29.8	455	2	JQ0158	gamma-aminobutyric
19	803	29.8	455	2	A39062	gamma-aminobutyric
20	800	29.7	443	2	S11396	gamma-aminobutyric
21	800	29.7	493	2	A34130	gamma-aminobutyric
22	799.5	29.7	456	2	A60652	gamma-aminobutyric
23	799.5	29.7	456	2	A27142	gamma-aminobutyric
24	798.5	29.7	492	2	I77911	gamma-aminobutyric
25	797.5	29.6	455	1	CHCHA1	gamma-aminobutyric
26	796.5	29.6	492	1	CHBOA3	gamma-aminobutyric
27	782.5	29.1	451	2	JH0370	gamma-aminobutyric
28	781	29.0	451	1	ACBOG2	gamma-aminobutyric
29	781	29.0	451	2	I57947	gamma-aminobutyric
30	709	26.3	488	2	JH0359	gamma-aminobutyric
31	691	25.7	354	2	A31588	gamma-amino butyri
32	673.5	25.0	474	2	B27142	gamma-aminobutyric
33	671.5	25.0	474	2	B60039	gamma-aminobutyric
34	671.5	25.0	474	2	A40336	gamma-aminobutyric
35	668.5	24.8	474	2	S53530	gamma-aminobutyric
36	668	24.8	473	2	A55275	gamma-aminobutyric
37	665	24.7	473	2	S04466	gamma-aminobutyric
38	665	24.7	473	2	S53532	gamma-aminobutyric
39	664	24.7	474	2	S04465	gamma-aminobutyric
40	664	24.7	474	2	S53531	gamma-aminobutyric
41	662.5	24.6	686	2	S60749	probable ligand-ga
42	660	24.5	474	2	JH0829	gamma-aminobutyric
43	652.5	24.2	449	2	A34625	gamma-aminobutyric
44	652	24.2	451	2	C49970	glycine receptor a
45	652	24.2	449	2	S12382	glycine receptor a

ALIGNMENTS

RESULT 1
S38296
gamma-aminobutyric acid receptor A gamma-4 chain precursor - chicken
N;Alternate names: GABA(A) receptor gamma-4 chain
C;Species: Gallus gallus (chicken)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S38296
R;Harvey, R.J.; Kim, H.C.; Darlison, M.G.
FEBS Lett. 331, 211-216, 1993
A;Title: Molecular cloning reveals the existence of a fourth gamma subunit of the ver
A;Reference number: S38296; MUID:93387470
A;Accession: S38296
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-457 <HAR>
A;Cross-references: EMBL:X73533; NID:g414021; PIDN:CAA51939.1; PID:g414022
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein

Query Match 44.7%; Score 1202.5; DB 2; Length 457;
Best Local Similarity 48.1%; Pred. No. 1.1e-88;
Matches 218; Conservative 82; Mismatches 94; Indels 59; Gaps 5;

```
Qy      70 EASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDE 129
           :|:::|||::| |||:|||| || ||| : |:| |||:||:|:: ||||||| |:|||||
Db      48 DATQILNSLLKNYDNKLRPDIGIKPTFIDVDIYVNSIGPVSVIQMEYTIDIFFAQTWYDR 107

Qy     130 RLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
           || :| | ::| || |:||::|||||||||||||   | || |||:||: |||||||:|:
Db     108 RLRFNSTLKALTLNTNMVSRIWIPDTFFRNSKRADSHWITTPNQLLRIWNDGKVLYTLRL 167

Qy     190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
           ||:| | | :  ||||:||||| ||||: ||  |::|:|  : :|:::: :|:|:||||||
Db     168 TIEAECLLQLQNFPMDTHSCPLVFSSYGYPREEIVYRWRRYSIEVSDQRTWRLYQFDFTG 227

Qy     250 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 309
           : | :|:: |  |::|||||: |::||| || | | |:|  :| :|||||||||| :| |||
Db     228 LRNTSEVLRTGAGEYMVMTVSFDLSRRMGYFAIQTYIPCILTVVLSWVSFWIKRDSTPAR 287

Qy     310 TSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQT 369
           ||||||:||||||| | |||: ||||||||:| ::::||:| | ||:|:| ||:|: |:
Db     288 TSLGITTVLTMTTLSTISRKHLPRVSYITAMDLFVSVCFIFVFAALMEYATLNYLVGNKK 347

Qy     370 K-AHASPKLRHP----------------RINSRAHARTRARSRACARQHQEAFVCQIVTTE 413
            |:| | | |                  ||:  |
Db     348 PLEHSSRKARLPPAGAQVMPSFTAININININNIMH------------------------ 382

Qy     414 GSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRL 473
                  |      :  ||||           | |  |  :::|| : ||:   |::||:
Db     382 -----WPPEIEEDEDDDPGSP----------CLEG-KECERFFCCIEDCQTGMWREGRV 424

Qy     474 CIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
           ||: |||:|||| ||  |  ||::||:  | |
Db     425 RIHISRLDSYSRVFFPTAFLLFNIVYWIAYLYL 457
```

RESULT 2

```
S16915
gamma-aminobutyric acid/benzodiazepine receptor gamma-3 chain precursor - mouse
N;Alternate names: GABA(A) receptor gamma-3 chain
C;Species: Mus musculus (house mouse)
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 20-Aug-1999
C;Accession: S16915; S15469
R;Wilson-Shaw, D.; Robinson, M.; Gambarana, C.; Siegel, R.E.; Sikela, J.M.
FEBS Lett. 284, 211-215, 1991
A;Title: A novel gamma subunit of the GABA(A) receptor identified using the polymerase c
A;Reference number: S16915; MUID:91285135
A;Accession: S16915
A;Molecule type: mRNA
A;Residues: 1-467 <WIL>
A;Cross-references: EMBL:X59300; NID:g51121; PIDN:CAA41988.1; PID:g51122
C;Superfamily: acetylcholine receptor
C;Keywords: disulfide bond; glycoprotein; ion channel; neurotransmitter receptor; transm
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-467/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-3 chain #status
F;255-277/Domain: transmembrane #status predicted <TM1>
F;281-303/Domain: transmembrane #status predicted <TM2>
F;315-337/Domain: transmembrane #status predicted <TM3>
F;444-467/Domain: transmembrane #status predicted <TM4>
F;110,228/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;171-185/Disulfide bonds: #status predicted


  Query Match             40.8%;  Score 1097.5;  DB 2;  Length 467;
  Best Local Similarity   42.8%;  Pred. No. 2.9e-80;
  Matches  222;  Conservative   91;  Mismatches  141;  Indels   65;  Gaps    9;

Qy       1 MLSKVLPVLLGILLILQS-------RVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEE 53
Db       1 MAAKLL-----LLLCLFSGLHARSRRVE--EDENEDSPSNQKWVLAPKPQD--------- 45

Qy      54 TKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILD 113
Db      45 --------------TDATLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSIN 89

Qy     114 MEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
Db      90 MEYQIDIFFAQTWTDSRLRFNSTMKTLTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQ 149

Qy     174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLE 233
Db     150 LLRIWNDGKILYTLRLTINAECQLQLHNFPMDAHACPLTFSSYGYPKEEMIYRWRKNSVE 209

Qy     234 INEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTM 293
Db     210 AADQKSWRLYQFDFMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVV 269

Qy     294 LSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFC 353
Db     270 LSWVSFWIKKDATPARTTLGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFA 329

Qy     354 ALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTE 413
Db     330 ALMEYATLNY--YSSCR---KPTIRKKKTSLLHPDSTRWIPDRISLQAPSNY-------- 377

Qy     414 GSDGEERPSCSAQQPPSPGSPEGPRSLC---SKLACCEWC---KRFKKYFCMVPDCEGST 467
Db     377 --------SLLDMRPPPPVMITLNNSMYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGS 428

Qy     468 WQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
Db     429 WRRGRIHIDVSELDSYSRVFFPTSFLLFNLVYWVGYLYL 467


RESULT   3
S13086
gamma-aminobutyric acid/benzodiazepine receptor A gamma-2 chain precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S13086
R;Glencorse, T.A.; Bateson, A.N.; Darlison, M.G.
Nucleic Acids Res. 18, 7157, 1990
A;Title: Sequence of the chicken GABA(A) receptor gamma-2-subunit cDNA.
A;Reference number: S13086; MUID:91088318
A;Accession: S13086
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <GLE>
A;Cross-references: EMBL:X54944; NID:g62896; PIDN:CAA38704.1; PID:g62897
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; phosphoprotein; transmembrane protein


  Query Match             40.4%;  Score 1087;  DB 2;  Length 474;
  Best Local Similarity   43.7%;  Pred. No. 2.1e-79;
  Matches  197;  Conservative   90;  Mismatches  110;  Indels   54;  Gaps    6;

Qy      70 EASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDE 129
Db      64 DVTLILNGLLEGYDNKLRPDIGVKPTVIHTDMYVNSIGPVNAINMEYTIDIFFAQTWYDR 123

Qy     130 RLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
Db     124 RLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVLYTLRL 183

Qy     190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
Db     184 TIDAECQLQLHNFPMDAHSCPLEFSSYGYPREEIIYQWKRSSVEVGDTRSWRLYQFSFTG 243

Qy     250 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 309
Db     244 LRNTTEVVKTTSGDYVVMSVYFNLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAVPAR 303

Qy     310 TSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYN-- 368
Db     304 TSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVSNRK 363

Qy     368 ----QTKAHASPKLR-----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGS 415
Db     364 PSKDKDKKKKNPLLRMFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------L 416

Qy     416 DGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCI 475
Db     417 DGKD---CAS----------------------------FFCCFEDCRTGAWRHGRIHI 443

Qy     476 HVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
Db     444 RIAKMDSYARIFFPTAFCLFNLVYWVSYLYL 474


RESULT   4
S19317
gamma-aminobutyric acid/benzodiazepine receptor gamma-3 chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: S19317; A40221
R;Knoflach, F.; Rhyner, T.; Villa, M.; Kellenberger, S.; Drescher, U.; Malherbe, P.;
FEBS Lett. 293, 191-194, 1991
A;Title: The gamma3-subunit of the GABA(A)-receptor confers sensitivity to benzodiaze
A;Reference number: S19317; MUID:92070559
A;Accession: S19317
A;Molecule type: mRNA
A;Residues: 1-467 <KNO>
A;Cross-references: EMBL:X63324; NID:g56181; PIDN:CAA44930.1; PID:g56182
R;Herb, A.; Wisden, W.; Luddens, H.; Puia, G.; Vicini, S.; Seeburg, P.H.
Proc. Natl. Acad. Sci. U.S.A. 89, 1433-1437, 1992
A;Title: The third gamma subunit of the gamma-aminobutyric acid type A receptor famil
A;Reference number: A40221; MUID:92159063
A;Accession: A40221
A;Molecule type: mRNA
A;Residues: 1-467 <HER>
A;Note: sequence extracted from NCBI backbone (NCBIP:82491)
C;Superfamily: acetylcholine receptor
```

```
C;Keywords: neurotransmitter receptor; transmembrane protein

  Query Match             40.3%;  Score 1083.5;  DB 2;  Length 467;
  Best Local Similarity   42.8%;  Pred. No. 3.8e-79;
  Matches  222;  Conservative   90;  Mismatches  142;  Indels   65;  Gaps   10;

Qy       1 MLSKVLPVLLGILLILQS-------RVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEE 53
Db       1 MAAKLL-----LLLCLFSGLHARSRRVE--EDDSEDSPSNQKWVLAP------------- 41

Qy      54 TKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILD 113
Db      41 -KSQDT----------DVTLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSIN 89

Qy     114 MEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
Db      90 MEYQIDIFFAQTWTDSRLRFNSTMKILTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQ 149

Qy     174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLE 233
Db     150 LLRIWNDGKILYTLRLTINAECQLQLHNFPMDAHACPLTFSSYGYPKEEMIYRWRKNSVE 209

Qy     234 INEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTM 293
Db     210 AADQKSWRLYQFDFMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVV 269

Qy     294 LSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFC 353
Db     270 LSWVSFWIKKDATPARTTLGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFA 329

Qy     354 ALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTE 413
Db     330 ALMEYATLNY--YSSCR---KPTIRKKKTSLLHPDSTRWIPDRISLQAPSNY-------- 377

Qy     414 GSDGEERPSCSAQQPPSPGSPEGPRSLC---SKLACCEWC---KRFKKYFCMVPDCEGST 467
Db     377 --------SLLDMRPPPPVMITLNNSMYWQEFEDTCVYECLDGKDCQTFFCCYEECKSGS 428

Qy     468 WQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
Db     429 WRRGRIHIDVSELDSYSRVFFPTSFLLFNLVYWVGYLYL 467


RESULT   5
JH0317
gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 13-Sep-1996
C;Accession: JH0317
R;Kofuji, P.; Wang, J.B.; Moss, S.J.; Huganir, R.L.; Burt, D.R.
J. Neurochem. 56, 713-715, 1991
A;Title: Generation of two forms of the gamma-aminobutyric acid A receptor gamma2-subuni
A;Reference number: JH0316; MUID:91108470
A;Accession: JH0317
A;Molecule type: mRNA
A;Residues: 1-474 <KOF>
A;Cross-references: GB:M57522
A;Experimental source: brain
C;Superfamily: acetylcholine receptor
C;Keywords: alternative splicing; glycoprotein; ion channel; neurotransmitter receptor;
F;1-38/Domain: signal sequence #status predicted <SIG>
F;29-375,384-474/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain,
F;39-474/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain, long fo
F;39-272/Domain: extracellular #status predicted <EXT>
F;273-295/Domain: transmembrane #status predicted <TM1>
F;299-321/Domain: transmembrane #status predicted <TM2>
F;333-355/Domain: transmembrane #status predicted <TM3>
F;356-450/Domain: intracellular #status predicted <INT>
F;451-473/Domain: transmembrane #status predicted <TM4>
F;51,128,246/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;381/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

  Query Match             40.2%;  Score 1081;  DB 2;  Length 474;
  Best Local Similarity   42.5%;  Pred. No. 6.2e-79;
  Matches  198;  Conservative   93;  Mismatches  119;  Indels   56;  Gaps    7;

Qy      57 TETETGSRVGKLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDM 114
Db      49 TSNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINM 108

Qy     115 EYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQM 174
Db     109 EYTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRM 168

Qy     175 VRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEI 234
Db     169 LRIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEV 228

Qy     235 NEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTML 294
Db     229 GDTRSWRLYQFSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVL 288

Qy     295 SWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCA 354
Db     289 SWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSA 348

Qy     355 LLEFAVLNFLIYN------QTKAHASPKLR-----HPRINSRAHARTRARSRAC---ARQ 400
Db     349 LVEYGTLHYFVSNRKPSKDKDKKKKNPLLRMFSFKAPTIDIRPRSATIQMNNATHLQERD 408

Qy     401 HQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMV 460
Db     409 EEYGYEC-------LDGKD---CAS-----------------------------FFCCF 428

Qy     461 PDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
Db     429 EDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLVYWVSYLYL 474


RESULT   6
JH0316
gamma-aminobutyric acid A receptor gamma 2 chain alternatively spliced precursor - mo
C;Species: Mus musculus (house mouse)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 04-Sep-1998
C;Accession: JH0316
R;Kofuji, P.; Wang, J.B.; Moss, S.J.; Huganir, R.L.; Burt, D.R.
J. Neurochem. 56, 713-715, 1991
A;Title: Generation of two forms of the gamma-aminobutyric acid A receptor gamma2-sub
A;Reference number: JH0316; MUID:91108470
A;Accession: JH0316
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-466 <KOF>
A;Cross-references: GB:M57522
C;Superfamily: acetylcholine receptor

  Query Match             40.1%;  Score 1080;  DB 2;  Length 466;
  Best Local Similarity   42.6%;  Pred. No. 7.3e-79;
  Matches  195;  Conservative   94;  Mismatches  121;  Indels   48;  Gaps    6;

Qy      57 TETETGSRVGKLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDM 114
Db      49 TSNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINM 108

Qy     115 EYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQM 174
Db     109 EYTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRM 168

Qy     175 VRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEI 234
Db     169 LRIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEV 228

Qy     235 NEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTML 294
```

```
          :  ||:|:|| | |: | ||:: |  ||::||:::|::||| ||   | |:| ::  :|
Db    229 GDTRSWRLYQFSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVL 288

Qy    295 SWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCA 354
          |||||||  :: |||||||||:||||||| | :||: |:|||:||:| ::::||:| | |
Db    289 SWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSA 348

Qy    355 LLEFAVLNFLIYNQTKAHASPKLRH---PRINSRAHARTRARSRAC---ARQHQEAFVCQ 408
          |:|:  |:: : |:  :    | :    | |: |  : |   : |     |  :  : |
Db    349 LVEYGTLHYFVSNRKPSKDKDKKKKNPAPTIDIRPRSATIQMNNATHLQERDEEYGYEC- 408

Qy    409 IVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTW 468
                ||::   |::                                :||   ||    |
Db    408 ------LDGKD---CAS-----------------------------FFCCFEDCRTGAW 428

Qy    469 QQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
          : ||: | : ::|:|:|: ||  |  ||::||:  | |
Db    429 RHGRIHIRIAKMDSYARIFFPTAFCLFNLVYWVSYLYL 466
```

RESULT 7
JQ0077
gamma-aminobutyric acid receptor A gamma-2 chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Aug-1999
C;Accession: JQ0077; A37164
R;Shivers, B.D.; Killisch, I.; Sprengel, R.; Sontheimer, H.; Koehler, M.; Schofield, P.R
Neuron 3, 327-337, 1989
A;Title: Two novel GABA-A receptor subunits exist in distinct neuronal subpopulations.
A;Reference number: JQ0076; MUID:90380375
A;Accession: JQ0077
A;Molecule type: mRNA
A;Residues: 1-466 <SHI>
A;Cross-references: GB:L08497; NID:g204217; PIDN:AAC42036.1; PID:g204218
A;Experimental source: brain
R;Malherbe, P.; Sigel, E.; Baur, R.; Persohn, E.; Richards, J.G.; Mohler, H.
J. Neurosci. 10, 2330-2337, 1990
A;Title: Functional characteristics and sites of gene expression of the alpha-1,beta-1,g
A;Reference number: A37164; MUID:90331051
A;Accession: A37164
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-21,'I',23-466 <MAL>
C;Comment: Neurotransmission effected by gamma-aminobutyric acid (GABA) is mediated main
C;Comment: The GABA-A receptor consists of subunits that are structurally related to lig
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F;1-38/Domain: signal sequence #status predicted <SIG>
F;39-466/Product: gamma-aminobutyric acid A receptor gamma-2 chain #status predicted <MA
F;273-295/Domain: transmembrane #status predicted <TM1>
F;299-321/Domain: transmembrane #status predicted <TM2>
F;333-355/Domain: transmembrane #status predicted <TM3>
F;443-465/Domain: transmembrane #status predicted <TM4>
F;51,128,246/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;189-203/Disulfide bonds: #status predicted

  Query Match 40.0%; Score 1077; DB 2; Length 466;
  Best Local Similarity 43.1%; Pred. No. 1.3e-78;
  Matches 193; Conservative 93; Mismatches 114; Indels 48; Gaps 6;

```
Qy     67 KLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
          |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|||||| |:|
Db     59 KVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFAQ 118

Qy    125 TWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVL 184
          |||| || :| | : | || |:| ::||||||||||:   | || ||:|:||: ||:||
Db    119 TWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVL 178

Qy    185 YTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQ 244
          ||:|:|||| | | :  |||| ||||| ||||: ||  |:::|:|:   :|: :  ||:|:|
Db    179 YTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQ 238

Qy    245 FDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTE 304
          | | |: | ||:: |  ||::|||:: ::||| ||   | |:| ::  :|||||||  :
Db    239 FSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKD 298

Qy    305 SAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL 364
          : ||||||||:|||||| | :||: |:|||:||:| ::::||:| | ||:|:  |::
Db    299 AVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYF 358

Qy    365 IYNQTKAHASPKLRH---PRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGE 418
          : |:  :    | :    | |: |  : |   : |     |  :  : |          ||:
Db    359 VSNRKPSKDKDKKKKNPAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGK 411

Qy    419 ERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVY 478
          :   |::                              :||   ||    |: ||: | :
Db    412 D---CAS-----------------------------FFCCFEDCRTGAWRHGRIHIRIA 438

Qy    479 RLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
          ::|:|:|: ||  |  ||::||:  | |
Db    439 KMDSYARIFFPTAFCLFNLVYWVSYLYL 466
```

RESULT 8
B39272
gamma-aminobutyric acid receptor A gamma-2L chain - bovine
N;Contains: gamma-aminobutyric acid receptor A gamma-2S chain
C;Species: Bos primigenius taurus (cattle)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 30-May-1997
C;Accession: B39272; A39272
R;Whiting, P.; McKernan, R.M.; Iversen, L.L.
Proc. Natl. Acad. Sci. U.S.A. 87, 9966-9970, 1990
A;Title: Another mechanism for creating diversity in gamma-aminobutyrate type A recep
sphorylation site.
A;Reference number: A39272; MUID:91088632
A;Accession: B39272
A;Molecule type: mRNA
A;Residues: 1-475 <WHI>
A;Cross-references: GB:M55563
A;Accession: A39272
A;Molecule type: mRNA
A;Residues: 1-376,385-475 <WH2>
A;Cross-references: GB:M55563
C;Superfamily: acetylcholine receptor
C;Keywords: alternative splicing; neurotransmitter receptor; phosphoprotein; transmem
F;1-475/Product: gamma-aminobutyric acid receptor A gamma-2L chain #status predicted
F;1-376,385-475/Product: gamma-aminobutyric acid receptor A gamma-2S chain #status pr
F;382/Binding site: phosphate (Ser) (covalent) #status predicted

  Query Match 39.9%; Score 1074; DB 2; Length 475;
  Best Local Similarity 43.0%; Pred. No. 2.3e-78;
  Matches 196; Conservative 91; Mismatches 113; Indels 56; Gaps 7;

```
Qy     67 KLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
          |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|||||| |:|
Db     60 KVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFAQ 119

Qy    125 TWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVL 184
          |||| || :| | : | || |:| ::||||||||||:   | || ||:|:||: ||:||
Db    120 TWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVL 179

Qy    185 YTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQ 244
          ||:|:|||| | | :  |||| ||||| ||||: ||  |:::|:|:   :|: :  ||:|:|
Db    180 YTLRLTIDAECQLQLHNFPMDGHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQ 239

Qy    245 FDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTE 304
          | | |: | ||:: |  ||::|||:: ::||| ||   | |:| ::  :|||||||  :
Db    240 FSFVGLRNTTEVVKTTSGDYVVMTVYSDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKD 299

Qy    305 SAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL 364
          : ||||||||:|||||| | :||: |:|||:||:| ::::||:| | ||:|:  |::
Db    300 AVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYF 359

Qy    365 IYN------QTKAHASPKLR-----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIV 410
```

```
Db    360 VSNRKPSKDKDKKKKNPLLRMFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYEC--- 417

Qy    411 TTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQ 470

Db    417 ----LDGKD---CAS----------------------------FFCCFEDCRTGAWRH 439

Qy    471 GRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506

Db    440 GRIHIRIAKMDSYARIFFPTAFCLFNLVYWVSYLYL 475


RESULT   9
S03905
gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Aug-1999
C;Accession: S03905
R;Pritchett, D.B.; Sontheimer, H.; Shivers, B.D.; Ymer, S.; Kettenmann, H.; Schofield, P
Nature 338, 582-585, 1989
A;Title: Importance of a novel GABA(A) receptor subunit for benzodiazepine pharmacology.
A;Reference number: S03905; MUID:89181956
A;Accession: S03905
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-467 <PRI>
A;Cross-references: GB:X15376; NID:g31636; PIDN:CAA33437.1; PID:g31637
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein
F;1-39/Domain: signal sequence #status predicted <SIG>
F;40-467/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain #status

  Query Match             39.7%;  Score 1067;  DB 2;  Length 467;
  Best Local Similarity   42.6%;  Pred. No. 8.1e-78;
  Matches  191;  Conservative   94;  Mismatches  115;  Indels   48;  Gaps    6;

Qy     67 KLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124

Db     60 KVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFAQ 119

Qy    125 TWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVL 184

Db    120 MWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVL 179

Qy    185 YTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQ 244

Db    180 YSLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQ 239

Qy    245 FDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTE 304

Db    240 FSFVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKD 299

Qy    305 SAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL 364

Db    300 AVPARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYF 359

Qy    365 IYNQTKAHASPKLRH---PRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGE 418

Db    360 VSNRKPSKDKDKKKKNPAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGK 412

Qy    419 ERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVY 478

Db    413 D---CAS----------------------------FFCCFEDCRTGAWRHGRIHIRIA 439

Qy    479 RLDNYSRVVFPVTFFFFNVLYWLVCLNL 506

Db    440 KMDSYARIFFPTAFCLFNLVYWVSYLYL 467


RESULT  10
S12056
gamma-aminobutyric acid/benzodiazepine receptor gamma-1 chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S12056
R;Ymer, S.; Draguhn, A.; Wisden, W.; Werner, P.; Keinaenen, K.; Schofield, P.R.; Spre
EMBO J. 9, 3261-3267, 1990
A;Title: Structural and functional characterization of the gamma(1) subunit of GABA(A
A;Reference number: S12056; MUID:91006020
A;Accession: S12056
A;Molecule type: mRNA
A;Residues: 1-465 <YME>
A;Cross-references: GB:X57514; NID:g56175; PIDN:CAA40739.1; PID:g56176
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein

  Query Match             39.2%;  Score 1054;  DB 2;  Length 465;
  Best Local Similarity   43.1%;  Pred. No. 8.8e-77;
  Matches  193;  Conservative   91;  Mismatches  108;  Indels   56;  Gaps    5;

Qy     70 EASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDE 129

Db     63 DITQILNSLLQGYDNKLRPDIGVRPTVIETDVYVNSIGPVDPINMEYTIDIIFAQTWFDS 122

Qy    130 RLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189

Db    123 RLKFNSTMKVLMLNSNMVGKIWIPDTFFRNSRKSDAHWITTPNRLLRIWSDGRVLYTLRL 182

Qy    190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249

Db    183 TINAECYLQLHNFPMDEHSCPLEFSSYGYPKNEIEYKWKKPSVEVADPKYWRLYQFAFVG 242

Qy    250 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 309

Db    243 LRNSTEISHTISGDYIIMTIFFDLSRRMGYFTIQTYIPCILTVVLSWVSFWINKDAVPAR 302

Qy    310 TSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYN-- 368

Db    303 TSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFAALMEYGTLHYFTSNNK 362

Qy    368 ---------QTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGE 418

Db    363 GKTTRDRKLKSKTSVSPGL-------HAGSTLIPMNNISMPQGEDDYGYQCL--EGKD-- 412

Qy    419 ERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVY 478

Db    412 ----CAT----------------------------FFCCFEDCRTGSWREGRIHIRIA 437

Qy    479 RLDNYSRVVFPVTFFFFNVLYWLVCLNL 506

Db    438 KIDSYSRIFFPTAFALFNLVYWVGYLYL 465


RESULT  11
JH0824
gamma-aminobutyric acid A receptor gamma 1 chain precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
C;Accession: JH0824
R;Glencorse, T.A.; Darlison, M.G.; Barnard, E.A.; Bateson, A.N.
J. Neurochem. 61, 2294-2302, 1993
A;Title: Sequence and novel distribution of the chicken homologue of the mammalian ga
A;Reference number: JH0824; MUID:94065817
A;Accession: JH0824
A;Molecule type: mRNA
A;Residues: 1-464 <GLE>
C;Comment: This protein mediates gamma-aminobutyric acid-induced synaptic inhibition
C;Superfamily: acetylcholine receptor
C;Keywords: ion channel; neurotransmitter receptor; transmembrane protein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-464/Product: gamma-aminobutyric acid A receptor gamma 1 chain #status predicted
F;269-290/Domain: transmembrane #status predicted <TM1>
F;295-316/Domain: transmembrane #status predicted <TM2>
F;328-349/Domain: transmembrane #status predicted <TM3>
```

```
F;441-464/Domain: transmembrane #status predicted <TM4>


  Query Match            39.1%;  Score 1051.5;  DB 2;  Length 464;
  Best Local Similarity  42.6%;  Pred. No. 1.4e-76;
  Matches  192;  Conservative   89;  Mismatches  111;  Indels   59;  Gaps    4;

Qy      70 EASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDE 129
           : : ||:::|  ||:|||| || : ||:  :: |||:||:  ::|||||||||:|||||
Db      59 DVTHILDSLLQGYDNKLRPDIGVRTTVIETDVYVNSIGPVDPINMEYTIDIIFAQTWYDS 118

Qy     130 RLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
           || :| : : |:|| |:| ::|||||||||||:::  | || ||:::||: ||:||||:|:
Db     119 RLKFNSSMKVLMLNSNMVGKIWIPDTFFRNSRKSDAHWITTPNRLLRIWSDGRVLYTLRL 178

Qy     190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
           ||:| | | :  |||| ||||| ||||: || ||: |||:   :|: :   |:|:|| | |
Db     179 TINAECYLQLHNFPMDEHSCPLEFSSYGYPRNEIEYKWKKTSVEVADPKYWRLYQFAFVG 238

Qy     250 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 309
           : | |||   |  ||:::|||||::||| ||    | |:|  :| :|||||||  :: |||
Db     239 LRNTTEISHTLSGDYIIMTIFFDLSRRMGYFTIQTYIPCILTVVLSWVSFWINKDAVPAR 298

Qy     310 TSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQT 369
           ||||||:|||||||  | :||: |:|||:||:| ::::||:|  | ||:|:  |::   |:
Db     299 TSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFAALMEYGTLHYFTSNR- 358

Qy     370 KAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPP 429
                                                  :|  |::: :      |
Db     358 ----------------------------------------KGDKGKDKKAKPKPSKP 374

Qy     430 S-----PGSPEGPRSLCSKL---------ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCI 475
           |     |||   | :  : |           | |  |    :||   ||   :|:::||: |
Db     375 SAIAVRPGSTLIPINNINNLPERDDDYGYECLEG-KDCASFFCCFEDCRTGSWREGRIHI 433

Qy     476 HVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL 506
             : ::|:|||: ||  |  ||::||:  | |
Db     434 RIAKIDSYSRIFFPTAFALFNLVYWIGYLYL 464


RESULT  12
S11087
gamma-aminobutyric acid receptor A, cerebellar - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Feb-1997
C;Accession: S11087
R;Lueddens, H.; Pritchett, D.B.; Koehler, M.; Killisch, I.; Keinaenen, K.; Monyer, H.; S
Nature 346, 648-651, 1990
A;Title: Cerebellar GABA(A) receptor selective for a behavioural alcohol antagonist.
A;Reference number: S11087; MUID:90348963
A;Accession: S11087
A;Molecule type: mRNA
A;Residues: 1-453 <LUE>
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein


  Query Match            31.9%;  Score 858;  DB 2;  Length 453;
  Best Local Similarity  37.7%;  Pred. No. 4.2e-61;
  Matches  171;  Conservative   88;  Mismatches  132;  Indels   62;  Gaps    6;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           ||||: :|  ||::|||| |   | |  :| | | ||:| ::|||||:|: | ||| ||||
Db      33 SRILDNLLEGYDNRLRPGFGGAVTEVKTDIYVTSFGPVSDVEMEYTMDVFFRQTWTDERL 92

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
             :   | | ||  :||::| |||||||  |::  | :| ||:: |:  :| :|||:|:||
Db      93 KFKGPAEILSLNNLMVSKIWTPDTFFRNGKKSIAHNMTTPNKLFRLMHNGTILYTMRLTI 152

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLEINEKNSWKLFQFDFT 248
           :| | : :: |||| |:||| | |::||::|:|| |:    : :|: |::|  | |:|
Db     153 NADCPMRLVNFPMDGHACPLKFGSYAYPKSEIIYTWKKGPLYSVEVPEESS-SLLQYDLI 211

Qy     249 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 308
           | :  :| | :  |::::||::|:: |: ||   | | |  :| :|| |||||  || ||
Db     212 GQTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPA 271

Qy     309 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 368
           ||  |||:|||||||   :| : |:||| ||:|::||:|| | | ||:||| :|:    |
Db     272 RTVFGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQ 331

Qy     369 TKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGS------------ 416
           ::             :  |:| |:      :  |:  :||    |
Db     332 SQ------------KAERQAQTAAKPPVAKSKTTESLEAEIVVHSDSKYHLKKRISSLTL 379

Qy     416 ---DGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGR 472
                 |     :: |  | :|  |  |                    :|   |::
Db     380 PIVPSSEASKVLSRTPILPSTPVTPPLL------------------LPAIGGTS----- 416

Qy     473 LCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
                ::| |||::||| |  ||::||:| |:
Db     416 ------KIDQYSRILFPVAFAGFNLVYWIVYLS 442


RESULT  13
S17551
gamma-aminobutyric acid/benzodiazepine receptor alpha-4 chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S17551
R;Wisden, W.; Herb, A.; Wieland, H.; Keinaenen, K.; Lueddens, H.; Seeburg, P.H.
FEBS Lett. 289, 227-230, 1991
A;Title: Cloning, pharmacological characteristics and expression pattern of the rat G
A;Reference number: S17551; MUID:92008629
A;Accession: S17551
A;Molecule type: mRNA
A;Residues: 1-552 <WIS>
A;Cross-references: GB:S55933; NID:g236011; PIDN:AAB19902.1; PID:g236012
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein


  Query Match            31.8%;  Score 855.5;  DB 2;  Length 552;
  Best Local Similarity  34.3%;  Pred. No. 8.7e-61;
  Matches  198;  Conservative   87;  Mismatches  172;  Indels  121;  Gaps   12;

Qy       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
           : | |   || :| :     | |   ||:|
Db      12 LCSGVSLALLHVLCLATCLNESPGQNSKDE---------------------------- 42

Qy      61 TGSRVGKL-PE-ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTI 118
                 || ||  :|||:::|  ||::|||| |   | |  :| | | ||:|  ::||||:
Db      42 ------KLCPENFTRILDSLLDGYDNRLRPGFGGPVTEVKTDIYVTSFGPVSDVEMEYTM 95

Qy     119 DIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIY 178
           |: | ||| |:|| |:   | | ||  :|:::| |||||||  |::  | :| ||:: ||
Db      96 DVFFRQTWIDKRLKYDGPIEILRLNNMMVTKVWTPDTFFRNGKKSVSHNMTAPNKLFRIM 155

Qy     179 KDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEIN 235
           ::| :|||:|:|| | | : :: |||| |:||| | |::||::|||| |        :|:
Db     156 RNGTILYTMRLTISAECPMRLVDFPMDGHACPLKFGSYAYPKSEMIYTWTKGPEKSVEV- 215

Qy     236 EKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLS 295
             | |  | |:|  | :  :| | :  |:::|||::|:: |: ||   | |:|  :| :||
Db     215 PKESSSLVQYDLIGQTVSSETIKSITGEYIVMTVYFHLRRKMGYFMIQTYIPCIMTVILS 274

Qy     296 WVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCAL 355
           |||||  || ||||  |||:|||||||   :| : |:||| ||:|::||:||| | | ||
Db     275 QVSFWINKESVPARTVFGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSAL 334

Qy     356 LEFAVLNFLIYNQ------------TKAHASPKLRHPRINS---RAHARTRARSRACARQ 400
           :||| :|:    |               :  |:| |:      :     ||    | |  |
Db     335 IEFAAVNYFTNIQMQKAKKKISKPPPEVPAAPVLKEKHTETSLQNTHANLNMRKRTNALV 394

Qy     401 HQEAFV---------CQIVTTEGSDGEERPSCSAQQPPSP------------------- 432
           | |: |             |      | |       |:|
```

```
Db    395 HSESDVNSRTEVGNHSSKTTAAQESSETTPKAHLASSPNPFSRANAAETISAAARGLSSA 454

Qy    432 --GSPEG---PRSLCSKLACCEWCKRFKKYFCMV------------------PDCEGST 467
Db    455 ASPSPHGTLQPAPLRSASARPAFGARLGRIKTTVNTTGVPGNVSATPPPSAPPPSGSGTS 514

Qy    468 WQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLN 505
Db    515 ----------KIDKYARILFPVTFGAFNMVYWVVYLS 541


RESULT  14
G01928
gamma-aminobutyric acid receptor A alpha-4 - human
N;Alternate names: GABA(A) receptor alpha-4 chain
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C;Accession: G01928; I38936
R;Yang, W.
submitted to the EMBL Data Library, June 1995
A;Reference number: G08852
A;Accession: G01928
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-554 <YAN>
A;Cross-references: EMBL:U30461; NID:g905392; PIDN:AAB52519.1; PID:g905393
R;McLean, P.J.; Farb, D.H.; Russek, S.J.
Genomics 26, 580-586, 1995
A;Title: Mapping of the alpha 4 subunit gene (GABRA4) to human chromosome 4 defines an a
ed from an ancestral cluster.
A;Reference number: I38936; MUID:95331795
A;Accession: I38936
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-57 <MCL>
A;Cross-references: EMBL:U20166; NID:g924604; PIDN:AAA74743.1; PID:g924605
C;Genetics:
A;Gene: GDB:GABRA4
A;Cross-references: GDB:370881; OMIM:137141
A;Map position: 4p14-4q12
A;Introns: 29/2
A;Note: the list of introns is incomplete
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; neurotransmitter receptor
F;144,157,402,408/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             31.6%;  Score 850;  DB 2;  Length 554;
  Best Local Similarity   35.1%;  Pred. No. 2.4e-60;
  Matches  189;  Conservative   90;  Mismatches  154;  Indels  106;  Gaps   12;

Qy     44 PLENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAV 103
Db     34 PGQNQ--KEEKLCTENFT----------RILDSLLDGYDNRLRPGFGGPVTEVKTDIYV 80

Qy    104 NSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRT 163
Db     81 TSFGPVSDVEMEYTMDVFFRQTWIDKRLKYDGPIEILRLNNMMVTKVWTPDTFFRNGKKS 140

Qy    164 HEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEM 223
Db    141 VSHNMTAPNKLFRIMRNGTILYTMRLTISAECPMRLVDFPMDGHACPLKFGSYAYPKSEM 200

Qy    224 IYKW---ENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYV 280
Db    201 IYTWTKGPEKSVEV-PKESSSLVQYDLIGQTVSSETIKSITGEYIVMTVYFHLRRKMGYF 259

Qy    281 AFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITAL 340
Db    260 MIQTYIPCIMTVILSQVSFWINKESVPARTVFGITTVLTMTTLSISARHSLPKVSYLTAM 319

Qy    341 DFYIAICFVFCFCALLEFAVLNFLIYNQ------------TKAHASP--KLRHPRINSR- 386
Db    320 DWFIAVCFAFVFSALIEFAAVNYFTNIQMEKAKRKTSKPPQEVPAAPVQREKHPEAPLQD 379

Qy    386 AHARTRARSRACARQHQEAFV------------CQIVTTEGSDGEERPSCSAQQPPSPGS 433
Db    380 TNANLNMRKRTNALVHSESDVGNRTEVGNHSSKSSTVVQESSKGTPRSYLASS--PNPFS 437

Qy    434 PEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRL----------CIHVY----- 479
Db    438 RANAAETISAARA------------LPSASPTSIRTGHMPRKASVGSASTRHVFGSRLQ 484

Qy    479 ------------------------------RLDNYSRVVFPVTFFFFNVLYWLVCLN 505
Db    485 RIKTTVNTIGATGKLSATPPPSAPPPSGSGTSKIDKYARILFPVTFGAFNMVYWVVYLS 543


RESULT  15
S06838
gamma-aminobutyric acid/benzodiazepine receptor alpha-4 chain precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
C;Accession: S06838
R;Ymer, S.; Draguhn, A.; Koehler, M.; Schofield, P.R.; Seeburg, P.H.
FEBS Lett. 258, 119-122, 1989
A;Title: Sequence and expression of a novel GABA(A) receptor alpha subunit.
A;Reference number: S06838; MUID:90076471
A;Accession: S06838
A;Molecule type: mRNA
A;Residues: 1-556 <YME>
A;Cross-references: EMBL:X61456; NID:g360; PIDN:CAA43696.1; PID:g361
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-556/Product: gamma-aminobutyric acid/benzodiazepine receptor alpha-4 chain #stat


  Query Match             31.3%;  Score 842;  DB 2;  Length 556;
  Best Local Similarity   36.4%;  Pred. No. 1.1e-59;
  Matches  196;  Conservative   83;  Mismatches  156;  Indels  104;  Gaps   14;

Qy     44 PLENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAV 103
Db     34 PGQNQ--KEEKLCPENFT----------RILDSLLDGYDNRLRPGFGGPVTEVKTDIYV 80

Qy    104 NSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRT 163
Db     81 TSFGPVSDVEMEYTMDVFFRQTWIDKRLKYDGPIEILRLNNMMVTKVWTPDTFFRNGKKS 140

Qy    164 HEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEM 223
Db    141 VSHNMTAPNKLFRIMRNGTILYTMRLTISAECPMRLVDFPMDGHACPLKFGSYAYPKSEM 200

Qy    224 IYKW---ENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYV 280
Db    201 IYTWTKGPEKSVEV-PKESSSLVQYDLIGQTVSSETIKSITGEYIVMTVYFHLRRKMGYF 259

Qy    281 AFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRK-NFPRVSYITA 339
Db    260 MIQTYIPCIMTVILSQVSFWINKESVPARTVFGITTVLTMTTLSISARPISLPKVSYATA 319

Qy    340 LDFYIAICFVFCFCALLEFAVLNFLIYNQ--------TKA----HASPKLR--HPRIN-S 384
Db    320 MDWFIAVCFAFVFSALIEFAAVNYFTNVQMEKAKRKTSKAPQEISAAPVLREKHPETPLQ 379

Qy    385 RAHARTRARSRACARQHQEAFV----------CQIVTTEGSDGEERPSCSAQQPPSPGSP 434
Db    380 NTNANLSMRKRANALVHSESDVGSRTDVGNHSSKSSTVVQGSSEATPQSYLASSPNPFSR 439

Qy    435 EG-----------PRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVY----- 479
Db    440 ANAAETISAARAIPSALPSTPSRTGYVPR------QVPVGSASTQ-------HVFGSRLQ 486

Qy    479 ------------------------------RLDNYSRVVFPVTFFFFNVLYWLVCLN 505
```

Db 487 RIKTTVNSIGTSGKLSATTTPSAPPPSGSGTSKIDKYARILFPVTFGAFNMVYWVVYLS 545

Search completed: March 11, 2000, 06:06:26
Job time: 124 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2000, 08:51:55 ; Search time 47.6 Seconds
(without alignments)
129.378 Million cell updates/sec

Title: US-09-030-832-42_COPY_1_260
Perfect score: 1357
Sequence: 1 MLSKVLPVLLGILLILQSRV.....KLFQFDFTGVSNKTEIITTP 260

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database : A_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 188963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1354	99.8	506	1	W59048	GABA-A receptor ep
2	1354	99.8	506	1	W61045	Human GABA recepto
3	1152	84.9	474	1	W59049	Variant of GABA-A
4	607	44.7	467	1	R83968	GABA-A receptor ga
5	485	35.7	453	1	R31187	GABA-A receptor al
6	485	35.7	453	1	R59865	Human GABA recepto
7	470.5	34.7	554	1	R97298	Human GABA-A recep
8	462.5	34.1	462	1	R31186	GABA-A receptor al
9	462.5	34.1	462	1	R59864	Human GABA recepto
10	461	34.0	492	1	R31185	GABA-A receptor al
11	461	34.0	492	1	R59863	Human GABA recepto
12	443	32.6	451	1	R31184	GABA-A receptor al
13	443	32.6	451	1	R59862	Human GABA recepto
14	431	31.8	686	1	W86162	Insect GABA recept
15	366	27.0	452	1	R97299	Human GABA-A recep
16	352	25.9	627	1	W85597	Human GABA-A recep
17	349	25.7	627	1	W85596	Human GABA-A recep
18	335.5	24.7	474	1	R31188	GABA-A receptor be
19	335.5	24.7	474	1	R59866	Human GABA recepto
20	325.5	24.0	561	1	W97413	Lucilia cuprina GA
21	312	23.0	488	1	W69285	GABA gated chlorid
22	312	23.0	488	1	W69286	GABA gated chlorid
23	309	22.8	496	1	W81633	GABA-gated chlorid
24	309	22.8	467	1	W81634	GABA-gated chlorid
25	308	22.7	496	1	R89336	GABA receptor subu
26	308	22.7	496	1	W86161	Insect GABA recept
27	307.5	22.7	455	1	W97860	Cat flea glutamate
28	306.5	22.6	637	1	R34035	Sequence of a GABA
29	305	22.5	487	1	R88361	Caenorhabditis ele
30	304	22.4	481	1	W81635	GABA-gated chlorid
31	304	22.4	459	1	W81636	GABA-gated chlorid
32	301	22.2	510	1	R88360	Caenorhabditis ele
33	293	21.6	456	1	W05246	Drosophila glutama
34	289.5	21.3	440	1	R93118	Human GABA-A recep
35	289.5	21.3	440	1	W26464	Human GABA-A recep
36	162	11.9	222	1	W81637	GABA-gated chlorid
37	154	11.3	522	1	R06265	Fish acetylcholine
38	141.5	10.4	495	1	R07143	Neuronal nicotinic
39	141	10.4	498	1	W09027	Neuronal nicotinic
40	140	10.3	502	1	W09026	Neuronal nicotinic
41	140	10.3	498	1	W44154	Human neuronal nic
42	140	10.3	502	1	W44157	Human neuronal nic
43	138	10.2	479	1	R89358	Alpha-9 nicotinic
44	135.5	10.0	520	1	R06261	Mouse acetylcholin
45	129.5	9.5	520	1	R06262	Calf acetylcholine

ALIGNMENTS

RESULT 1
W59048
ID W59048 standard; Protein; 506 AA.
AC W59048;
DT 25-SEP-1998 (first entry)
DE GABA-A receptor epsilon sub-unit related protein.
KW GABA-A receptor; diagnosis; therapy; drug screening.
OS Mammalia.
PN DE19644501-A1.
PD 30-APR-1998.
PF 25-OCT-1996; 044501.
PR 25-OCT-1996; DE-044501.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR WPI; 98-252096/23.
DR N-PSDB; V11776.
PT Protein related to GABA-A receptor sub-unit epsilon - useful for
PT diagnosis, therapy or drug screening
PS Example 1; Fig 1; 12pp; German.
CC The GABA-A receptor sub-unit epsilon related protein is used for the
CC diagnosis and/or therapy of related disorders. It can also be used to
CC screen for substances that modulate the activity of the protein.
SQ Sequence 506 AA;

Query Match 99.8%; Score 1354; DB 1; Length 506;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60

Qy      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
           ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEISVNSLGPLSILDMEYTIDI 120

Qy     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180

Qy     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240

Qy     241 KLFQFDFTGVSNKTEIITTP 260
           ||||||||||||||||||||
Db     241 KLFQFDFTGVSNKTEIITTP 260
```

RESULT 2
W61045
ID W61045 standard; Protein; 506 AA.
AC W61045;
DT 12-OCT-1998 (first entry)
DE Human GABA receptor epsilon subunit.
KW GABA receptor; gamma-amino butyric acid receptor; human;
KW appetite; cognition.
OS Homo sapiens.
PN WO9823742-A1.
PD 04-JUN-1998.
PF 18-NOV-1997; G03159.

PR 03-OCT-1997; GB-020995.
PR 25-NOV-1996; GB-024442.
PA (MERI) MERCK SHARP & DOHME LTD.
PI Whiting PJ;
DR WPI; 98-322722/28.
DR N-PSDB; V36319.
PT New isolated GABA receptor subunit, epsilon - used to develop
PT products for the screening and design of drugs, e.g. for modulating
PT appetite behaviours, hormonal interactions and cognition
PS Claim 15; Fig 1; 37pp; English.
CC This polypeptide comprises a novel class of subunit, classified as
CC as epsilon, within the human GABA receptor gene family. Its amino
CC acid sequence was deduced from a cDNA clone (see V36319) isolated
CC from a human brain cDNA library. A stably co-transfected eukaryotic
CC cell line capable of expressing the GABA epsilon receptor subunit,
CC at least one alpha receptor subunit and at least one beta receptor
CC subunit is claimed. A recombinant expression vector, and protein
CC and membrane preparations of the GABA receptor obtained from the
CC co-transfected cells are also claimed. The new GABA-A receptor
CC epsilon subunit and products can be used in the screening and
CC design of drugs which act upon the GABA receptor. The ligands or
CC drug candidates identified may be used as therapeutic agents, e.g.
CC for the modulation of appetite behaviours, hormonal interactions
CC and cognition. They can also be used for the study of structure,
CC pharmacology and function of the various GABA receptor subtypes.
SQ Sequence 506 AA;

Query Match 99.8%; Score 1354; DB 1; Length 506;
Best Local Similarity 99.6%; Pred. No. 1.5e-133;
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60

Qy      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
          ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEISVNSLGPLSILDMEYTIDI 120

Qy     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180

Qy     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240

Qy     241 KLFQFDFTGVSNKTEIITTP 260
          ||||||||||||||||||||
Db     241 KLFQFDFTGVSNKTEIITTP 260
```

RESULT 3
W59049
ID W59049 standard; Protein; 474 AA.
AC W59049;
DT 25-SEP-1998 (first entry)
DE Variant of GABA-A receptor epsilon sub-unit related protein.
KW GABA-A receptor; diagnosis; therapy; drug screening.
OS Mammalia.
PN DE19644501-A1.
PD 30-APR-1998.
PF 25-OCT-1996; 044501.
PR 25-OCT-1996; DE-044501.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR WPI; 98-252096/23.
DR N-PSDB; V11777.
PT Protein related to GABA-A receptor sub-unit epsilon - useful for
PT diagnosis, therapy or drug screening
PS Disclosure; Fig 2; 12pp; German.
CC The GABA-A receptor sub-unit epsilon related protein is used for the
CC diagnosis and/or therapy of related disorders. It can also be used to
CC screen for substances that modulate the activity of the protein.
SQ Sequence 474 AA;

Query Match 84.9%; Score 1152; DB 1; Length 474;
Best Local Similarity 87.3%; Pred. No. 2e-112;
Matches 227; Conservative 1; Mismatches 0; Indels 32; Gaps 1;

```
Qy       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60

Qy      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
          ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEISVNSLGPLSILDMEYTIDI 120

Qy     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
          ||||||                                        ||||||||||||||||||||
Db     121 IFSQTW----------------------------------NSKRTHEHEITMPNQMVRIYKD 148

Qy     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     149 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 208

Qy     241 KLFQFDFTGVSNKTEIITTP 260
          ||||||||||||||||||||
Db     209 KLFQFDFTGVSNKTEIITTP 228
```

RESULT 4
R83968
ID R83968 standard; Protein; 467 AA.
AC R83968;
DT 02-FEB-1996 (first entry)
DE GABA-A receptor gamma-3 subunit.
KW GABA-A receptor; gamma-aminobutyric acid receptor; gamma-3 subunit.
OS Homo sapiens.
PN WO9529234-A1.
PD 02-NOV-1995.
PF 12-APR-1995; G00834.
PR 22-APR-1994; GB-008064.
PA (MERI) MERCK SHARP & DOHME LTD.
PI Whiting PJ;
DR WPI; 95-382983/49.
DR N-PSDB; T02334.
PT New cell line expressing human GABA-A receptor sub-units - useful in
PT drug screening and design
PS Disclosure; Page 21-23; 30pp; English.
CC A cDNA clone isolated from a human foetal brain cDNA library
CC encoded the GABA-A receptor gamma-3 subunit (R83968).
CC The cDNA can be expressed in eukaryotic (pref. rodent fibroblast)
CC cell lines to produce recombinant gamma-3 subunit or hybrid
CC GABA-A receptors having novel subunit compositions.
SQ Sequence 467 AA;

Query Match 44.7%; Score 607; DB 1; Length 467;
Best Local Similarity 48.2%; Pred. No. 2.4e-55;
Matches 122; Conservative 37; Mismatches 74; Indels 20; Gaps 3;

```
Qy       7 PVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETETGSRVG 66
          | || :|| | | :          | || |          ||      || :|
Db       3 PKLL-LLLCLFSGL---------HARSRKVEEDEYEDSSSNQKWVLAPKSQDT------- 46

Qy      67 KLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTW 126
             : : ||| :|  || |||| || ||||: |:| |||:||:|  ::||| ||| |:|||
Db      46 ---DVTLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSINMEYQIDIFFAQTW 102

Qy     127 YDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYT 186
           | || :| | : | || |:|  :||||| |||||    | || |||::||: |||:|||
Db     103 TDSRLRFNSTMKILTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQLLRIWNDGKILYT 162
```

```
Qy    187 IRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFD 246
          :|:||:| | | :  |||| ||||| ||||: ||: :|||:|    ::  :: ||:|:|||
Db    163 LRLTINAECQLQLHNFPMDEHSCPLIFSSYGYPKEQMIYRWRKNSVQAADQKSWRLYQFD 222

Qy    247 FTGVSNKTEIITT 259
          | |: | |||:||
Db    223 FMGLRNTTEIVTT 235


RESULT   5
R31187
ID   R31187 standard; Protein; 453 AA.
AC   R31187;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-6 subunit.
KW   Primer; human; alpha-6; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta.
OS   Homo sapiens.
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   N-PSDB; Q33130.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Disclosure; Fig 5; 43pp; English.
CC   This sequence represents the human alpha-6 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Rat alpha-6 cDNA was used as a probe
CC   and a human alpha-6 cDNA clone was isolated from a cerebellum cDNA
CC   library.  No full length cDNA's were isolated. To obtain a full length
CC   cDNA 3 clones were joined together using convenient restriction sites.
CC   GABA-A receptor comprises a multimeric protein of molecular size
CC   230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   453 AA;

  Query Match             35.7%;  Score 485;  DB 1;  Length 453;
  Best Local Similarity   44.6%;  Pred. No. 1.4e-42;
  Matches   91;  Conservative   44;  Mismatches   57;  Indels   12;  Gaps    3;

Qy     65 VGKL--------PEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEY 116
          :|||           ||||: :|  ||::|||| |   | |  :| | | ||:| ::|||
Db     18 LGKLEVEGNFYSENVSRILDNLLEGYDNRLRPGFGGAVTEVKTDIYVTSFGPVSDVEMEY 77

Qy    117 TIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVR 176
          |:|: | ||| |||| :    | | ||  :||::| ||||||| |::  | :| ||:: |
Db     78 TMDVFFRQTWTDERLKFGGPTEILSLNNLMVSKIWTPDTFFRNGKKSIAHNMTTPNKLFR 137

Qy    177 IYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLE 233
          | ::| :|||:|:||:| | : :: |||| |:||| | |::||::|:|| |:    : :|
Db    138 IMQNGTILYTMRLTINADCPMRLVNFPMDGHACPLKFGSYAYPKSEIIYTWKKGPLYSVE 197

Qy    234 INEKNSWKLFQFDFTGVSNKTEII 257
          : |::|  | |:|  | :  :| |
Db    198 VPEESS-SLLQYDLIGQTVSSETI 220


RESULT   6
R59865
ID   R59865 standard; Protein; 453 AA.
AC   R59865;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha6 subunit DNA.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   N-PSDB; Q69142.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.5; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   453 AA;

  Query Match             35.7%;  Score 485;  DB 1;  Length 453;
  Best Local Similarity   44.6%;  Pred. No. 1.4e-42;
  Matches   91;  Conservative   44;  Mismatches   57;  Indels   12;  Gaps    3;

Qy     65 VGKL--------PEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEY 116
          :|||           ||||: :|  ||::|||| |   | |  :| | | ||:| ::|||
Db     18 LGKLEVEGNFYSENVSRILDNLLEGYDNRLRPGFGGAVTEVKTDIYVTSFGPVSDVEMEY 77

Qy    117 TIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVR 176
          |:|: | ||| |||| :    | | ||  :||::| ||||||| |::  | :| ||:: |
Db     78 TMDVFFRQTWTDERLKFGGPTEILSLNNLMVSKIWTPDTFFRNGKKSIAHNMTTPNKLFR 137

Qy    177 IYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLE 233
          | ::| :|||:|:||:| | : :: |||| |:||| | |::||::|:|| |:    : :|
Db    138 IMQNGTILYTMRLTINADCPMRLVNFPMDGHACPLKFGSYAYPKSEIIYTWKKGPLYSVE 197

Qy    234 INEKNSWKLFQFDFTGVSNKTEII 257
          : |::|  | |:|  | :  :| |
Db    198 VPEESS-SLLQYDLIGQTVSSETI 220


RESULT   7
R97298
ID   R97298 standard; Protein; 554 AA.
AC   R97298;
DT   06-JAN-1997  (first entry)
DE   Human GABA-A receptor alpha 4 subunit.
KW   GABA-A receptor; gamma-aminobutyric acid; alpha-4 subunit.
OS   Homo sapiens.
PN   WO9610637-A1.
PD   11-APR-1996.
PF   29-SEP-1995; G02323.
PR   01-OCT-1994; GB-020010.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Le Bourdelles B,  Whiting PJ;
DR   WPI; 96-209359/21.
DR   N-PSDB; T28988.
PT   DNA encoding alpha-4 and delta subunit(s) of the human GABAa
PT   receptor  - also stably co-transfected eukaryotic cells expressing
PT   receptors contg. these subunit(s), used for screening and designing
PT   drugs
PS   Example 1; Fig 2; 45pp; English.
CC   The amino acid sequence (R97298) of the alpha-4 subunit of the
```

```
CC   human GABA-A receptor was deduced from a cDNA clone (T28988)
CC   isolated from a human brain thalamus cDNA library.  The alpha-4
CC   subunit can be produced in transfected host cells, partic. rodent
CC   fibroblasts.  Co-transfected host cells capable of expressing the
CC   alpha-4, delta (see also R97299) and beta subunits can be used to
CC   screen or design drugs that act on GABA-A receptors, e.g.
CC   benzodiazepines, barbiturates, beta-carbolines and neurosteroids.
CC   Construction of recombinant receptors contg. the alpha-4 and
CC   delta subunits becomes possible for the first time.
SQ   Sequence   554 AA;


  Query Match             34.7%;  Score 470.5;  DB 1;  Length 554;
  Best Local Similarity   42.9%;  Pred. No. 6.2e-41;
  Matches   93;  Conservative   43;  Mismatches   64;  Indels   17;  Gaps    4;

Qy      44 PLENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAV 103
           | :||   ||   ||  |           |||:::|  ||::|||| |   | |  :| |
Db      34 PGQNQ--KEEKLCTENFT----------RILDSLLDGYDNRLRPGFGGPVTEVKTDIYV 80

Qy     104 NSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRT 163
           | ||:| :::|||:|: | ||| |:|| |:   | | ||  :|:::| ||||||| |::
Db      81 TSFGPVSDVEVEYTMDVFFRQTWIDKRLKYDGPIEILRLNNMMVTKVWTPDTFFRNGKKS 140

Qy     164 HEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEM 223
           | :| ||:: || ::| :|||:|:|| | | : :: |||| |:||: | |::||::||
Db     141 VSHNMTAPNKLFRIMRNGTILYTMRLTISAECPMRLVDFPMDGHACPVKFGSYAYPKSEM 200

Qy     224 IYKW---ENFKLEINEKNSWKLFQFDFTGVSNKTEII 257
           || |       :|:  | |  | |:|  | :  :| |
Db     201 IYTWTKGPEKSVEV-PKESSSLVQYDLIGQTVSSETI 236


RESULT   8
R31186
ID   R31186 standard; Protein; 462 AA.
AC   R31186;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-5 subunit.
KW   Primer; human; alpha-5; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta.
OS   Homo sapiens.
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   N-PSDB; Q33129.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Disclosure; Fig 4; 43pp; English.
CC   This sequence represents the human alpha-5 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Rat alpha-5 cDNA was used as a probe
CC   and a human alpha-5 cDNA clone was isolated from a hippocampal cDNA
CC   library.  GABA-A receptor comprises a multimeric protein of molecular
CC   size 230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   462 AA;


  Query Match             34.1%;  Score 462.5;  DB 1;  Length 462;
  Best Local Similarity   42.3%;  Pred. No. 3.3e-40;
  Matches   88;  Conservative   45;  Mismatches   70;  Indels    5;  Gaps    2;

Qy      54 TKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILD 113
           | | : ||   :      :|||: :|  ||::||||:||: | |  :| | | ||:|  :
Db      35 TSSVKDETNDNITIF---TRILDGLLDGYDNRLRPGLGERITQVRTDIYVTSFGPVSDTE 91

Qy     114 MEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
           ||||||: | |:| |||| :    : | ||  : |::| ||||| | |::  | :| ||:
Db      92 MEYTIDVFFRQSWKDERLRFKGPMQRLPLNNLLASKIWTPDTFFHNGKKSIAHNMTTPNK 151

Qy     174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN--FK 231
           ::|:  || :|||:|:|| | | : :  ||||:|:||| | |::|| :|::| | |   |
Db     152 LLRLEDDGTLLYTMRLTISAECPMQLEDFPMDAHACPLKFGSYAYPNSEVVYVWTNGSTK 211

Qy     232 LEINEKNSWKLFQFDFTGVSNKTEIITT 259
           :  ::  :| |:   | :  || |:|
Db     212 SVVVAEDGSRLNQYHLMGQTVGTENIST 239


RESULT   9
R59864
ID   R59864 standard; Protein; 462 AA.
AC   R59864;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha5 subunit.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   N-PSDB; Q69141.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.4; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   462 AA;


  Query Match             34.1%;  Score 462.5;  DB 1;  Length 462;
  Best Local Similarity   42.3%;  Pred. No. 3.3e-40;
  Matches   88;  Conservative   45;  Mismatches   70;  Indels    5;  Gaps    2;

Qy      54 TKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILD 113
           | | : ||   :      :|||: :|  ||::||||:||: | |  :| | | ||:|  :
Db      35 TSSVKDETNDNITIF---TRILDGLLDGYDNRLRPGLGERITQVRTDIYVTSFGPVSDTE 91

Qy     114 MEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
           |||||: | |:| |||| :    : | ||  : |::| ||||| | |::  | :| ||:
Db      92 MEYTIDVFFRQSWKDERLRFKGPMQRLPLNNLLASKIWTPDTFFHNGKKSIAHNMTTPNK 151

Qy     174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN--FK 231
           ::|:  || :|||:|:|| | | : :  ||||:|:||| | |::|| :|::| | |   |
Db     152 LLRLEDDGTLLYTMRLTISAECPMQLEDFPMDAHACPLKFGSYAYPNSEVVYVWTNGSTK 211

Qy     232 LEINEKNSWKLFQFDFTGVSNKTEIITT 259
           :  ::  :| |:   | :  || |:|
Db     212 SVVVAEDGSRLNQYHLMGQTVGTENIST 239
```

```
RESULT  10
R31185
ID   R31185 standard; Protein; 492 AA.
AC   R31185;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-3 subunit.
KW   Primer; human; alpha-3; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta.
OS   Homo sapiens.
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   N-PSDB; Q33128.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Disclosure; Fig 3; 43pp; English.
CC   This sequence represents the human alpha-3 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Bovine alpha-3 cDNA was used as a
CC   probe and an alpha-3 cDNA clone was isolated from a human foetal
CC   brain cDNA library, which was missing approx. 100 bp of the 5' end.
CC   This missing fragment was isolated by PCR.  The two fragments were
CC   ligated together to give a full length alpha-3 cDNA.    GABA-A
CC   receptor comprises a multimeric protein of molecular size 230-370 kD
CC   with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   492 AA;

  Query Match             34.0%;  Score 461;  DB 1;  Length 492;
  Best Local Similarity   45.5%;  Pred. No. 5.2e-40;
  Matches   86;  Conservative   41;  Mismatches   58;  Indels    4;  Gaps    2;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           :|||: :|  ||::|||||:|:  | |  :| | | ||:|  |||||||: | |||:||||
Db      68 TRILDRLLDGYDNRLRPGLGDAVTEVKTDIYVTSFGPVSDTDMEYTIDVFFRQTWHDERL 127

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
           ::   : | ||  : |::| |||||  | |::  | :| ||:::|:  :| :|||:|:||
Db     128 KFDGPMKILPLNNLLASKIWTPDTFFHNGKKSVAHNMTTPNKLLRLVDNGTLLYTMRLTI 187

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEINEKNSWKLFQFDFT 248
           | | :|:  |||| |:||| | |::|   |::| |   :|  :|: :  | :| |:|
Db     188 HAECPMHLEDFPMDVHACPLKFGSYAYTTAEVVYSWTLGKNKSVEVAQDGS-RLNQYDLL 246

Qy     249 GVSNKTEII 257
           |    ||||
Db     247 GHVVGTEII 255


RESULT  11
R59863
ID   R59863 standard; Protein; 492 AA.
AC   R59863;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha3 subunit.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   N-PSDB; Q69140.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.3; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   492 AA;

  Query Match             34.0%;  Score 461;  DB 1;  Length 492;
  Best Local Similarity   45.5%;  Pred. No. 5.2e-40;
  Matches   86;  Conservative   41;  Mismatches   58;  Indels    4;  Gaps    2;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           :|||: :|  ||::|||||:|:  | |  :| | | ||:|  |||||||: | |||:||||
Db      68 TRILDRLLDGYDNRLRPGLGDAVTEVKTDIYVTSFGPVSDTDMEYTIDVFFRQTWHDERL 127

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
           ::   : | ||  : |::| |||||  | |::  | :| ||:::|:  :| :|||:|:||
Db     128 KFDGPMKILPLNNLLASKIWTPDTFFHNGKKSVAHNMTTPNKLLRLVDNGTLLYTMRLTI 187

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEINEKNSWKLFQFDFT 248
           | | :|:  |||| |:||| | |::|   |::| |   :|  :|: :  | :| |:|
Db     188 HAECPIHLEDFPMDVHACPLKFGSYAYTTAEVVYSWTLGKNKSVEVAQDGS-RLNQYDLL 246

Qy     249 GVSNKTEII 257
           |    ||||
Db     247 GHVVGTEII 255


RESULT  12
R31184
ID   R31184 standard; Protein; 451 AA.
AC   R31184;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-2 subunit.
KW   Primer; human; alpha-3; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta.
OS   Homo sapiens.
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   N-PSDB; Q33127.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Disclosure; Fig 2; 43pp; English.
CC   This sequence represents the human alpha-2 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Bovine alpha-2 cDNA was used as a
CC   probe and an alpha-2 cDNA clone was isolated from a human foetal
CC   brain cDNA library. GABA-A receptor comprises a multimeric protein
CC   of molecular size 230-270 kD with specific binding sites for various
CC   drugs including benzodiazepines, barbiturates, and beta-carbolines,
CC   in addition to the agonist ligand GABA.  The receptor is composed of
```

```
CC   several distinct types of subunit, which are divided into four classes
CC   (alpha, beta, gamma and delta) based on sequence homology.  To date
CC   six types of alpha, three types of beta, two types of gamma and one
CC   type of delta subunit have been identified.  It has been found that
CC   in addition to an alpha and a beta subunit, either gamma-1 or gamma-2
CC   is also required to confer benzodiazipine sensitivity.  The benzo-
CC   diazepine pharmacology of the receptor is largely dependent on the
CC   identity of the alpha and gamma subunits present.  Receptors
CC   containing a delta subunit do not appear to bind benzodiazepines.
SQ   Sequence   451 AA;

  Query Match             32.6%;  Score 443;  DB 1;  Length 451;
  Best Local Similarity   45.0%;  Pred. No. 3.5e-38;
  Matches   85;  Conservative   36;  Mismatches   64;  Indels    4;  Gaps    2;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           :|||: :|  ||::||||:|:  | |   | | | ||:|  |||||||: | | | ||||
Db      43 TRILDRLLDGYDNRLRPGLGDSITEVFTNIYVTSFGPVSDTDMEYTIDVFFRQKWKDERL 102

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
           :      | ||  : |::| ||||| | |::  | :||||:::||  || :|||:|:|:
Db     103 KFKGPMNILRLNNLMASKIWTPDTFFHNGKKSVAHNMTMPNKLLRIQDDGTLLYTMRLTV 162

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEINEKNSWKLFQFDFT 248
           | | :|:  ||||:||||| | |::|  :|: | |    :  :::    | :| |:|
Db     163 QAECPMHLEDFPMDAHSCPLKFGSYAYTTSEVTYIWTYNASDSVQVAPDGS-RLNQYDLL 221

Qy     249 GVSNKTEII 257
           | |   | |
Db     222 GQSIGKETI 230


RESULT  13
R59862
ID   R59862 standard; Protein; 451 AA.
AC   R59862;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha2 subunit.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   N-PSDB; Q69139.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.2; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   451 AA;

  Query Match             32.6%;  Score 443;  DB 1;  Length 451;
  Best Local Similarity   45.0%;  Pred. No. 3.5e-38;
  Matches   85;  Conservative   36;  Mismatches   64;  Indels    4;  Gaps    2;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           :|||: :|  ||::||||:|:  | |   | | | ||:|  |||||||: | | | ||||
Db      43 TRILDRLLDGYDNRLRPGLGDSITEVFTNIYVTSFGPVSDTDMEYTIDVFFRQKWKDERL 102

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
           :      | ||  : |::| ||||| | |::  | :||||:::||  || :|||:|:|:
Db     103 KFKGPMNILRLNNLMASKIWTPDTFFHNGKKSVAHNMTMPNKLLRIQDDGTLLYTMRLTV 162

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEINEKNSWKLFQFDFT 248
           | | :|:  ||||:||||| | |::|  :|: | |    :  :::    | :| |:|
Db     163 QAECPMHLEDFPMDAHSCPLKFGSYAYTTSEVTYIWTYNASDSVQVAPDGS-RLNQYDLL 221

Qy     249 GVSNKTEII 257
           | |   | |
Db     222 GQSIGKETI 230


RESULT  14
W86162
ID   W86162 standard; Protein; 686 AA.
AC   W86162;
DT   04-MAR-1999  (first entry)
DE   Insect GABA receptor subunit Grd.
KW   GABA; gamma-aminobutyric acid receptor; LCCH3; GABA recognition site;
KW   Grd; insecticide; insect; pharmacological; screening.
OS   Drosophila sp.
PN   US5854002-A.
PD   29-DEC-1998.
PF   17-DEC-1996; 768301.
PR   17-DEC-1996; US-768301.
PA   (RHON ) RHONE-POULENC INC.
PI   Gant DB, Tomalski MD;
DR   WPI; 99-094901/08.
DR   N-PSDB; V84686.
PT   Host cells that express LCCH3 and Grd subunits of insect
PT   gamma-aminobutyric acid receptor - comprises separate vectors or a
PT   single vector, used for screening compounds for insecticidal
PT   activity
PS   Claim 1; Columns 23-26; 27pp; English.
CC   This represents an insect gamma-aminobutyric acid (GABA) receptor subunit
CC   Grd. The invention provides host cells comprising (i) two expression
CC   vectors, one containing a sequence encoding the GABA receptor subunit
CC   LCCH3 and the other containing a sequence encoding the GABA receptor Grd
CC   subunit, with the sequences under control of separate promoters; or (ii)
CC   a single expression vector containing both GABA receptor subunits LCCH3
CC   and Grd linked to one or more regulatory elements. Membrane preparation
CC   from these cells are used to screen compounds for their ability to bind
CC   to the GABA recognition site of an insect GABA receptor, specifically to
CC   identify new insecticides. Co-expression of LCCH3 and Grd generates a
CC   GABA recognition site in the host cell membrane that has pharmacological
CC   properties very similar to those of the native receptor. The cells and
CC   membrane preparations are suitable for high throughput screening.
SQ   Sequence   686 AA;

  Query Match             31.8%;  Score 431;  DB 1;  Length 686;
  Best Local Similarity   40.4%;  Pred. No. 1.2e-36;
  Matches   76;  Conservative   45;  Mismatches   65;  Indels    2;  Gaps    1;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           | :|: :|  ||: :||  |  |  : |:| | |:||:| :|| |::|  | |:| |:||
Db     110 SELLDNLLRGYDNSIRPDFGGPPATIEVDIMVRSMGPISEVDMTYSMDCYFRQSWVDKRL 169

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
           :    ::| |: ::::::| |||:| | |::: | || ||: ||||::|:|||: |:||
Db     170 AFEGAQDTLALSVSMLARIWKPDTYFYNGKQSYLHTITTPNKFVRIYQNGRVLYSSRLTI 229

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG-- 250
           ||| :::  ||||   ||| | || |  :::||:|   :  :      || |||
Db     230 KAGCPMNLADFPMDIQKCPLKFGSFGYTTSDVIYRWNKERPPVAIAEDMKLSQFDLVDCP 289

Qy     250 VSNKTEII 257
           | |:|:
Db     290 AGNLTDIV 297


RESULT  15
R97299
ID   R97299 standard; Protein; 452 AA.
AC   R97299;
```

DT 06-JAN-1997 (first entry)
DE Human GABA-A receptor delta subunit.
KW GABA-A receptor; gamma-aminobutyric acid; delta subunit.
OS Homo sapiens.
PN WO9610637-A1.
PD 11-APR-1996.
PF 29-SEP-1995; G02323.
PR 01-OCT-1994; GB-020010.
PA (MERI) MERCK SHARP & DOHME LTD.
PI Le Bourdelles B, Whiting PJ;
DR WPI; 96-209359/21.
DR N-PSDB; T28989.
PT DNA encoding alpha-4 and delta subunit(s) of the human GABAa
PT receptor - also stably co-transfected eukaryotic cells expressing
PT receptors contg. these subunit(s), used for screening and designing
PT drugs
PS Example 2; Fig 3; 45pp; English.
CC The amino acid sequence (R97299) of the delta subunit of the
CC human GABA-A receptor was deduced from a cDNA clone (T28989)
CC isolated from a human hippocampus cDNA library. The delta
CC subunit can be produced in transfected host cells, partic. rodent
CC fibroblasts. Co-transfected host cells capable of expressing the
CC delta, alpha-4 (see also R97298) and beta subunits can be used to
CC screen or design drugs that act on GABA-A receptors, e.g.
CC benzodiazepines, barbiturates, beta-carbolines and neurosteroids.
CC Construction of recombinant receptors contg. the alpha-4 and
CC delta subunits becomes possible for the first time.
SQ Sequence 452 AA;

Query Match 27.0%; Score 366; DB 1; Length 452;
Best Local Similarity 33.8%; Pred. No. 4.1e-30;
Matches 72; Conservative 46; Mismatches 91; Indels 4; Gaps 2;

```
Qy      49 LLSEETKSTE--TETGSRVGKLPEASRI--LNTILSNYDHKLRPGIGEKPTVVTVEIAVN 104
           | ::: : |    : |  ||   | | :  |: ::: |    |||||  |  | : : |
Db      14 LCAQQLRGTRAMNDIGDYVGSNLEISWLPNLDGLIAGYARNFRPGIGGPPVNVALALEVA 73

Qy     105 SLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTH 164
           |:  :|  :||||: :   |:| | || || | |:| |:   | :||:||||  |:|
Db      74 SIDHISEANMEYTMTVFLHQSWRDSRLSYNHTNETLGLDSRFVDKLWLPDTFIVNAKSAW 133

Qy     165 EHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMI 224
            |::|: |:::|:  || :||:||:|    | : : :||||   | |   |: |   :::
Db     134 FHDVTVENKLIRLQPDGVILYSIRITSTVACDMDLAKFPMDEQECMLDLESYGYSSEDIV 193

Qy     225 YKWENFKLEINEKNSWKLFQFDFTGVSNKTEII 257
           | |   :  |:  :  :| ||  |     ||::
Db     194 YYWSESQEHIHGLDKLQLAQFTITSYRFTTELM 226
```

Search completed: March 10, 2000, 08:51:56
Job time: 5289 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:01:25 ; Search time 34.6 Seconds
(without alignments)
99.924 Million cell updates/sec

Title: US-09-030-832-42_COPY_1_260
Perfect score: 1357
Sequence: 1 MLSKVLPVLLGILLILQSRV.....KLFQFDFTGVSNKTEIITTP 260

Scoring table: BLOSUM62

Searched: 133990 seqs, 13297546 residues

Database : Issued_Patents_AA:*

Word size : 0

Number of hits that pass the threshold : 133990
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/PCTUS9_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	608	44.8	467	1	US-08-459-100A-3	Sequence 3, Appli
2	485	35.7	453	1	US-08-417-330A-18	Sequence 18, Appl
3	462.5	34.1	462	1	US-08-417-330A-16	Sequence 16, Appl
4	461	34.0	492	1	US-08-417-330A-14	Sequence 14, Appl
5	443	32.6	451	1	US-08-417-330A-12	Sequence 12, Appl
6	431	31.8	686	2	US-08-768-301-4	Sequence 4, Appli
7	357.5	26.3	474	1	US-08-459-100A-4	Sequence 4, Appli
8	339.5	25.0	617	1	US-08-137-614A-25	Sequence 25, Appl
9	335.5	24.7	474	1	US-08-417-330A-20	Sequence 20, Appl
10	314.5	23.2	637	3	US-08-072-064-1	Sequence 1, Appli
11	314.5	23.2	637	3	US-08-072-064-4	Sequence 4, Appli
12	314.5	23.2	637	3	US-08-072-064-6	Sequence 6, Appli
13	314.5	23.2	637	3	US-08-072-064-8	Sequence 8, Appli
14	314.5	23.2	637	4	PCT-US92-08558-1	Sequence 1, Appli
15	312	23.0	488	1	US-08-554-659-2	Sequence 2, Appli
16	312	23.0	488	1	US-08-554-659-4	Sequence 4, Appli
17	311.5	23.0	617	1	US-08-137-614A-24	Sequence 24, Appl
18	308	22.7	496	1	US-08-137-614A-2	Sequence 2, Appli
19	308	22.7	496	2	US-08-768-301-2	Sequence 2, Appli
20	305	22.5	617	1	US-08-137-614A-26	Sequence 26, Appl
21	305	22.5	487	1	US-08-249-112-4	Sequence 4, Appli
22	305	22.5	487	4	PCT-US95-06556-4	Sequence 4, Appli
23	301	22.2	510	1	US-08-249-112-3	Sequence 3, Appli
24	301	22.2	510	4	PCT-US95-06556-3	Sequence 3, Appli
25	293	21.6	456	1	US-08-435-933-6	Sequence 6, Appli
26	293	21.6	456	4	PCT-US96-06035-6	Sequence 6, Appli
27	289.5	21.3	440	1	US-08-459-100A-2	Sequence 2, Appli
28	289.5	21.3	440	4	PCT-US94-09589-2	Sequence 2, Appli
29	141	10.4	498	1	US-08-496-855A-6	Sequence 6, Appli
30	141	10.4	498	2	US-08-466-589-12	Sequence 12, Appl
31	141	10.4	498	2	US-08-700-636-12	Sequence 12, Appl
32	140	10.3	502	1	US-08-496-855A-4	Sequence 4, Appli
33	140	10.3	502	2	US-08-466-589-10	Sequence 10, Appl
34	140	10.3	502	2	US-08-700-636-10	Sequence 10, Appl
35	138	10.2	479	1	US-08-278-635B-2	Sequence 2, Appli
36	131	9.7	629	1	US-08-278-635B-6	Sequence 6, Appli
37	131	9.7	528	2	US-08-466-589-2	Sequence 2, Appli
38	131	9.7	528	2	US-08-700-636-2	Sequence 2, Appli
39	128.5	9.5	529	1	US-08-496-855A-2	Sequence 2, Appli
40	122.5	9.0	627	2	US-08-466-589-6	Sequence 6, Appli
41	122.5	9.0	627	2	US-08-700-636-6	Sequence 6, Appli
42	116	8.5	511	1	US-08-278-635B-8	Sequence 8, Appli
43	115.5	8.5	449	5	5468481-1	Patent No. 5468481
44	114	8.4	510	1	US-08-278-635B-4	Sequence 4, Appli
45	113.5	8.4	497	1	US-08-278-635B-5	Sequence 5, Appli

ALIGNMENTS

```
RESULT   1
US-08-459-100A-3
; Sequence 3, Application US/08459100A
; Patent No. 5654172
;  GENERAL INFORMATION:
;    APPLICANT:  Li, ET AL.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,100A
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09589
;      FILING DATE:  26 AUG 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-325
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-459-100A-3


  Query Match             44.8%;  Score 608;  DB 1;  Length 467;
  Best Local Similarity   53.3%;  Pred. No. 2.1e-61;
  Matches  104;  Conservative   41;  Mismatches   48;  Indels    2;  Gaps    1;

Qy      67 KLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
           |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|||||||  |:|
Db      60 KVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFAQ 119

Qy     125 TWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVL 184
           ||| || :| | : | || |:| ::||||||||||||:   | || ||:|:||: ||:||
Db     120 MWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVL 179
```

```
Qy    185 YTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQ 244
          |::|:|||| | | :  |||| ||||| ||||: ||  |::|:|:   :|: :  ||:|:|
Db    180 YSLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQ 239

Qy    245 FDFTGVSNKTEIITT 259
          | | |: | ||:: |
Db    240 FSFVGLRNTTEVVKT 254


RESULT   2
US-08-417-330A-18
; Sequence 18, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  453 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-18


  Query Match             35.7%;  Score 485;  DB 1;  Length 453;
  Best Local Similarity   44.6%;  Pred. No. 2.7e-47;
  Matches   91;  Conservative   44;  Mismatches   57;  Indels   12;  Gaps    3;

Qy     65 VGKL--------PEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEY 116
          :|||          ||||: :|  ||::|||| |   | |  :| | | ||:| ::|||
Db     18 LGKLEVEGNFYSENVSRILDNLLEGYDNRLRPGFGGAVTEVKTDIYVTSFGPVSDVEMEY 77

Qy    117 TIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVR 176
          |:|: | ||| |||| :    | | ||  :||::| ||||||| |::  | :| ||:: |
Db     78 TMDVFFRQTWTDERLKFGGPTEILSLNNLMVSKIWTPDTFFRNGKKSIAHNMTTPNKLFR 137

Qy    177 IYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLE 233
          | ::| :|||:|:||:| | : :: |||| |:||| | |::||::|:|| |:    : :|
Db    138 IMQNGTILYTMRLTINADCPMRLVNFPMDGHACPLKFGSYAYPKSEIIYTWKKGPLYSVE 197

Qy    234 INEKNSWKLFQFDFTGVSNKTEII 257
          : |::|  | |:|  | :  :| |
Db    198 VPEESS-SLLQYDLIGQTVSSETI 220


RESULT   3
US-08-417-330A-16
; Sequence 16, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  462 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-16


  Query Match             34.1%;  Score 462.5;  DB 1;  Length 462;
  Best Local Similarity   42.3%;  Pred. No. 1.1e-44;
  Matches   88;  Conservative   45;  Mismatches   70;  Indels    5;  Gaps    2;

Qy     54 TKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILD 113
          | | : ||   :      :|||: :|  ||::||||:||: | |  :| | | ||:|  :
Db     35 TSSVKDETNDNITIF---TRILDGLLDGYDNRLRPGLGERITQVRTDIYVTSFGPVSDTE 91

Qy    114 MEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
          ||||||: | |:| |||| :    : | ||  : |::| ||||| | |::  | :| ||:
Db     92 MEYTIDVFFRQSWKDERLRFKGPMQRLPLNNLLASKIWTPDTFFHNGKKSIAHNMTTPNK 151

Qy    174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN--FK 231
          ::|:  || :|||:|:|| | | : :  ||||:|:||| | |::|| :|::| | |   |
```

```
Db    152 LLRLEDDGTLLYTMRLTISAECPMQLEDFPMDAHACPLKFGSYAYPNSEVVYVWTNGSTK 211

Qy    232 LEINEKNSWKLFQFDFTGVSNKTEIITT 259
Db    212 SVVVAEDGSRLNQYHLMGQTVGTENIST 239


RESULT   4
US-08-417-330A-14
; Sequence 14, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  492 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-14


  Query Match           34.0%;  Score 461;  DB 1;  Length 492;
  Best Local Similarity  45.5%;  Pred. No. 1.7e-44;
  Matches   86;  Conservative   41;  Mismatches   58;  Indels    4;  Gaps    2;

Qy     72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
Db     68 TRILDRLLDGYDNRLRPGLGDAVTEVKTDIYVTSFGPVSDTDMEYTIDVFFRQTWHDERL 127

Qy    132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
Db    128 KFDGPMKILPLNNLLASKIWTPDTFFHNGKKSVAHNMTTPNKLLRLVDNGTLLYTMRLTI 187

Qy    192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEINEKNSWKLFQFDFT 248
Db    188 HAECPMHLEDFPMDVHACPLKFGSYAYTTAEVVYSWTLGKNKSVEVAQDGS-RLNQYDLL 246

Qy    249 GVSNKTEII 257
Db    247 GHVVGTEII 255


RESULT   5
US-08-417-330A-12
; Sequence 12, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  451 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-12


  Query Match           32.6%;  Score 443;  DB 1;  Length 451;
  Best Local Similarity  45.0%;  Pred. No. 1.8e-42;
  Matches   85;  Conservative   36;  Mismatches   64;  Indels    4;  Gaps    2;

Qy     72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
Db     43 TRILDRLLDGYDNRLRPGLGDSITEVFTNIYVTSFGPVSDTDMEYTIDVFFRQKWKDERL 102

Qy    132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
Db    103 KFKGPMNILRLNNLMASKIWTPDTFFHNGKKSVAHNMTMPNKLLRIQDDGTLLYTMRLTV 162

Qy    192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEINEKNSWKLFQFDFT 248
Db    163 QAECPMHLEDFPMDAHSCPLKFGSYAYTTSEVTYIWTYNASDSVQVAPDGS-RLNQYDLL 221
```

```
Qy    249 GVSNKTEII 257
          | |   | |
Db    222 GQSIGKETI 230
```

```
RESULT   6
US-08-768-301-4
; Sequence 4, Application US/08768301
; Patent No. 5854002
;  GENERAL INFORMATION:
;    APPLICANT:  Tomalski, Michael D.
;    APPLICANT:  Gant, Daniel B.
;    TITLE OF INVENTION:  METHOD OF IDENTIFYING COMPOUNDS THAT BIND
;    TITLE OF INVENTION:  TO THE INSECT GABA RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brumbaugh, Graves, Donohue & Raymond
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  10112-0228
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/768,301
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacLeod, Janet M
;      REGISTRATION NUMBER:  35,263
;      REFERENCE/DOCKET NUMBER:  A30693
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-408-2500
;      TELEFAX:  212-765-2519
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  686 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
US-08-768-301-4
```

```
  Query Match            31.8%;  Score 431;  DB 2;  Length 686;
  Best Local Similarity  40.4%;  Pred. No. 8.3e-41;
  Matches   76;  Conservative   45;  Mismatches   65;  Indels    2;  Gaps    1;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           | :|: :|  ||: :||  |  |  : |:| | |:||:| :|| |::|  | |:| |:||
Db     110 SELLDNLLRGYDNSIRPDFGGPPATIEVDIMVRSMGPISEVDMTYSMDCYFRQSWVDKRL 169

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
           :   ::| |: ::::::| |||:| | |::: | || ||: ||||::|:|||: |:||
Db     170 AFEGAQDTLALSVSMLARIWKPDTYFYNGKQSYLHTITTPNKFVRIYQNGRVLYSSRLTI 229

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG-- 250
           ||| :::  |||   ||| | || |  :::||:|   :  :      || |||
Db     230 KAGCPMNLADFPMDIQKCPLKFGSFGYTTSDVIYRWNKERPPVAIAEDMKLSQFDLVDCP 289

Qy     250 VSNKTEII 257
```

```
           | |:|:
Db     290 AGNLTDIV 297
```

```
RESULT   7
US-08-459-100A-4
; Sequence 4, Application US/08459100A
; Patent No. 5654172
;  GENERAL INFORMATION:
;    APPLICANT:  Li, ET AL.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,100A
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09589
;      FILING DATE:  26 AUG 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-325
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  474 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-459-100A-4
```

```
  Query Match            26.3%;  Score 357.5;  DB 1;  Length 474;
  Best Local Similarity  35.1%;  Pred. No. 1.3e-32;
  Matches   68;  Conservative   44;  Mismatches   79;  Indels    3;  Gaps    1;

Qy      68 LPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWY 127
           :|      :: :|  || :|||  |  |  | : | | |:  :| ::|:||: : | |:|
Db      34 MPYVKETVDRLLKGYDIRLRPDFGGPPVDVGMRIDVASIDMVSEVNMDYTLTMYFQQSWK 93

Qy     128 DERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTI 187
           |:|| |:    :| |:  |  |||:|||:| | |::  | :|: |:|:|:: || ||| :
Db      94 DKRLSYSGIPLNLTLDNRVADQLWVPDTYFLNDKKSFVHGVTVKNRMIRLHPDGTVLYGL 153

Qy     188 RMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQF-- 246
           |:|  | | : : |:|:|  :| |   |: |  ::: : |   :  :   |  :| ||
Db     154 RITTTAACMMDLRRYPLDEQNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELPQFSI 213

Qy     246 -DFTGVSNKTEIIT 258
            |:  || | |  |
Db     214 VDYKMVSKKVEFTT 227
```

```
RESULT   8
US-08-137-614A-25
; Sequence 25, Application US/08137614A
```

```
; Patent No. 5487976
;  GENERAL INFORMATION:
;    APPLICANT:  Soderlund, David M.
;    APPLICANT:  Knipple, Douglas C.
;    APPLICANT:  Henderson, Joseph E.
;    TITLE OF INVENTION:  Gene Encoding An Insect
;    TITLE OF INVENTION:  Gamma-Aminobutyric Acid (GABA) Receptor Subunit
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,614A
;      FILING DATE:  15-OCT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716)263-1636
;      TELEFAX:  (716)263-1600
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  617 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-137-614A-25


  Query Match             25.0%;  Score 339.5;  DB 1;  Length 617;
  Best Local Similarity   33.7%;  Pred. No. 2.3e-30;
  Matches   67;  Conservative   42;  Mismatches   75;  Indels   15;  Gaps    2;

Qy      75 LNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERLCYN 134
           :: :|  || :|||  |  |  | : | | |:  :| ::|:||: : | |:| |:|| |
Db      63 VDRLLKGYDIRLRPDFGGPPVDVGMRIDVASIDMVSEVNMDYTLTMYFQQSWKDKRLSYX 122

Qy     135 DTFE-----------SLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGK 182
                         :| |:  |  |||:|||:| | |::  | :|: |:|:|:: ||
Db     123 XXXXXXXXXXXSGIPLNLTLDNRVADQLWVPDTYFLNDKKSFVHGVTVKNRMIRLHPDGT 182

Qy     183 VLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKL 242
           ||| :|:|  | | : : |:|:|  :| |   |: |  ::: : |   :  :   |  :|
Db     183 VLYGLRITTTAACMMDLRRYPLDEQNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIEL 242

Qy     243 FQF---DFTGVSNKTEIIT 258
             ||   |:  || | |  |
Db     243 PQFSIVDYKMVSKKVEFTT 261


RESULT   9
US-08-417-330A-20
; Sequence 20, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  474 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-20


  Query Match             24.7%;  Score 335.5;  DB 1;  Length 474;
  Best Local Similarity   33.7%;  Pred. No. 4.3e-30;
  Matches   63;  Conservative   43;  Mismatches   78;  Indels    3;  Gaps    1;

Qy      75 LNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERLCYN 134
           :: :|  || :|||  |  |  | : | : |:  :| ::|:||: : | | | |:|| ||
Db      40 VDRLLKGYDIRLRPDFGGPPVAVGMNIDIASIDMVSEVNMDYTLTMYFQQAWRDKRLSYN 99

Qy     135 DTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAG 194
                :| |:  |  |||:|||:| | |::  | :|: |:|:|:: || ||| :|:|  |
Db     100 VIPLNLTLDNRVADQLWVPDTYFLNDKKSFVHGVTVKNRMIRLHPDGTVLYGLRITTTAA 159

Qy     195 CSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQF---DFTGVS 251
           | : : |:|:|  :| |   |: |  ::: : |      :      :| ||   |:  ::
Db     160 CMMDLRRYPLDEQNCTLEIESYGYTTDDIEFYWRGDDNAVTGVTKIELPQFSIVDYKLIT 219

Qy     252 NKTEIIT 258
               |  |
Db     220 KKVVFST 226


RESULT  10
US-08-072-064-1
; Sequence 1, Application US/08072064
; Patent No. 6008046
;  GENERAL INFORMATION:
;    APPLICANT:  FFRENCH-CONSTANT, RICHARD H.
;    APPLICANT:  JACKSON, MEYER B.
;    TITLE OF INVENTION:  DRUG AND PESTICIDE SCREENING
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER G. CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
```

```
;       STATE:  California
;       COUNTRY:  United States of America
;       ZIP:  94104
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/072,064
;       FILING DATE:  19930602
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 770,881
;       FILING DATE:  04-OCT-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  CARROLL, PETER G.
;       REGISTRATION NUMBER:  32,837
;       REFERENCE/DOCKET NUMBER:  OPHD-00574
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/705-8410
;       TELEFAX:  415/397-8338
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  637 amino acids
;       TYPE:  AMINO ACID
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  peptide
;     ORIGINAL SOURCE:
;       ORGANISM:  Drosophila melanogaster
;     POSITION IN GENOME:
;       CHROMOSOME/SEGMENT:  III; polytene subregion 66F
;       MAP POSITION:  approximately map unit 26
US-08-072-064-1


  Query Match             23.2%;  Score 314.5;  DB 3;  Length 637;
  Best Local Similarity   30.1%;  Pred. No. 1.8e-27;
  Matches   78;  Conservative   49;  Mismatches  109;  Indels   23;  Gaps    7;

Qy      23 PQTESKNEASSR-DVVYGPQPQP----------LENQLLSEETKSTETET-------GSR 64
           |:| |   : |: | :    | |          :   |:::||      |        ||
Db      25 PKTHSTTMSDSKMDKLARMAPLPRTPLLTIWLAINMALIAQETGHKRIHTVQAATGGGSM 84

Qy      65 VGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
           :| :   | ||::   :|| ::||  |  |  | | : | |:  :| : |::|:|  | |
Db      85 LGDV-NISAILDSFSVSYDKRVRPNYGGPPVEVGVTMYVLSISSVSEVLMDFTLDFYFRQ 143

Qy     125 TWYDERLCYNDT--FESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGK 182
            | | || |      |:| :    :  :|:|||| | |::: |  |  |: :|::  |
Db     144 FWTDPRLAYRKRPGVETLSVGSEFIKNIWVPDTFFVNEKQSYFHIATTSNEFIRVHHSGS 203

Qy     183 VLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKL 242
           :  :||:|| | | :::  ||||   | :   || |   :: | | :    :   :  :|
Db     204 ITRSIRLTITASCPMNLQYFPMDRQLCHIEIESFGYTMRDIRYFWRDGLSSVGMSSEVEL 263

Qy     243 FQFDFTGVSNK-TEI-ITT 259
           ||   |   : ||| :||
Db     264 PQFRVLGHRQRATEINLTT 282


RESULT  11
US-08-072-064-4
; Sequence 4, Application US/08072064
; Patent No. 6008046
;  GENERAL INFORMATION:
;    APPLICANT:  FFRENCH-CONSTANT, RICHARD H.
;    APPLICANT:  JACKSON, MEYER B.
;    TITLE OF INVENTION:  DRUG AND PESTICIDE SCREENING
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER G. CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/072,064
;      FILING DATE:  19930602
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 770,881
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  OPHD-00574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  637 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-072-064-4


  Query Match             23.2%;  Score 314.5;  DB 3;  Length 637;
  Best Local Similarity   30.1%;  Pred. No. 1.8e-27;
  Matches   78;  Conservative   49;  Mismatches  109;  Indels   23;  Gaps    7;

Qy      23 PQTESKNEASSR-DVVYGPQPQP----------LENQLLSEETKSTETET-------GSR 64
           |:| |   : |: | :    | |          :   |:::||      |        ||
Db      25 PKTHSTTMSDSKMDKLARMAPLPRTPLLTIWLAINMALIAQETGHKRIHTVQAATGGGSM 84

Qy      65 VGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
           :| :   | ||::   :|| ::||  |  |  | | : | |:  :| : |::|:|  | |
Db      85 LGDV-NISAILDSFSVSYDKRVRPNYGGPPVEVGVTMYVLSISSVSEVLMDFTLDFYFRQ 143

Qy     125 TWYDERLCYNDT--FESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGK 182
            | | || |      |:| :    :  :|:|||| | |::: |  |  |: :|::  |
Db     144 FWTDPRLAYRKRPGVETLSVGSEFIKNIWVPDTFFVNEKQSYFHIATTSNEFIRVHHSGS 203

Qy     183 VLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKL 242
           :  :||:|| | | :::  ||||   | :   || |   :: | | :    :   :  :|
Db     204 ITRSIRLTITASCPMNLQYFPMDRQLCHIEIESFGYTMRDIRYFWRDGLSSVGMSSEVEL 263

Qy     243 FQFDFTGVSNK-TEI-ITT 259
           ||   |   : ||| :||
Db     264 PQFRVLGHRQRATEINLTT 282


RESULT  12
US-08-072-064-6
; Sequence 6, Application US/08072064
; Patent No. 6008046
;  GENERAL INFORMATION:
;    APPLICANT:  FFRENCH-CONSTANT, RICHARD H.
;    APPLICANT:  JACKSON, MEYER B.
;    TITLE OF INVENTION:  DRUG AND PESTICIDE SCREENING
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER G. CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
```

```
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/072,064
;      FILING DATE:  19930602
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 770,881
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  OPHD-00574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  637 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-072-064-6


  Query Match             23.2%;  Score 314.5;  DB 3;  Length 637;
  Best Local Similarity   30.1%;  Pred. No. 1.8e-27;
  Matches   78;  Conservative   49;  Mismatches  109;  Indels   23;  Gaps    7;

Qy      23 PQTESKNEASSR-DVVYGPQPQP----------LENQLLSEETKSTETET-------GSR 64
           |:| |   : |: | :    | |          :   |:::||      |       ||
Db      25 PKTHSTTMSDSKMDKLARMAPLPRTPLLTIWLAINMALIAQETGHKRIHTVQAATGGGSM 84

Qy      65 VGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
           :| :   | ||::   :|| ::||  |  |  | : | |:  :| : |::|:|  | |
Db      85 LGDV-NISAILDSFSVSYDKRVRPNYGGPPVEVGVTMYVLSISSVSEVLMDFTLDFYFRQ 143

Qy     125 TWYDERLCYNDT--FESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGK 182
           | | || |      |:| :    :  :|:|||||| | |::: |  |  |: :|::  |
Db     144 FWTDPRLAYRKRPGVETLSVGSEFIKNIWVPDTFFVNEKQSYFHIATTSNEFIRVHHSGS 203

Qy     183 VLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKL 242
           :  :||:|| | | :::  ||||   | :   || |   :: | | :    :   :  :|
Db     204 ITRSIRLTITASCPMNLQYFPMDRQLCHIEIESFGYTMRDIRYFWRDGLSSVGMSSEVEL 263

Qy     243 FQFDFTGVSNK-TEI-ITT 259
           ||   |   : ||| :||
Db     264 PQFRVLGHRQRATEINLTT 282


RESULT  13
US-08-072-064-8
; Sequence 8, Application US/08072064
; Patent No. 6008046
;  GENERAL INFORMATION:
;    APPLICANT:  FFRENCH-CONSTANT, RICHARD H.
;    APPLICANT:  JACKSON, MEYER B.
;    TITLE OF INVENTION:  DRUG AND PESTICIDE SCREENING
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER G. CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/072,064
;      FILING DATE:  19930602
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 770,881
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  OPHD-00574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  637 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-072-064-8


  Query Match             23.2%;  Score 314.5;  DB 3;  Length 637;
  Best Local Similarity   30.1%;  Pred. No. 1.8e-27;
  Matches   78;  Conservative   49;  Mismatches  109;  Indels   23;  Gaps    7;

Qy      23 PQTESKNEASSR-DVVYGPQPQP----------LENQLLSEETKSTETET-------GSR 64
           |:| |   : |: | :    | |          :   |:::||      |       ||
Db      25 PKTHSTTMSDSKMDKLARMAPLPRTPLLTIWLAINMALIAQETGHKRIHTVQAATGGGSM 84

Qy      65 VGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
           :| :   | ||::   :|| ::||  |  |  | : | |:  :| : |::|:|  | |
Db      85 LGDV-NISAILDSFSVSYDKRVRPNYGGPPVEVGVTMYVLSISSVSEVLMDFTLDFYFRQ 143

Qy     125 TWYDERLCYNDT--FESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGK 182
           | | || |      |:| :    :  :|:|||||| | |::: |  |  |: :|::  |
Db     144 FWTDPRLAYRKRPGVETLSVGSEFIKNIWVPDTFFVNEKQSYFHIATTSNEFIRVHHSGS 203

Qy     183 VLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKL 242
           :  :||:|| | | :::  ||||   | :   || |   :: | | :    :   :  :|
Db     204 ITRSIRLTITASCPMNLQYFPMDRQLCHIEIESFGYTMRDIRYFWRDGLSSVGMSSEVEL 263

Qy     243 FQFDFTGVSNK-TEI-ITT 259
           ||   |   : ||| :||
Db     264 PQFRVLGHRQRATEINLTT 282


RESULT  14
PCT-US92-08558-1
; Sequence 1, Application PC/TUS9208558
;  GENERAL INFORMATION:
;    APPLICANT:  Cornell Research Foundation, Inc.
;    TITLE OF INVENTION:  MOLECULAR CLONING AND TRANSFORMATION OF CYCLODIENE RESISTAN
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Yahwak & Associates
;      STREET:  25 Skytop Drive
;      CITY:  Trumbull
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06611
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Microsoft Word 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/08558
;      FILING DATE:  19921002
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  US/07/770,881
;      FILING DATE:  October 4th 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  George M. Yahwak
;      REGISTRATION NUMBER:  26,824
;      REFERENCE/DOCKET NUMBER:  CRF D-1052
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203)268-1951
;      TELEFAX:  (203)268-1951
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  637 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Drosophila melanogaster
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  III
;      MAP POSITION:  approximately map unit 26
PCT-US92-08558-1


  Query Match             23.2%;  Score 314.5;  DB 4;  Length 637;
  Best Local Similarity   30.1%;  Pred. No. 1.8e-27;
  Matches   78;  Conservative   49;  Mismatches  109;  Indels   23;  Gaps    7;

Qy      23 PQTESKNEASSR-DVVYGPQPQP----------LENQLLSEETKSTETET-------GSR 64
           |:| |   : |: | :    | |          :   |:::||      |        ||
Db      25 PKTHSTTMSDSKMDKLARMAPLPRTPLLTIWLAINMALIAQETGHKRIHTVQAATGGGSM 84

Qy      65 VGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
           :| :   | ||::   :|| ::||  |  |  | | : | |:  :| : |::|:|  | |
Db      85 LGDV-NISAILDSFSVSYDKRVRPNYGGPPVEVGVTMYVLSISSVSEVLMDFTLDFYFRQ 143

Qy     125 TWYDERLCYNDT--FESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGK 182
           | | || |      |:| :    :  :|:|||| | |::: |  |  |: :|::  |
Db     144 FWTDPRLAYRKRPGVETLSVGSEFIKNIWVPDTFFVNEKQSYFHIATTSNEFIRVHHSGS 203

Qy     183 VLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKL 242
           : :||:|| | | :::  ||||   | :   || |   :: | | :    :  :  :|
Db     204 ITRSIRLTITASCPMNLQYFPMDRQLCHIEIESFGYTMRDIRYFWRDGLSSVGMSSEVEL 263

Qy     243 FQFDFTGVSNK-TEI-ITT 259
           ||   |   : ||| :||
Db     264 PQFRVLGHRQRATEINLTT 282


RESULT  15
US-08-554-659-2
; Sequence 2, Application US/08554659
; Patent No. 5767261
;  GENERAL INFORMATION:
;    APPLICANT:  Wingate, Vincent
;    APPLICANT:  Wolff, Mark
;    TITLE OF INVENTION:  LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
;    TITLE OF INVENTION:  AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/554,659
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9732
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  488 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-554-659-2


  Query Match             23.0%;  Score 312;  DB 1;  Length 488;
  Best Local Similarity   34.4%;  Pred. No. 2.3e-27;
  Matches   62;  Conservative   34;  Mismatches   82;  Indels    2;  Gaps    1;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           | ||:::  :|| ::||  |  |  | | : | |:  || : |::|:|  | | | | ||
Db      44 SAILDSLSVSYDKRVRPNYGGPPVDVGVNMYVLSISSLSEVKMDFTLDFYFRQFWTDPRL 103

Qy     132 CYNDT--FESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
           |  :   |:| :    :  :|:|||| | |::: |  |  |: :||:  | :  :||:
Db     104 AYKKSTGVETLSVGSEFIRNIWVPDTFFVNEKQSYFHIATTSNEFIRIHHSGSITRSIRL 163

Qy     190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
           || | | : :  ||||   | :   || |   :: |||      :   :   | ||   |
Db     164 TITASCPMDLQYFPMDRQLCNIEIESFGYTMRDIRYKWNEGPNSVGVSSEVSLPQFKVLG 223


Search completed: March 11, 2000, 06:01:26
Job time: 1115 sec
```

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:06:27 ; Search time 52.39 Seconds
(without alignments)
234.091 Million cell updates/sec

Title: US-09-030-832-42_COPY_1_260
Perfect score: 1357
Sequence: 1 MLSKVLPVLLGILLILQSRV.....KLFQFDFTGVSNKTEIITTP 260

Scoring table: BLOSUM62

Searched: 142080 seqs, 47169319 residues

Database : PIR_62:*

Word size : 0

Number of hits that pass the threshold : 142080
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	661	48.7	457	2	S38296	gamma-aminobutyric
2	631	46.5	467	2	S16915	gamma-aminobutyric
3	622	45.8	474	2	S13086	gamma-aminobutyric
4	621	45.8	474	2	JH0317	gamma-aminobutyric
5	621	45.8	466	2	JH0316	gamma-aminobutyric
6	618	45.5	467	2	S19317	gamma-aminobutyric
7	618	45.5	475	2	B39272	gamma-aminobutyric
8	618	45.5	466	2	JQ0077	gamma-aminobutyric
9	608	44.8	467	2	S03905	gamma-aminobutyric
10	598	44.1	465	2	S12056	gamma-aminobutyric
11	585	43.1	464	2	JH0824	gamma-aminobutyric
12	480	35.4	453	2	S11087	gamma-aminobutyric
13	477.5	35.2	554	2	G01928	gamma-aminobutyric
14	473	34.9	552	2	S17551	gamma-aminobutyric
15	471.5	34.7	556	2	S06838	gamma-aminobutyric
16	464	34.2	493	2	A34130	gamma-aminobutyric
17	462.5	34.1	462	2	A48933	gamma-aminobutyric
18	461	34.0	492	1	CHBOA3	gamma-aminobutyric
19	461	34.0	492	2	I77911	gamma-aminobutyric
20	460	33.9	455	2	JQ0158	gamma-aminobutyric
21	460	33.9	455	2	A39062	gamma-aminobutyric
22	458.5	33.8	464	2	B34130	gamma-aminobutyric
23	456.5	33.6	456	2	A60652	gamma-aminobutyric
24	456.5	33.6	456	2	A27142	gamma-aminobutyric
25	453	33.4	455	1	CHCHA1	gamma-aminobutyric
26	447.5	33.0	451	2	JH0370	gamma-aminobutyric
27	443	32.6	451	1	ACBOG2	gamma-aminobutyric
28	443	32.6	451	2	I57947	gamma-aminobutyric
29	431	31.8	686	2	S60749	probable ligand-ga
30	429	31.6	443	2	S11396	gamma-aminobutyric
31	408	30.1	354	2	A31588	gamma-amino butyri
32	366	27.0	488	2	JH0359	gamma-aminobutyric
33	359	26.5	449	2	A34625	gamma-aminobutyric
34	356	26.2	449	2	A36303	gamma-aminobutyric
35	356	26.2	449	2	I52630	GABAA receptor del
36	351.5	25.9	474	2	B60039	gamma-aminobutyric
37	351.5	25.9	474	2	A40336	gamma-aminobutyric
38	351.5	25.9	474	2	S53530	gamma-aminobutyric
39	351.5	25.9	474	2	B27142	gamma-aminobutyric
40	336.5	24.8	473	2	A38627	gamma-aminobutyric
41	335.5	24.7	474	2	S04465	gamma-aminobutyric
42	335.5	24.7	474	2	S53531	gamma-aminobutyric
43	335.5	24.7	512	2	I52656	gamma-aminobutyric
44	333	24.5	474	2	JH0829	gamma-aminobutyric
45	333	24.5	491	2	JH0828	gamma-aminobutyric

ALIGNMENTS

RESULT 1
S38296
gamma-aminobutyric acid receptor A gamma-4 chain precursor - chicken
N;Alternate names: GABA(A) receptor gamma-4 chain
C;Species: Gallus gallus (chicken)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S38296
R;Harvey, R.J.; Kim, H.C.; Darlison, M.G.
FEBS Lett. 331, 211-216, 1993
A;Title: Molecular cloning reveals the existence of a fourth gamma subunit of the ver
A;Reference number: S38296; MUID:93387470
A;Accession: S38296
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-457 <HAR>
A;Cross-references: EMBL:X73533; NID:g414021; PIDN:CAA51939.1; PID:g414022
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein

Query Match 48.7%; Score 661; DB 2; Length 457;
Best Local Similarity 57.9%; Pred. No. 3.9e-49;
Matches 110; Conservative 44; Mismatches 36; Indels 0; Gaps 0;

```
Qy      70 EASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDE 129
           :|::|||::| |||:|||| || ||| : |:| |||:||:|:: ||||||| |:|||||
Db      48 DATQILNSLLKNYDNKLRPDIGIKPTFIDVDIYVNSIGPVSVIQMEYTIDIFFAQTWYDR 107

Qy     130 RLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
           || :| | ::| || |:||::|||||||||||||    | || |||::||: |||||||:|:
Db     108 RLRFNSTLKALTLNTNMVSRIWIPDTFFRNSKRADSHWITTPNQLLRIWNDGKVLYTLRL 167

Qy     190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
           ||:| | | :  ||||:|||| ||||: ||  |::|:|  : :|:::: :|:|:||||||
Db     168 TIEAECLLQLQNFPMDTHSCPLVFSSYGYPREEIVYRWRRYSIEVSDQRTWRLYQFDFTG 227

Qy     250 VSNKTEIITT 259
           : | :|:: |
Db     228 LRNTSEVLRT 237
```

RESULT 2
S16915
gamma-aminobutyric acid/benzodiazepine receptor gamma-3 chain precursor - mouse
N;Alternate names: GABA(A) receptor gamma-3 chain
C;Species: Mus musculus (house mouse)
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 20-Aug-1999
C;Accession: S16915; S15469
R;Wilson-Shaw, D.; Robinson, M.; Gambarana, C.; Siegel, R.E.; Sikela, J.M.
FEBS Lett. 284, 211-215, 1991
A;Title: A novel gamma subunit of the GABA(A) receptor identified using the polymeras
A;Reference number: S16915; MUID:91285135
A;Accession: S16915
A;Molecule type: mRNA
A;Residues: 1-467 <WIL>
A;Cross-references: EMBL:X59300; NID:g51121; PIDN:CAA41988.1; PID:g51122
C;Superfamily: acetylcholine receptor
C;Keywords: disulfide bond; glycoprotein; ion channel; neurotransmitter receptor; tra

```
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-467/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-3 chain #status
F;255-277/Domain: transmembrane #status predicted <TM1>
F;281-303/Domain: transmembrane #status predicted <TM2>
F;315-337/Domain: transmembrane #status predicted <TM3>
F;444-467/Domain: transmembrane #status predicted <TM4>
F;110,228/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;171-185/Disulfide bonds: #status predicted


  Query Match             46.5%;  Score 631;  DB 2;  Length 467;
  Best Local Similarity   46.6%;  Pred. No. 1.5e-46;
  Matches  124;  Conservative   46;  Mismatches   58;  Indels   38;  Gaps    4;

Qy       1 MLSKVLPVLLGILLILQS-------RVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEE 53
           | :|:|     :|| | |       |||  : |::: |::  |  |:||
Db       1 MAAKLL-----LLLCLFSGLHARSRRVE--EDENEDSPSNQKWVLAPKPQD--------- 45

Qy      54 TKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILD 113
                    :|: ||| :|  || |||| || ||||: |:| |||:||:| ::
Db      45 --------------TDATLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSIN 89

Qy     114 MEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
           ||| ||| |:||| | || :| | ::| || |:|  :||||| |||||    | || |||
Db      90 MEYQIDIFFAQTWTDSRLRFNSTMKTLTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQ 149

Qy     174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLE 233
           ::||: |||:|||:|:||:| | | :  ||||:|:|||:|||: ||: ||||:|    :|
Db     150 LLRIWNDGKILYTLRLTINAECQLQLHNFPMDAHACPLTFSSYGYPKEEMIYRWRKNSVE 209

Qy     234 INEKNSWKLFQFDFTGVSNKTEIITT 259
             :: ||:|:|||| |: | |||:||
Db     210 AADQKSWRLYQFDFMGLRNTTEIVTT 235


RESULT   3
S13086
gamma-aminobutyric acid/benzodiazepine receptor A gamma-2 chain precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S13086
R;Glencorse, T.A.; Bateson, A.N.; Darlison, M.G.
Nucleic Acids Res. 18, 7157, 1990
A;Title: Sequence of the chicken GABA(A) receptor gamma-2-subunit cDNA.
A;Reference number: S13086; MUID:91088318
A;Accession: S13086
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <GLE>
A;Cross-references: EMBL:X54944; NID:g62896; PIDN:CAA38704.1; PID:g62897
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; phosphoprotein; transmembrane protein


  Query Match             45.8%;  Score 622;  DB 2;  Length 474;
  Best Local Similarity   55.8%;  Pred. No. 9.2e-46;
  Matches  106;  Conservative   39;  Mismatches   45;  Indels    0;  Gaps    0;

Qy      70 EASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDE 129
           : : ||| :|  ||:|||| || ||||:  :: |||:||:: ::|||||| |:|||||
Db      64 DVTLILNGLLEGYDNKLRPDIGVKPTVIHTDMYVNSIGPVNAINMEYTIDIFFAQTWYDR 123

Qy     130 RLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
           || :| | : | || |:| ::|||||||||||:   |.|| ||:|:||: ||:||||:|:
Db     124 RLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVLYTLRL 183

Qy     190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
           |||| | | :  ||||:|||| |||: ||  |:||:|:   :|: :  ||:|:|| |||
Db     184 TIDAECQLQLHNFPMDAHSCPLEFSSYGYPREEIIYQWKRSSVEVGDTRSWRLYQFSFTG 243

Qy     250 VSNKTEIITT 259
           : | ||:: |
Db     244 LRNTTEVVKT 253


RESULT   4
JH0317
gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 13-Sep-1996
C;Accession: JH0317
R;Kofuji, P.; Wang, J.B.; Moss, S.J.; Huganir, R.L.; Burt, D.R.
J. Neurochem. 56, 713-715, 1991
A;Title: Generation of two forms of the gamma-aminobutyric acid A receptor gamma2-sub
A;Reference number: JH0316; MUID:91108470
A;Accession: JH0317
A;Molecule type: mRNA
A;Residues: 1-474 <KOF>
A;Cross-references: GB:M57522
A;Experimental source: brain
C;Superfamily: acetylcholine receptor
C;Keywords: alternative splicing; glycoprotein; ion channel; neurotransmitter recepto
F;1-38/Domain: signal sequence #status predicted <SIG>
F;29-375,384-474/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-2 cha
F;39-474/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain, long
F;39-272/Domain: extracellular #status predicted <EXT>
F;273-295/Domain: transmembrane #status predicted <TM1>
F;299-321/Domain: transmembrane #status predicted <TM2>
F;333-355/Domain: transmembrane #status predicted <TM3>
F;356-450/Domain: intracellular #status predicted <INT>
F;451-473/Domain: transmembrane #status predicted <TM4>
F;51,128,246/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;381/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicte


  Query Match             45.8%;  Score 621;  DB 2;  Length 474;
  Best Local Similarity   52.7%;  Pred. No. 1.1e-45;
  Matches  108;  Conservative   41;  Mismatches   54;  Indels    2;  Gaps    1;

Qy      57 TETETGSRVGKLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDM 114
           |  :|     |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|
Db      49 TSNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINM 108

Qy     115 EYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQM 174
           |||||| |:||||| || :| | : | || |:| ::||||||||||:   | || ||:|
Db     109 EYTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRM 168

Qy     175 VRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEI 234
           :||: ||:||||:|:|||| | | :  |||| ||||| |||: ||  |::|:|:   :|:
Db     169 LRIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEV 228

Qy     235 NEKNSWKLFQFDFTGVSNKTEIITT 259
             :  ||:|:|| | |: | ||:: |
Db     229 GDTRSWRLYQFSFVGLRNTTEVVKT 253


RESULT   5
JH0316
gamma-aminobutyric acid A receptor gamma 2 chain alternatively spliced precursor - mo
C;Species: Mus musculus (house mouse)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 04-Sep-1998
C;Accession: JH0316
R;Kofuji, P.; Wang, J.B.; Moss, S.J.; Huganir, R.L.; Burt, D.R.
J. Neurochem. 56, 713-715, 1991
A;Title: Generation of two forms of the gamma-aminobutyric acid A receptor gamma2-sub
A;Reference number: JH0316; MUID:91108470
A;Accession: JH0316
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-466 <KOF>
A;Cross-references: GB:M57522
C;Superfamily: acetylcholine receptor


  Query Match             45.8%;  Score 621;  DB 2;  Length 466;
  Best Local Similarity   52.7%;  Pred. No. 1.1e-45;
```

```
  Matches  108;  Conservative   41;  Mismatches   54;  Indels    2;  Gaps    1;

Qy      57 TETETGSRVGKLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDM 114
           |  :|     |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|
Db      49 TSNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINM 108

Qy     115 EYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQM 174
           |||||| |:||||| || :| | : | || |:| ::||||||||||:   | || ||:|
Db     109 EYTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRM 168

Qy     175 VRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEI 234
           :||: ||:||||:|:|||| | |. :  |||| ||||| ||||: ||  |::|:|:   :|:
Db     169 LRIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEV 228

Qy     235 NEKNSWKLFQFDFTGVSNKTEIITT 259
           :  ||:|:|| | |: | ||:: |
Db     229 GDTRSWRLYQFSFVGLRNTTEVVKT 253


RESULT   6
S19317
gamma-aminobutyric acid/benzodiazepine receptor gamma-3 chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: S19317; A40221
R;Knoflach, F.; Rhyner, T.; Villa, M.; Kellenberger, S.; Drescher, U.; Malherbe, P.; Sig
FEBS Lett. 293, 191-194, 1991
A;Title: The gamma3-subunit of the GABA(A)-receptor confers sensitivity to benzodiazepin
A;Reference number: S19317; MUID:92070559
A;Accession: S19317
A;Molecule type: mRNA
A;Residues: 1-467 <KNO>
A;Cross-references: EMBL:X63324; NID:g56181; PIDN:CAA44930.1; PID:g56182
R;Herb, A.; Wisden, W.; Luddens, H.; Puia, G.; Vicini, S.; Seeburg, P.H.
Proc. Natl. Acad. Sci. U.S.A. 89, 1433-1437, 1992
A;Title: The third gamma subunit of the gamma-aminobutyric acid type A receptor family.
A;Reference number: A40221; MUID:92159063
A;Accession: A40221
A;Molecule type: mRNA
A;Residues: 1-467 <HER>
A;Note: sequence extracted from NCBI backbone (NCBIP:82491)
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein


  Query Match             45.5%;  Score 618;  DB 2;  Length 467;
  Best Local Similarity   46.6%;  Pred. No. 2e-45;
  Matches  124;  Conservative   45;  Mismatches   59;  Indels   38;  Gaps    5;

Qy       1 MLSKVLPVLLGILLILQS-------RVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEE 53
           | :|:|     :|| | |       |||  : :|::  |::  |  |
Db       1 MAAKLL-----LLLCLFSGLHARSRRVE--EDDSEDSPSNQKWVLAP------------- 41

Qy      54 TKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILD 113
            || :|          : : ||| :|  || |||| || ||||: |:| |||:||:| ::
Db      41 -KSQDT----------DVTLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSIN 89

Qy     114 MEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
           ||| ||| |:||| | || :| | : | || |:|  :|||| |||||    | || |||
Db      90 MEYQIDIFFAQTWTDSRLRFNSTMKILTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQ 149

Qy     174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLE 233
           ::||: |||:|||:|:|||:| | | :  ||||:|:|||:|||: ||: ||||:|    :|
Db     150 LLRIWNDGKILYTLRLTINAECQLQLHNFPMDAHACPLTFSSYGYPKEEMIYRWRKNSVE 209

Qy     234 INEKNSWKLFQFDFTGVSNKTEIITT 259
             :: ||:|:|||| |: | |||:||
Db     210 AADQKSWRLYQFDFMGLRNTTEIVTT 235


RESULT   7
B39272
gamma-aminobutyric acid receptor A gamma-2L chain - bovine
N;Contains: gamma-aminobutyric acid receptor A gamma-2S chain
C;Species: Bos primigenius taurus (cattle)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 30-May-1997
C;Accession: B39272; A39272
R;Whiting, P.; McKernan, R.M.; Iversen, L.L.
Proc. Natl. Acad. Sci. U.S.A. 87, 9966-9970, 1990
A;Title: Another mechanism for creating diversity in gamma-aminobutyrate type A recep
sphorylation site.
A;Reference number: A39272; MUID:91088632
A;Accession: B39272
A;Molecule type: mRNA
A;Residues: 1-475 <WHI>
A;Cross-references: GB:M55563
A;Accession: A39272
A;Molecule type: mRNA
A;Residues: 1-376,385-475 <WH2>
A;Cross-references: GB:M55563
C;Superfamily: acetylcholine receptor
C;Keywords: alternative splicing; neurotransmitter receptor; phosphoprotein; transmem
F;1-475/Product: gamma-aminobutyric acid receptor A gamma-2L chain #status predicted
F;1-376,385-475/Product: gamma-aminobutyric acid receptor A gamma-2S chain #status pr
F;382/Binding site: phosphate (Ser) (covalent) #status predicted


  Query Match             45.5%;  Score 618;  DB 2;  Length 475;
  Best Local Similarity   54.4%;  Pred. No. 2e-45;
  Matches  106;  Conservative   40;  Mismatches   47;  Indels    2;  Gaps    1;

Qy      67 KLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
           |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|||||||| |:|
Db      60 KVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFAQ 119

Qy     125 TWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVL 184
           |||| || :| | : | || |:| ::||||||||||:   | || ||:|:||: ||:||
Db     120 TWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVL 179

Qy     185 YTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQ 244
           ||:|:|||| | | :  |||| ||||| |||: ||  |::|:|:   :|: :  ||:|:|
Db     180 YTLRLTIDAECQLQLHNFPMDGHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQ 239

Qy     245 FDFTGVSNKTEIITT 259
           | | |: | ||:: |
Db     240 FSFVGLRNTTEVVKT 254


RESULT   8
JQ0077
gamma-aminobutyric acid receptor A gamma-2 chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Aug-1999
C;Accession: JQ0077; A37164
R;Shivers, B.D.; Killisch, I.; Sprengel, R.; Sontheimer, H.; Koehler, M.; Schofield,
Neuron 3, 327-337, 1989
A;Title: Two novel GABA-A receptor subunits exist in distinct neuronal subpopulations
A;Reference number: JQ0076; MUID:90380375
A;Accession: JQ0077
A;Molecule type: mRNA
A;Residues: 1-466 <SHI>
A;Cross-references: GB:L08497; NID:g204217; PIDN:AAC42036.1; PID:g204218
A;Experimental source: brain
R;Malherbe, P.; Sigel, E.; Baur, R.; Persohn, E.; Richards, J.G.; Mohler, H.
J. Neurosci. 10, 2330-2337, 1990
A;Title: Functional characteristics and sites of gene expression of the alpha-1,beta-
A;Reference number: A37164; MUID:90331051
A;Accession: A37164
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-21,'I',23-466 <MAL>
C;Comment: Neurotransmission effected by gamma-aminobutyric acid (GABA) is mediated m
C;Comment: The GABA-A receptor consists of subunits that are structurally related to
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F;1-38/Domain: signal sequence #status predicted <SIG>
```

```
F;39-466/Product: gamma-aminobutyric acid A receptor gamma-2 chain #status predicted <MA
F;273-295/Domain: transmembrane #status predicted <TM1>
F;299-321/Domain: transmembrane #status predicted <TM2>
F;333-355/Domain: transmembrane #status predicted <TM3>
F;443-465/Domain: transmembrane #status predicted <TM4>
F;51,128,246/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;189-203/Disulfide bonds: #status predicted


  Query Match             45.5%;  Score 618;  DB 2;  Length 466;
  Best Local Similarity   54.4%;  Pred. No. 2e-45;
  Matches  106;  Conservative   40;  Mismatches   47;  Indels    2;  Gaps    1;

Qy      67 KLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
           |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|||||||| |:|
Db      59 KVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFAQ 118

Qy     125 TWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVL 184
           |||| || :| | : | || |:| ::|||||||||||:   | || ||:|:||: ||:||
Db     119 TWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVL 178

Qy     185 YTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQ 244
           ||:|:|||| | | :  |||| ||||| |||: ||  |::|:|:   :|: :  ||:|:|
Db     179 YTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQ 238

Qy     245 FDFTGVSNKTEIITT 259
           | | |: | ||:: |
Db     239 FSFVGLRNTTEVVKT 253


RESULT   9
S03905
gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Aug-1999
C;Accession: S03905
R;Pritchett, D.B.; Sontheimer, H.; Shivers, B.D.; Ymer, S.; Kettenmann, H.; Schofield, P
Nature 338, 582-585, 1989
A;Title: Importance of a novel GABA(A) receptor subunit for benzodiazepine pharmacology.
A;Reference number: S03905; MUID:89181956
A;Accession: S03905
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-467 <PRI>
A;Cross-references: GB:X15376; NID:g31636; PIDN:CAA33437.1; PID:g31637
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein
F;1-39/Domain: signal sequence #status predicted <SIG>
F;40-467/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain #status


  Query Match             44.8%;  Score 608;  DB 2;  Length 467;
  Best Local Similarity   53.3%;  Pred. No. 1.4e-44;
  Matches  104;  Conservative   41;  Mismatches   48;  Indels    2;  Gaps    1;

Qy      67 KLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
           |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|||||||| |:|
Db      60 KVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFAQ 119

Qy     125 TWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVL 184
            ||| || :| | : | || |:| ::|||||||||||:   | || ||:|:||: ||:||
Db     120 MWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVL 179

Qy     185 YTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQ 244
           |::|:|||| | | :  |||| ||||| |||: ||  |::|:|:   :|: :  ||:|:|
Db     180 YSLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQ 239

Qy     245 FDFTGVSNKTEIITT 259
           | | |: | ||:: |
Db     240 FSFVGLRNTTEVVKT 254


RESULT  10
S12056
gamma-aminobutyric acid/benzodiazepine receptor gamma-1 chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S12056
R;Ymer, S.; Draguhn, A.; Wisden, W.; Werner, P.; Keinaenen, K.; Schofield, P.R.; Spre
EMBO J. 9, 3261-3267, 1990
A;Title: Structural and functional characterization of the gamma(1) subunit of GABA(A
A;Reference number: S12056; MUID:91006020
A;Accession: S12056
A;Molecule type: mRNA
A;Residues: 1-465 <YME>
A;Cross-references: GB:X57514; NID:g56175; PIDN:CAA40739.1; PID:g56176
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein


  Query Match             44.1%;  Score 598;  DB 2;  Length 465;
  Best Local Similarity   53.7%;  Pred. No. 1e-43;
  Matches  102;  Conservative   44;  Mismatches   44;  Indels    0;  Gaps    0;

Qy      70 EASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDE 129
           : ::|||::|  ||:|||| || :|||:  :: |||:||:  ::|||||||||:|||:|
Db      63 DITQILNSLLQGYDNKLRPDIGVRPTVIETDVYVNSIGPVDPINMEYTIDIIFAQTWFDS 122

Qy     130 RLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
           || :| | : |:|| |:| ::|||||||||||:::  | || ||:::||: ||:||||:|:
Db     123 RLKFNSTMKVLMLNSNMVGKIWIPDTFFRNSRKSDAHWITTPNRLLRIWSDGRVLYTLRL 182

Qy     190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
           ||:| | | :  |||| ||||| |||: ||:||: |||:   :|: :   |:|:|| | |
Db     183 TINAECYLQLHNFPMDEHSCPLEFSSYGYPKNEIEYKWKKPSVEVADPKYWRLYQFAFVG 242

Qy     250 VSNKTEIITT 259
           : | |||  |
Db     243 LRNSTEISHT 252


RESULT  11
JH0824
gamma-aminobutyric acid A receptor gamma 1 chain precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
C;Accession: JH0824
R;Glencorse, T.A.; Darlison, M.G.; Barnard, E.A.; Bateson, A.N.
J. Neurochem. 61, 2294-2302, 1993
A;Title: Sequence and novel distribution of the chicken homologue of the mammalian ga
A;Reference number: JH0824; MUID:94065817
A;Accession: JH0824
A;Molecule type: mRNA
A;Residues: 1-464 <GLE>
C;Comment: This protein mediates gamma-aminobutyric acid-induced synaptic inhibition
C;Superfamily: acetylcholine receptor
C;Keywords: ion channel; neurotransmitter receptor; transmembrane protein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-464/Product: gamma-aminobutyric acid A receptor gamma 1 chain #status predicted
F;269-290/Domain: transmembrane #status predicted <TM1>
F;295-316/Domain: transmembrane #status predicted <TM2>
F;328-349/Domain: transmembrane #status predicted <TM3>
F;441-464/Domain: transmembrane #status predicted <TM4>


  Query Match             43.1%;  Score 585;  DB 2;  Length 464;
  Best Local Similarity   52.6%;  Pred. No. 1.3e-42;
  Matches  100;  Conservative   43;  Mismatches   47;  Indels    0;  Gaps    0;

Qy      70 EASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDE 129
           : : ||:::|  ||:|||| || : ||:  :: |||:||:  ::|||||||||:|||||
Db      59 DVTHILDSLLQGYDNKLRPDIGVRTTVIETDVYVNSIGPVDPINMEYTIDIIFAQTWYDS 118

Qy     130 RLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
           || :| : : |:|| |:| ::|||||||||||:::  | || ||:::||: ||:||||:|:
Db     119 RLKFNSSMKVLMLNSNMVGKIWIPDTFFRNSRKSDAHWITTPNRLLRIWSDGRVLYTLRL 178
```

```
Qy    190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
          ||:| | | :  |||| ||||| |||: || ||: |||:   :|: :   |:|:|| | |
Db    179 TINAECYLQLHNFPMDEHSCPLEFSSYGYPRNEIEYKWKKTSVEVADPKYWRLYQFAFVG 238

Qy    250 VSNKTEIITT 259
          : | |||  |
Db    239 LRNTTEISHT 248
```

RESULT 12
S11087
gamma-aminobutyric acid receptor A, cerebellar - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Feb-1997
C;Accession: S11087
R;Lueddens, H.; Pritchett, D.B.; Koehler, M.; Killisch, I.; Keinaenen, K.; Monyer, H.; S
Nature 346, 648-651, 1990
A;Title: Cerebellar GABA(A) receptor selective for a behavioural alcohol antagonist.
A;Reference number: S11087; MUID:90348963
A;Accession: S11087
A;Molecule type: mRNA
A;Residues: 1-453 <LUE>
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein

```
  Query Match             35.4%;  Score 480;  DB 2;  Length 453;
  Best Local Similarity   46.0%;  Pred. No. 1.3e-33;
  Matches   87;  Conservative   43;  Mismatches   55;  Indels    4;  Gaps    2;

Qy     72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
          ||||: :|  ||::|||| |   | |  :| | | ||:| ::|||||:|: | ||| ||||
Db     33 SRILDNLLEGYDNRLRPGFGGAVTEVKTDIYVTSFGPVSDVEMEYTMDVFFRQTWTDERL 92

Qy    132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
          :   | | ||  :||::| ||||||| |::  | :| ||:: |:  :| :|||:|:||
Db     93 KFKGPAEILSLNNLMVSKIWTPDTFFRNGKKSIAHNMTTPNKLFRLMHNGTILYTMRLTI 152

Qy    192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLEINEKNSWKLFQFDFT 248
          :| | : :: |||| |:||| | |::||::|:|| |:    : :|: |::|  | |:|
Db    153 NADCPMRLVNFPMDGHACPLKFGSYAYPKSEIIYTWKKGPLYSVEVPEESS-SLLQYDLI 211

Qy    249 GVSNKTEII 257
          | :  :| |
Db    212 GQTVSSETI 220
```

RESULT 13
G01928
gamma-aminobutyric acid receptor A alpha-4 - human
N;Alternate names: GABA(A) receptor alpha-4 chain
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C;Accession: G01928; I38936
R;Yang, W.
submitted to the EMBL Data Library, June 1995
A;Reference number: G08852
A;Accession: G01928
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-554 <YAN>
A;Cross-references: EMBL:U30461; NID:g905392; PIDN:AAB52519.1; PID:g905393
R;McLean, P.J.; Farb, D.H.; Russek, S.J.
Genomics 26, 580-586, 1995
A;Title: Mapping of the alpha 4 subunit gene (GABRA4) to human chromosome 4 defines an a
ed from an ancestral cluster.
A;Reference number: I38936; MUID:95331795
A;Accession: I38936
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-57 <MCL>
A;Cross-references: EMBL:U20166; NID:g924604; PIDN:AAA74743.1; PID:g924605
C;Genetics:
A;Gene: GDB:GABRA4
A;Cross-references: GDB:370881; OMIM:137141
A;Map position: 4p14-4q12
A;Introns: 29/2
A;Note: the list of introns is incomplete
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; neurotransmitter receptor
F;144,157,402,408/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
  Query Match             35.2%;  Score 477.5;  DB 2;  Length 554;
  Best Local Similarity   43.8%;  Pred. No. 2.8e-33;
  Matches   95;  Conservative   41;  Mismatches   64;  Indels   17;  Gaps    4;

Qy     44 PLENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAV 103
          | :||   ||   ||  |              |||:::|  ||::|||| |   | |  :| |
Db     34 PGQNQ--KEEKLCTENFT----------RILDSLLDGYDNRLRPGFGGPVTEVKTDIYV 80

Qy    104 NSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRT 163
          | ||:| ::|||||:|: | ||| |:|| |:   | | ||  :|:::| ||||||| |::
Db     81 TSFGPVSDVEMEYTMDVFFRQTWIDKRLKYDGPIEILRLNNMMVTKVWTPDTFFRNGKKS 140

Qy    164 HEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEM 223
          | :| ||:: || ::| :|||:|:|| | | : :: |||| |:||| | |::||::||
Db    141 VSHNMTAPNKLFRIMRNGTILYTMRLTISAECPMRLVDFPMDGHACPLKFGSYAYPKSEM 200

Qy    224 IYKW---ENFKLEINEKNSWKLFQFDFTGVSNKTEII 257
          || |       :|:  | |  | |:|  | :  :| |
Db    201 IYTWTKGPEKSVEV-PKESSSLVQYDLIGQTVSSETI 236
```

RESULT 14
S17551
gamma-aminobutyric acid/benzodiazepine receptor alpha-4 chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S17551
R;Wisden, W.; Herb, A.; Wieland, H.; Keinaenen, K.; Lueddens, H.; Seeburg, P.H.
FEBS Lett. 289, 227-230, 1991
A;Title: Cloning, pharmacological characteristics and expression pattern of the rat G
A;Reference number: S17551; MUID:92008629
A;Accession: S17551
A;Molecule type: mRNA
A;Residues: 1-552 <WIS>
A;Cross-references: GB:S55933; NID:g236011; PIDN:AAB19902.1; PID:g236012
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein

```
  Query Match             34.9%;  Score 473;  DB 2;  Length 552;
  Best Local Similarity   38.5%;  Pred. No. 6.8e-33;
  Matches  101;  Conservative   45;  Mismatches   74;  Indels   42;  Gaps    5;

Qy      1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
          : | |   || :| :     | |   ||:|
Db     12 LCSGVSLALLHVLCLATCLNESPGQNSKDE---------------------------- 42

Qy     61 TGSRVGKL-PE-ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTI 118
                || ||  :|||:::|  ||::|||| |   | |  :| | | ||:| ::||||:
Db     42 ------KLCPENFTRILDSLLDGYDNRLRPGFGGPVTEVKTDIYVTSFGPVSDVEMEYTM 95

Qy    119 DIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIY 178
          |: | ||| |:|| |:   | | ||  :|:::| |||||| |::  | :| ||:: ||
Db     96 DVFFRQTWIDKRLKYDGPIEILRLNNMMVTKVWTPDTFFRNGKKSVSHNMTAPNKLFRIM 155

Qy    179 KDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEIN 235
          ::| :|||:|:|| | | : :: |||| |:||| | |::||::|||| |       :|:
Db    156 RNGTILYTMRLTISAECPMRLVDFPMDGHACPLKFGSYAYPKSEMIYTWTKGPEKSVEV- 215

Qy    236 EKNSWKLFQFDFTGVSNKTEII 257
          | |  | |:|  | :  :| |
Db    215 PKESSSLVQYDLIGQTVSSETI 236
```

```
RESULT  15
S06838
gamma-aminobutyric acid/benzodiazepine receptor alpha-4 chain precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
C;Accession: S06838
R;Ymer, S.; Draguhn, A.; Koehler, M.; Schofield, P.R.; Seeburg, P.H.
FEBS Lett. 258, 119-122, 1989
A;Title: Sequence and expression of a novel GABA(A) receptor alpha subunit.
A;Reference number: S06838; MUID:90076471
A;Accession: S06838
A;Molecule type: mRNA
A;Residues: 1-556 <YME>
A;Cross-references: EMBL:X61456; NID:g360; PIDN:CAA43696.1; PID:g361
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-556/Product: gamma-aminobutyric acid/benzodiazepine receptor alpha-4 chain #status


  Query Match             34.7%;  Score 471.5;  DB 2;  Length 556;
  Best Local Similarity   43.3%;  Pred. No. 9.3e-33;
  Matches   94;  Conservative   41;  Mismatches   65;  Indels   17;  Gaps    4;

Qy      44 PLENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAV 103
           | :||   ||    |  |           |||:::|  ||::|||| |   | |  :| |
Db      34 PGQNQ--KEEKLCPENFT----------RILDSLLDGYDNRLRPGFGGPVTEVKTDIYV 80

Qy     104 NSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRT 163
            | ||:| ::|||||:|: | ||| |:|| |:   | | ||  :|:::| ||||||| |::
Db      81 TSFGPVSDVEMEYTMDVFFRQTWIDKRLKYDGPIEILRLNNMMVTKVWTPDTFFRNGKKS 140

Qy     164 HEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEM 223
              | :| ||:: || ::| :|||:|:|| | | : :: |||| |:||| | |::||::||
Db     141 VSHNMTAPNKLFRIMRNGTILYTMRLTISAECPMRLVDFPMDGHACPLKFGSYAYPKSEM 200

Qy     224 IYKW---ENFKLEINEKNSWKLFQFDFTGVSNKTEII 257
           || |       :|:  | |  | |:|  | :  :| |
Db     201 IYTWTKGPEKSVEV-PKESSSLVQYDLIGQTVSSETI 236


Search completed: March 11, 2000, 06:06:28
Job time: 126 sec
```

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:18:29 ; Search time 41.51 Seconds
(without alignments)
434.278 Million cell updates/sec

Title: US-09-030-832-42_COPY_1_260
Perfect score: 1357
Sequence: 1 MLSKVLPVLLGILLILQSRV.....KLFQFDFTGVSNKTEIITTP 260

Scoring table: BLOSUM62

Searched: 225878 seqs, 69334122 residues

Database : SPTREMBL_12:*

Word size : 0

Number of hits that pass the threshold : 225878
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1357	100.0	505	4	Q99520	Q99520 homo sapien
2	1354	99.8	506	4	O15346	O15346 homo sapien
3	647	47.7	384	11	O55209	O55209 rattus norv
4	481.5	35.5	438	13	Q90288	Q90288 carassius a
5	477	35.2	286	11	O54736	O54736 mus musculu
6	431	31.8	686	5	Q24352	Q24352 drosophila
7	362.5	26.7	545	5	O18276	O18276 caenorhabdi
8	347.5	25.6	466	13	Q9YGQ3	Q9ygq3 morone amer
9	340	25.1	499	5	O17555	O17555 caenorhabdi
10	339.5	25.0	476	13	Q9YGQ4	Q9ygq4 morone amer
11	338	24.9	472	5	Q25035	Q25035 haemonchus
12	337	24.8	1187	5	Q19146	Q19146 caenorhabdi
13	335.5	24.7	512	4	Q16323	Q16323 homo sapien
14	333	24.5	430	13	Q90590	Q90590 gallus gall
15	329	24.2	478	5	P92023	P92023 caenorhabdi
16	328	24.2	479	13	Q9YGQ5	Q9ygq5 morone amer
17	326	24.0	449	4	O75816	O75816 homo sapien
18	325	23.9	473	13	O42157	O42157 morone amer
19	324	23.9	478	5	O17548	O17548 caenorhabdi
20	323	23.8	453	13	O57430	O57430 fugu rubrip
21	322	23.7	606	5	Q24561	Q24561 drosophila
22	319	23.5	657	5	O17547	O17547 caenorhabdi
23	319	23.5	448	5	Q9Y0I2	Q9y0i2 caenorhabdi
24	318.5	23.5	347	5	Q23074	Q23074 caenorhabdi
25	314.5	23.2	444	13	O93430	O93430 brachydanio
26	311	22.9	494	5	Q9XZW0	Q9xzw0 heliothis v
27	310.5	22.9	550	5	O17145	O17145 lucilia cup
28	310	22.8	601	5	P92138	P92138 drosophila
29	309	22.8	496	5	O18468	O18468 heliothis v
30	307.5	22.7	243	5	O17308	O17308 tribolium c
31	305	22.5	434	5	Q17328	Q17328 caenorhabdi
32	304	22.4	481	5	O18471	O18471 heliothis v
33	302.5	22.3	533	5	Q16896	Q16896 aedes aegyp
34	301.5	22.2	487	5	Q9Y0I5	Q9y0i5 caenorhabdi
35	301.5	22.2	475	5	Q9Y0I4	Q9y0i4 caenorhabdi
36	301.5	22.2	506	5	Q9Y0I3	Q9y0i3 caenorhabdi
37	301	22.2	438	5	O46124	O46124 haemonchus
38	301	22.2	461	5	Q17327	Q17327 caenorhabdi
39	301	22.2	495	5	O17793	O17793 caenorhabdi
40	298	22.0	469	5	O46123	O46123 haemonchus
41	297.5	21.9	416	5	Q17367	Q17367 caenorhabdi
42	297.5	21.9	430	5	Q17369	Q17369 caenorhabdi
43	297.5	21.9	654	5	O01436	O01436 caenorhabdi
44	295	21.7	453	5	O77295	O77295 drosophila
45	293	21.6	456	5	Q94900	Q94900 drosophila

ALIGNMENTS

RESULT 1
Q99520
ID Q99520 PRELIMINARY; PRT; 505 AA.
AC Q99520;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE PUTATIVE GABA-GATED CHLORIDE CHANNEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97238072.
RA GARRET M., BASCLES L., BOUE-GRABOT E., SARTOR P., CHARRON G.,
RA BLOCH B., MARGOLSKEE R.F.;
RT "An mRNA encoding a putative GABA-gated chloride channel is expressed
RT in the human cardiac conduction system.";
RL J. Neurochem. 68:1382-1389(1997).
DR EMBL; Y07637; CAA68914.1; -.
DR PFAM; PF00065; neur_chan; 2.
DR PRINTS; PR00253; GABAARECEPTR.
SQ SEQUENCE 505 AA; 57856 MW; 1E6B104C CRC32;

Query Match 100.0%; Score 1357; DB 4; Length 505;
Best Local Similarity 100.0%; Pred. No. 9.7e-113;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60

Qy      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120

Qy     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180

Qy     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240

Qy     241 KLFQFDFTGVSNKTEIITTP 260
           ||||||||||||||||||||
Db     241 KLFQFDFTGVSNKTEIITTP 260
```

```
RESULT   2
O15346
ID   O15346      PRELIMINARY;      PRT;   506 AA.
AC   O15346;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GABA RECEPTOR EPSILON SUBUNIT.
GN   GABRE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 97480709.
RA   WILKE K., GAUL R., KLAUCK S.M., POUSTKA A.;
RT   "A gene in human chromosome band Xq28 (GABRE) defines a putative new
RT   subunit class of the GABAA neurotransmitter receptor.";
RL   Genomics 45:1-10(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   HANNA M.C., HALES T.G., KIRKNESS E.F.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Y09765; CAA70904.1; -.
DR   EMBL; U92283; AAB94645.1; -.
DR   EMBL; U92281; AAB94645.1; JOINED.
DR   EMBL; U92282; AAB94645.1; JOINED.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00253; GABAARECEPTR.
SQ   SEQUENCE   506 AA;  57971 MW;  95B5B1C4 CRC32;

  Query Match             99.8%;  Score 1354;  DB 4;  Length 506;
  Best Local Similarity   99.6%;  Pred. No. 1.8e-112;
  Matches  259;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60

Qy      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
           ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEISVNSLGPLSILDMEYTIDI 120

Qy     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180

Qy     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240

Qy     241 KLFQFDFTGVSNKTEIITTP 260
           ||||||||||||||||||||
Db     241 KLFQFDFTGVSNKTEIITTP 260


RESULT   3
O55209
ID   O55209      PRELIMINARY;      PRT;   384 AA.
AC   O55209;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   GABA-A RECEPTOR EPSILON SUBUNIT (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   HANNA M.C., HALES T.G., KIRKNESS E.F.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U92284; AAB93879.1; -.
DR   PFAM; PF00065; neur_chan; 2.
FT   NON_TER       1      1
SQ   SEQUENCE   384 AA;  45465 MW;  E5D0E1B9 CRC32;

  Query Match             47.7%;  Score 647;  DB 11;  Length 384;
  Best Local Similarity   82.7%;  Pred. No. 9.1e-50;
  Matches  115;  Conservative   15;  Mismatches    9;  Indels    0;  Gaps    0;

Qy     122 FSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDG 181
           | |||||||||||||||:|:|:||||||||||||||||||||| |::||:|||| |:|||
Db       1 FYQTWYDERLCYNDTFETLILHGNVVSQLWIPDTFFRNSKRTQEYDITIPNQMALIHKDG 60

Qy     182 KVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWK 241
           |||||:|||||| |||||| |||||||||||||||| |:||||||||||:|: ||:||
Db      61 KVLYTVRMTIDARCSLHMLNFPMDSHSCPLSFSSFSYDEHEMIYKWENFKLKIDAKNTWK 120

Qy     242 LFQFDFTGVSNKTEIITTP 260
           | :||||||:||||||:||
Db     121 LLEFDFTGVNNKTEIISTP 139


RESULT   4
Q90288
ID   Q90288      PRELIMINARY;      PRT;   438 AA.
AC   Q90288;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   NEUROTRANSMITTER RECEPTOR ALPHA SUBUNIT PRECURSOR.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC   Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC   Cyprinoidea; Cyprinidae; Cyprininae; Carassius.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 96373714.
RA   BAHN S., HARVEY R.J., DARLISON M.G., WISDEN W.;
RT   "Conservation of gamma-aminobutyric acid type A receptor alpha 6
RT   subunit gene expression in cerebellar granule cells.";
RL   J. Neurochem. 66:1810-1818(1996).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; X94342; CAA64068.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
DR   PRINTS; PR01079; GABAARALPHA.
KW   Signal; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW   Transmembrane.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    483       NEUROTRANSMITTER RECEPTOR ALPHA SUBUNIT.
SQ   SEQUENCE   438 AA;  49982 MW;  ED9DBE5C CRC32;

  Query Match             35.5%;  Score 481.5;  DB 13;  Length 438;
  Best Local Similarity   45.5%;  Pred. No. 5.6e-35;
  Matches   90;  Conservative   44;  Mismatches   59;  Indels    5;  Gaps    3;

Qy      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
           | :|| |   :|||: :|  ||::|||| |   | |  :| | | ||:| ::||||:|:
Db      22 TETRV-YLDNITRILDRLLDGYDNRLRPGFGGPVTEVKTDIFVTSFGPVSDVEMEYTMDV 80

Qy     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
           | ||| |:|| :    | | ||  :||::| ||||||| ||:  | :| ||:: || ::
Db      81 FFRQTWIDDRLKFEGPIEILRLNNLMVSKIWTPDTFFRNGKRSISHNMTTPNKLFRIMQN 140

Qy     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLEINEK 237
```

```
          | :|||:|:||:| | : :: |||| ||||| | |::|| :|:::| |:    | :|: ::
Db    141 GTILYTMRLTINAECPMRLINFPMDGHSCPLKFGSYAYPMSEIVYTWKKGPLFSVEVPQE 200

Qy    238 NSWKLFQFDFTGVSNKTE 255
          :|  | |:|  | :  :|
Db    201 SS-SLLQYDLIGQTVSSE 217


RESULT   5
O54736
ID   O54736      PRELIMINARY;      PRT;   286 AA.
AC   O54736;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GAMMA-AMINOBUTYRIC ACID A RECPTOR, SUBUNIT ALPHA 6 (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=BRAIN, CEREBELLUM;
RX   MEDLINE; 97404410.
RA   BAHN S., JONES A., WISDEN W.;
RT   "Directing gene expression to cerebellar granule cells using gamma-
RT   aminobutyric acid type A receptor alpha6 subunit transgenes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:9417-9421(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=BRAIN, CEREBELLUM;
RX   MEDLINE; 96355730.
RA   JONES A., BAHN S., GRANT A.L., KOHLER M., WISDEN W.;
RT   "Characterization of a cerebellar granule cell-specific gene encoding
RT   the gamma-aminobutyric acid type A receptor alpha 6 subunit.";
RL   J. Neurochem. 67:907-916(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=BRAIN, CEREBELLUM;
RX   MEDLINE; 97160644.
RA   JONES A., KORPI E.R., MCKERNAN R.M., PELZ R., NUSSER Z., MAKELA R.,
RA   MELLOR J.R., POLLARD S., BAHN S., STEPHENSON F.A., RANDALL A.D.,
RA   SIEGHART W., SOMOGYI P., SMITH A.J., WISDEN W.;
RT   "Ligand-gated ion channel subunit partnerships: GABAA receptor alpha6
RT   subunit gene inactivation inhibits delta subunit expression.";
RL   J. Neurosci. 17:1350-1362(1997).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=BRAIN, CEREBELLUM;
RX   MEDLINE; 96373714.
RA   BAHN S., HARVEY R.J., DARLISON M.G., WISDEN W.;
RT   "Conservation of gamma-aminobutyric acid type A receptor alpha 6
RT   subunit gene expression in cerebellar granule cells.";
RL   J. Neurochem. 66:1810-1818(1996).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; AJ222970; CAA11024.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
FT   NON_TER     286    286
SQ   SEQUENCE   286 AA;  32983 MW;  4C3C2E4E CRC32;


  Query Match             35.2%;  Score 477;  DB 11;  Length 286;
  Best Local Similarity   45.7%;  Pred. No. 8e-35;
  Matches   86;  Conservative   43;  Mismatches   55;  Indels    4;  Gaps    2;

Qy     73 RILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERLC 132
          |||: :|  ||::|||| |   | |  :| | | ||:| ::|||:|: | ||| ||||
Db     34 RILDNLLEGYDNRLRPGFGGAVTEVKTDIYVTSFGPVSDVEMEYTMDVFFRQTWTDERLK 93

Qy    133 YNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTID 192
          :    | | ||  :||::| |||||| |::  | :| ||:: |: ::| :|||:|:||:
Db     94 FKGPAEILSLNNLMVSKIWTPDTFFRNGKKSIAHNMTTPNKLFRLMQNGTILYTMRLTIN 153

Qy    193 AGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLEINEKNSWKLFQFDFTG 249
          | | : :: |||| |:||| | |::||: |:|| |:    : :|: |::|  | |:|  |
Db    154 ADCPMRLVNFPMDGHACPLKFGSYAYPKTEIIYTWKKGPLYSVEVPEESS-SLLQYDLIG 212

Qy    250 VSNKTEII 257
            :  :| |
Db    213 QTVSSETI 220


RESULT   6
Q24352
ID   Q24352      PRELIMINARY;      PRT;   686 AA.
AC   Q24352;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GLYCINE RECEPTOR PRECURSOR.
GN   GRD.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERLIN K; TISSUE=HEAD;
RX   MEDLINE; 94246427.
RA   HARVEY R.J., SCHMITT B., HERMANS-BORGMEYER I., GUNDELFINGER E.D.,
RA   BETZ H., DARLISON M.G.;
RT   "Sequence of a Drosophila ligand-gated ion-channel polypeptide with an
RT   unusual amino-terminal extracellular domain.";
RL   J. Neurochem. 62:2480-2483(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; X78349; CAA55144.1; -.
DR   FLYBASE; FBgn0001134; Grd.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 3.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
KW   Signal.
FT   SIGNAL        1     72       POTENTIAL.
FT   CHAIN        73    686       GLYCINE RECEPTOR.
SQ   SEQUENCE   686 AA;  76557 MW;  D70F536E CRC32;


  Query Match             31.8%;  Score 431;  DB 5;  Length 686;
  Best Local Similarity   40.4%;  Pred. No. 3.2e-30;
  Matches   76;  Conservative   45;  Mismatches   65;  Indels    2;  Gaps    1;

Qy     72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
          | :|: :|  ||: :||  |  |  : |:| | |:||:| :|| |::|  | |:| |:||
Db    110 SELLDNLLRGYDNSIRPDFGGPPATIEVDIMVRSMGPISEVDMTYSMDCYFRQSWVDKRL 169

Qy    132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
          :    ::| |: :::::::| |||:| | |::: | || ||: ||||::|:|||: |:||
Db    170 AFEGAQDTLALSVSMLARIWKPDTYFYNGKQSYLHTITTPNKFVRIYQNGRVLYSSRLTI 229

Qy    192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG-- 250
          ||| :::  ||||   ||| | || |  :::||:|   :  :      || |||
Db    230 KAGCPMNLADFPMDIQKCPLKFGSFGYTTSDVIYRWNKERPPVAIAEDMKLSQFDLVDCP 289

Qy    250 VSNKTEII 257
            | |:|:
Db    290 AGNLTDIV 297


RESULT   7
O18276
ID   O18276      PRELIMINARY;      PRT;   545 AA.
AC   O18276;
```

```
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   ZC482.1 PROTEIN.
GN   ZC482.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC   Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   MCMURRAY A.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94150718.
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA   GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA   JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA   LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA   THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA   WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; Z93397; CAB07719.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   545 AA;  61601 MW;  26207FDB CRC32;


  Query Match             26.7%;  Score 362.5;  DB 5;  Length 545;
  Best Local Similarity   35.6%;  Pred. No. 2.9e-24;
  Matches   68;  Conservative   47;  Mismatches   73;  Indels    3;  Gaps    2;

Qy      71 ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDER 130
           || :|: :| :|| :|||| |    ::|::| : |  :| :||:||: :   | | |||
Db      16 ASSLLSDLLLDYDIRLRPGFGGDALLLTMDIIIASFDSISEVDMDYTLTMYLHQYWTDER 75

Qy     131 LCYND--TFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIR 188
           | :::    : : |:|     :|:|||| | | :: ||:|  |:|:||  |||| | :|
Db      76 LRWSNEIPIDEMTLSGEFSQNIWVPDTFLANDKHSYLHEVTERNKMLRINVDGKVAYGMR 135

Qy     189 MTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFT 248
           :|    ||::: ||:|| :| :   |: |  :|:: || |: | ::      : ||  |
Db     136 LTSTLSCSMNLRNFPLDSQNCTVEIESYGYTTSEVLMKW-NYPLAVHGVEQADVPQFTIT 194

Qy     249 GVSNKTEIITT 259
           |   :  |::|
Db     195 GFHTEDSIVST 205


RESULT   8
Q9YGQ3
ID   Q9YGQ3      PRELIMINARY;      PRT;   466 AA.
AC   Q9YGQ3;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-1B SUBUNIT PRECURSOR.
OS   Morone americana (white perch).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC   Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC   Perciformes; Percoidei; Moronidae; Morone.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=RETINA;
RX   MEDLINE; 99022091.
RA   QIAN H., DOWLING J.E., RIPPS H.;
RT   "Molecular and pharmacological properties of GABA-rho subunits from
RT   white perch retina.";
RL   J. Neurobiol. 37:305-320(1998).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; AF101036; AAD17895.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW   Transmembrane.
SQ   SEQUENCE   466 AA;  53592 MW;  B48737DE CRC32;


  Query Match             25.6%;  Score 347.5;  DB 13;  Length 466;
  Best Local Similarity   30.7%;  Pred. No. 5e-23;
  Matches   71;  Conservative   55;  Mismatches   82;  Indels   23;  Gaps    4;

Qy      16 LQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETETGSRVGKLPEASRIL 75
           |:|| | | ||  :      ::          :   : ||:  |:|            :|
Db      30 LRSRTEMPLTEEPHRKIGSPIL----------KRSPDITKAWGTKT----------EHLL 69

Qy      76 NTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERLCY-N 134
           : ::|  :||| |      | |:: | ||  :| :||::|: :     | |||| : :
Db      70 R--IEDHDFTMRPGFGGPAVPVGVDVQVESLDAISEVDMDFTMTLYLRHYWKDERLSFRS 127

Qy     135 DTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAG 194
           :| :|:  :  :| ::|:|| || :||::  |: |  | |:|:| ||||||::|:|: |
Db     128 NTNQSMTFDSRLVKKIWVPDMFFVHSKKSFTHDTTTDNVMLRVYPDGKVLYSLRVTVTAM 187

Qy     195 CSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQF 245
           ||: : |||:|: :| |   |::| :::::  |:     :|      | ||
Db     188 CSMDLSRFPLDTQTCSLEIESYAYTDDDLMLYWKEGNRSLNTDERISLSQF 238


RESULT   9
O17555
ID   O17555      PRELIMINARY;      PRT;   499 AA.
AC   O17555; O18279;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   ZC482.5 PROTEIN.
GN   ZC482.5.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC   Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   MCMURRAY A.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94150718.
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA   GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA   JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA   LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA   THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA   WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; Z93397; CAB07722.1; -.
DR   EMBL; Z93372; CAB07722.1; JOINED.
DR   EMBL; Z93372; CAB07549.1; -.
```

```
DR   EMBL; Z93397; CAB07549.1; JOINED.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   499 AA;  57553 MW;  34743390 CRC32;


  Query Match             25.1%;  Score 340;  DB 5;  Length 499;
  Best Local Similarity   29.5%;  Pred. No. 2.6e-22;
  Matches   72;  Conservative   52;  Mismatches   88;  Indels   32;  Gaps    5;

Qy       5 VLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETETGSR 64
           ::|:   | ||     :      :   |||   |         || |   |
Db       6 IIPI---IALIHGHHSQAVIDMKRQRLSSRSTTY--------NQTLIRYT---------- 45

Qy      65 VGKLPEASRILNTILSNYDHKLRP-GIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFS 123
                ::|:|||| | |   ||       |  | |:|:: |:|||:|  :||:::|  |
Db      45 -------TKVLDTILLNQDKNFRPVNPDNSPLQVEVDISIRSMGPVSEQNMEFSLDCYFR 97

Qy     124 QTWYDERLCY---NDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
           | | | || :   | :   : | :  :|||||: || :::: | :|:|| : |:  |
Db      98 QKWLDRRLAFTPINPSKPEIPLASKMLKDIWIPDTYIRNGRKSYLHTLTVPNILFRVRSD 157

Qy     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
           |:|  : |:|| : | : : :||||: :||:   |  |   :::|||:: :|:    |:
Db     158 GQVHVSQRLTIRSRCQMFLKKFPMDTQACPIEVGSLGYFSKDVVYKWKDVELDAKMGNTL 217

Qy     241 KLFQ 244
             :|
Db     218 SQYQ 221


RESULT  10
Q9YGQ4
ID   Q9YGQ4      PRELIMINARY;      PRT;   476 AA.
AC   Q9YGQ4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-1A SUBUNIT PRECURSOR.
OS   Morone americana (white perch).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC   Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC   Perciformes; Percoidei; Moronidae; Morone.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=RETINA;
RX   MEDLINE; 99022091.
RA   QIAN H., DOWLING J.E., RIPPS H.;
RT   "Molecular and pharmacological properties of GABA-rho subunits from
RT   white perch retina.";
RL   J. Neurobiol. 37:305-320(1998).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; AF101035; AAD17894.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW   Transmembrane.
SQ   SEQUENCE   476 AA;  54703 MW;  945F8375 CRC32;


  Query Match             25.0%;  Score 339.5;  DB 13;  Length 476;
  Best Local Similarity   31.6%;  Pred. No. 2.7e-22;
  Matches   77;  Conservative   53;  Mismatches   99;  Indels   15;  Gaps    5;

Qy       8 VLLGILLILQ---SRVEGPQTE--SKNEASSRDVVYGPQPQPLENQLLSEETKSTETETG 62
           ||  : | :|     ||| |       : : ||   |       :|: |   | :   |
Db       8 VLFCVWLAVQLEDGPVEGSQAGDLQTEQVAKRDQNGG----GWRSQIRSPIYKQSPDMTK 63

Qy      63 SRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIF 122
           | : |  :  ||      ::|  :||  |  |  | |:: | ||  :| :||::|: :

Db      64 SLMTKSEQLLRI-----DDHDFTMRPAFGGPPIPVGVDVQVESLDTISEVDMDFTMTLYL 118

Qy     123 SQTWYDERLCYNDT-FESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDG 181
             | |||| :  |  :|:  :  :| ::|:|| || :|||:  |: |  | |:|:| ||
Db     119 RHYWKDERLSFPSTNNQSMTFDSRLVKKIWVPDMFFVHSKRSFIHDTTTDNVMLRVYPDG 178

Qy     182 KVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWK 241
           |||::|:|: | |:: : |||:|: :| |   |::| :::::  |:     :|  :
Db     179 NVLYSLRVTVTAMCNMDLSRFPLDTQTCSLEIESYAYTDDDLMLSWKKGNESLNTDDRIS 238

Qy     242 LFQF 245
           | ||
Db     239 LSQF 242


RESULT  11
Q25035
ID   Q25035      PRELIMINARY;      PRT;   472 AA.
AC   Q25035;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GABA A/GLYCINE RECEPTOR SUBUNIT.
GN   HG1.
OS   Haemonchus contortus.
OC   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Strongylida;
OC   Trichostrongyloidea; Trichostrongylidae; Haemonchinae; Haemonchus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95041083.
RA   LAUGHTON D.L., AMAR M., THOMAS P., TOWNER P., HARRIS P., LUNT G.C.,
RA   WOLSTENHOLME A.J.;
RT   "Cloning of a putative inhibitory amino acid receptor subunit from the
RT   parasitic nematode Haemonchus contortus.";
RL   Recept. Channels 2:155-163(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; X73584; CAA51991.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
FT   VARIANT     231    231       G -> D.
FT   VARIANT     329    329       S -> A.
SQ   SEQUENCE   472 AA;  54732 MW;  7B8A2213 CRC32;


  Query Match             24.9%;  Score 338;  DB 5;  Length 472;
  Best Local Similarity   35.0%;  Pred. No. 3.6e-22;
  Matches   64;  Conservative   44;  Mismatches   69;  Indels    6;  Gaps    3;

Qy      72 SRILNTILSNYDHKLRP-GIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDER 130
           :::|||||  | | | ||      |  | ::|:| |:||:|  |||:::|  | | | | |
Db      37 TKLLNTILLNQDKKFRPTNPDSSPLNVEIDISVRSMGPISEQDMEFSLDCYFRQKWLDRR 96

Qy     131 LCY---NDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTI 187
           | :   |     : |   ::  :|:|||: || :::: | :|:|| : |:  ||:|  :
Db      97 LAFTPINPDKPVMPLASKMLKDIWVPDTYIRNGRKSYLHTLTVPNILFRVRSDGQVHVSQ 156

Qy     188 RMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDF 247
           |:||   | : : :||||  :||:   |  |  |:::| |::  :|:: |    | |:
Db     157 RLTIKTKCLMFLKKFPMDVQACPIEIGSLGYFSNDVVYYWKD--VELDAKMGNMLSQYKI 214

Qy     248 TGV 250
             |:
Db     215 LGL 217


RESULT  12
Q19146
ID   Q19146      PRELIMINARY;      PRT;  1187 AA.
AC   Q19146; Q22565;
```

```
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   T19B10.10 PROTEIN.
GN   T19B10.10.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC   Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   WHITE S.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94150718.
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA   GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA   JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA   LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA   THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA   WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   LENNARD N.;
RL   Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z77656; CAB01143.1; -.
DR   EMBL; Z74043; CAB01143.1; JOINED.
DR   EMBL; Z74043; CAA98549.1; -.
DR   EMBL; Z77656; CAA98549.1; JOINED.
DR   PFAM; PF00065; neur_chan; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
SQ   SEQUENCE   1187 AA;  136410 MW;  FDC06409 CRC32;

  Query Match             24.8%;  Score 337;  DB 5;  Length 1187;
  Best Local Similarity   34.4%;  Pred. No. 1.5e-21;
  Matches   66;  Conservative   47;  Mismatches   71;  Indels    8;  Gaps    3;

Qy      66 GKLPEASRILNTILSNYDHKLRPGIGE-KPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
           |     : :|| :| |||   |||    ||| | ::: : ::||:| |   |: :  | |
Db      57 GVAQNVTHLLNNVLKNYDQHFRPGFNSGKPTKVYIDLFIRTMGPVSDLFNTYSFNCYFRQ 116

Qy     125 TWYDERLCYNDT---FESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDG 181
           | |:|| :|::   |  | |:  :: ::| |||:| |   :: | ||  |::||:  ||
Db     117 KWTDDRLHFNNSGIGFRQLSLSMAMLDKIWKPDTYFWNGAGSYVHGITTSNRLVRLEPDG 176

Qy     182 KVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW----ENFKLEINEK 237
           :||: |:|: | | : | |:|:|  :| |   |::|  :|: |||    ::  ::|: :
Db     177 TILYSSRITVKAKCQMDMSRYPLDKQACRLVIGSYAYSSDEVQYKWRIMGDDNGVKIDYE 236

Qy     238 NSWKLFQFDFTG 249
           :   | ||  :|
Db     237 SIADLPQFSLSG 248


RESULT  13
Q16323
ID   Q16323      PRELIMINARY;      PRT;   512 AA.
AC   Q16323;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GABAA RECEPTOR BETA 2 SUBUNIT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95223118.
RA   MCKINLEY D.D., LENNON D.J., CARTER D.B.;
RT   "Cloning, sequence analysis and expression of two forms of mRNA coding
RT   for the human beta 2 subunit of the GABAA receptor.";
RL   Brain Res. Mol. Brain Res. 28:175-179(1995).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; S77553; AAB33982.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
DR   PRINTS; PR01160; GABAARBETA.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   512 AA;  59150 MW;  FF0E2B52 CRC32;

  Query Match             24.7%;  Score 335.5;  DB 4;  Length 512;
  Best Local Similarity   33.7%;  Pred. No. 6.7e-22;
  Matches   63;  Conservative   43;  Mismatches   78;  Indels    3;  Gaps    1;

Qy      75 LNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERLCYN 134
           :: :|  || :|||  |  |  | : | : |:  :| ::|:||: : | | | |:|| ||
Db      40 VDRLLKGYDIRLRPDFGGPPVAVGMNIDIASIDMVSEVNMDYTLTMYFQQAWRDKRLSYN 99

Qy     135 DTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAG 194
              :| |:  |  |||:|||:| | |::  | :|: |:|:|:: || ||| :|:|  |
Db     100 VIPLNLTLDNRVADQLWVPDTYFLNDKKSFVHGVTVKNRMIRLHPDGTVLYGLRITTTAA 159

Qy     195 CSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQF---DFTGVS 251
           | : : |:|:|  :| |   |: |  ::: : |      :      :| ||   |:  ::
Db     160 CMMDLRRYPLDEQNCTLEIESYGYTTDDIEFYWRGDDNAVTGVTKIELPQFSIVDYKLIT 219

Qy     252 NKTEIIT 258
           |    |
Db     220 KKVVFST 226


RESULT  14
Q90590
ID   Q90590      PRELIMINARY;      PRT;   430 AA.
AC   Q90590;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GABA-A RECEPTOR BETA 2 SUBUNIT PRECURSOR (FRAGMENT).
GN   GABARB.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 94087186.
RA   HARVEY R.J., CHINCHETRU M.A., DARLISON M.G.;
RT   "Alternative splicing of a 51-nucleotide exon that encodes a putative
RT   protein kinase C phosphorylation site generates two forms of the
RT   chicken gamma-aminobutyric acidA receptor beta 2 subunit.";
RL   J. Neurochem. 62:10-16(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; X72806; CAA51326.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Signal; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW   Transmembrane.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25   >430       GABA-A RECEPTOR BETA 2 SUBUNIT.
FT   NON_TER     430    430
SQ   SEQUENCE   430 AA;  49101 MW;  D21C7CBE CRC32;
```

```
  Query Match             24.5%;  Score 333;  DB 13;  Length 430;
  Best Local Similarity   37.3%;  Pred. No. 8.8e-22;
  Matches   57;  Conservative   38;  Mismatches   58;  Indels    0;  Gaps    0;

Qy      75 LNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERLCYN 134
           :: :|  || :|||  |  |  | : | : |:  :| ::|:||: : | | | |:|| ||
Db      40 VDRLLKGYDIRLRPDFGGPPVAVGMNIDIASIDMVSEVNMDYTLTMYFQQAWRDKRLSYN 99

Qy     135 DTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAG 194
             :| |:  |  |||:|||:| | |::  | :|: |:|:|:: || ||| :|:|  |
Db     100 VIPLNLTLDNRVADQLWVPDTYFLNDKKSFVHGVTVKNRMIRLHPDGTVLYGLRITTTAA 159

Qy     195 CSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW 227
           | : : |:|:|  :| |   |: |  ::: : |
Db     160 CMMDLRRYPLDEQNCTLEIESYGYTTDDIEFYW 192


RESULT  15
P92023
ID   P92023      PRELIMINARY;      PRT;   478 AA.
AC   P92023;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   T10G3.7 PROTEIN.
GN   T10G3.7.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC   Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   BURTON J.;
RL   Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94150718.
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA   GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA   JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA   LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA   THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA   WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; Z81118; CAB03329.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 3.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   478 AA;  54746 MW;  5F34B651 CRC32;


  Query Match             24.2%;  Score 329;  DB 5;  Length 478;
  Best Local Similarity   28.6%;  Pred. No. 2.3e-21;
  Matches   76;  Conservative   66;  Mismatches   84;  Indels   40;  Gaps   10;

Qy      10 LGILLILQSRVEGPQTES---KNEASSRDVVYGPQPQPLENQLLSEETKSTETETGSRVG 66
           :|:|| : :    |::|    |: ||| |             |  :: :||  |: :|:
Db      12 VGLLLGVHAYHSRPKSEEHSPKHAASSSD------------LFEDDDQSTTLESIARLS 58

Qy      67 -------KLPEAS--RILNTILS-NYDHKLRPGIGEK------PTVVTVEIAVNSLGPLS 110
                  : |: |   ||  :|:  |||::||  ||       | ||:| : : |:  :
Db      59 APAHVPIEQPQTSDTEILEHLLTRGYDHRVRPP-GEDGTIHGGPVVVSVNMLLRSISKID 117

Qy     111 ILDMEYTIDIIFSQTWYDERLCYNDTFES----LVLNGNVVSQLWIPDTFFRNSKRTHEH 166
           ::|||:: : | ::| |:|| :    ::    |:|      ::|:||:||:| |: ::|
Db     118 NVNMEYSVQLTFRESWVDKRLSFGVKGDAQPDFLILTAG--QEIWMPDSFFQNEKQAYKH 175

Qy     167 EITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYK 226
           |  || ::|::||| :||::|:::   | :|:  :|||   | :  :|::|   :: |
Db     176 MIDKPNVLIRVHKDGTILYSVRISLVLSCPMHLQYYPMDVQQCFIDLASYAYTTKDIEYV 235

Qy     227 W-ENFKLEINEKNSWKLFQFDFTGVS 251
           | |   :::    |  |  |  |  |
Db     236 WKEETPVQLKAGLSSSLPSFQLTNTS 261


Search completed: March 11, 2000, 06:18:30
Job time: 58 sec
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:26:40 ; Search time 22.24 Seconds
(without alignments)
349.140 Million cell updates/sec

Title: US-09-030-832-42_COPY_1_260
Perfect score: 1357
Sequence: 1 MLSKVLPVLLGILLILQSRV.....KLFQFDFTGVSNKTEIITTP 260

Scoring table: BLOSUM62

Searched: 82229 seqs, 29864866 residues

Database : SwissProt_38:*

Word size : 0

Number of hits that pass the threshold : 82229

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1357	100.0	506	1	GAE_HUMAN	P78334 homo sapien
2	661	48.7	457	1	GAC4_CHICK	P34904 gallus gall
3	631	46.5	467	1	GAC3_MOUSE	P27681 mus musculu
4	622	45.8	474	1	GAC2_CHICK	P21548 gallus gall
5	621	45.8	474	1	GAC2_MOUSE	P22723 mus musculu
6	618	45.5	475	1	GAC2_BOVIN	P22300 bos taurus
7	618	45.5	466	1	GAC2_RAT	P18508 rattus norv
8	618	45.5	467	1	GAC3_RAT	P28473 rattus norv
9	613	45.2	467	1	GAC3_HUMAN	Q99928 homo sapien
10	608	44.8	467	1	GAC2_HUMAN	P18507 homo sapien
11	598	44.1	465	1	GAC1_RAT	P23574 rattus norv
12	485	35.7	453	1	GAA6_HUMAN	Q16445 homo sapien
13	480	35.4	453	1	GAA6_RAT	P30191 rattus norv
14	477.5	35.2	554	1	GAA4_HUMAN	P48169 homo sapien
15	473	34.9	552	1	GAA4_RAT	P28471 rattus norv
16	472	34.8	465	1	GAA6_CHICK	Q90845 gallus gall
17	471.5	34.7	556	1	GAA4_BOVIN	P20237 bos taurus
18	464	34.2	492	1	GAA3_MOUSE	P26049 mus musculu
19	464	34.2	493	1	GAA3_RAT	P20236 rattus norv
20	463.5	34.2	464	1	GAA5_RAT	P19969 rattus norv
21	462.5	34.1	462	1	GAA5_HUMAN	P31644 homo sapien
22	461	34.0	492	1	GAA3_BOVIN	P10064 bos taurus
23	461	34.0	492	1	GAA3_HUMAN	P34903 homo sapien
24	460	33.9	455	1	GAA1_MOUSE	P18504 mus musculu
25	456.5	33.6	456	1	GAA1_BOVIN	P08219 bos taurus
26	453	33.4	455	1	GAA1_CHICK	P19150 gallus gall
27	447.5	33.0	451	1	GAA2_RAT	P23576 rattus norv
28	443	32.6	451	1	GAA2_BOVIN	P10063 bos taurus
29	443	32.6	451	1	GAA2_HUMAN	P47869 homo sapien
30	443	32.6	451	1	GAA2_MOUSE	P26048 mus musculu
31	442.5	32.6	456	1	GAA1_HUMAN	P14867 homo sapien
32	429	31.6	443	1	GAA6_MOUSE	P16305 mus musculu
33	366	27.0	488	1	GAB4_CHICK	P24045 gallus gall
34	363	26.8	452	1	GAD_HUMAN	O14764 homo sapien
35	359	26.5	449	1	GAD_RAT	P18506 rattus norv
36	357.5	26.3	474	1	GAB1_HUMAN	P18505 homo sapien
37	356	26.2	449	1	GAD_MOUSE	P22933 mus musculu
38	351.5	25.9	474	1	GAB1_BOVIN	P08220 bos taurus
39	351.5	25.9	474	1	GAB1_MOUSE	P50571 mus musculu
40	351.5	25.9	474	1	GAB1_RAT	P15431 rattus norv
41	336.5	24.8	473	1	GAR1_HUMAN	P24046 homo sapien
42	336	24.8	474	1	GAR1_RAT	P50572 rattus norv
43	335.5	24.7	474	1	GAB2_HUMAN	P47870 homo sapien
44	335.5	24.7	474	1	GAB2_MOUSE	P15432 mus musculu
45	331	24.4	473	1	GAB3_HUMAN	P28472 homo sapien

ALIGNMENTS

```
RESULT   1
GAE_HUMAN
ID   GAE_HUMAN      STANDARD;      PRT;   506 AA.
AC   P78334; O15345;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR EPSILON SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97192095.
RA   DAVIES P.A., HANNA M.C., HALES T.G., KIRKNESS E.F.;
RT   "Insensitivity to anaesthetic agents conferred by a class of GABA(A)
RT   receptor subunit.";
RL   Nature 385:820-823(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97480709.
RA   WILKE K., GAUL R., KLAUCK S.M., POUSTKA A.;
RT   "A gene in human chromosome band Xq28 (GABRE) defines a putative new
RT   subunit class of the GABAA neurotransmitter receptor.";
RL   Genomics 45:1-10(1997).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. ASSOCIATES WITH ALPHA AND BETA
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: FOUND IN MANY TISSUE. HIGHEST LEVELS OF
CC       EXPRESSION IN ADULT HEART AND PLACENTA.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U66661; AAB49284.1; -.
DR   EMBL; Y09763; CAA70903.1; -.
DR   EMBL; Y09764; CAA70903.1; JOINED.
DR   MIM; 300093; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane.
FT   SIGNAL        1      ?       POTENTIAL.
FT   CHAIN         ?    506       GAMMA-AMINOBUTYRIC-ACID RECEPTOR EPSILON
FT                                SUBUNIT.
FT   DOMAIN        ?    253       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    254    274       POTENTIAL.
FT   TRANSMEM    281    301       POTENTIAL.
FT   TRANSMEM    344    364       POTENTIAL.
FT   DOMAIN      365    485       CYTOPLASMIC (PROBABLE).
```

```
FT   TRANSMEM    486    506       POTENTIAL.
FT   CARBOHYD    134    134       POTENTIAL.
FT   CARBOHYD    252    252       POTENTIAL.
FT   DISULFID    195    209       BY SIMILARITY.
FT   CONFLICT    102    102       A -> S (IN REF. 2).
FT   CONFLICT    245    245       F -> L (IN REF. 2).
FT   CONFLICT    471    471       G -> A (IN REF. 2).
FT   CONFLICT    502    502       V -> F (IN REF. 2).
SQ   SEQUENCE   506 AA;  57955 MW;  6BC8394B CRC32;
```

```
  Query Match             100.0%;  Score 1357;  DB 1;  Length 506;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-106;
  Matches  260;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60

Qy      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDI 120

Qy     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 IFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKD 180

Qy     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSW 240

Qy     241 KLFQFDFTGVSNKTEIITTP 260
           ||||||||||||||||||||
Db     241 KLFQFDFTGVSNKTEIITTP 260
```

```
RESULT   2
GAC4_CHICK
ID   GAC4_CHICK     STANDARD;      PRT;   457 AA.
AC   P34904;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG4.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93387470.
RA   HARVEY R.J., KIM H.-C., DARLISON M.G.;
RT   "Molecular cloning reveals the existence of a fourth gamma subunit of
RT   the vertebrate brain GABAA receptor.";
RL   FEBS Lett. 331:211-216(1993).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: ABUNDANT IN SEVERAL BRAIN REGIONS, INCLUDING
CC       THE ECTOSTRIATUM, NUCLEUS ROTUNDUS AND HYPERSTRIATUM VENTRALE.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X73533; CAA51939.1; -.
DR   PIR; S38296; S38296.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    457       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4
FT                                SUBUNIT.
FT   DOMAIN       22    256       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    257    279       PROBABLE.
FT   TRANSMEM    283    305       PROBABLE.
FT   TRANSMEM    317    339       PROBABLE.
FT   DOMAIN      340    433       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    434    457       PROBABLE.
FT   CARBOHYD     35     35       POTENTIAL.
FT   CARBOHYD    112    112       POTENTIAL.
FT   CARBOHYD    230    230       POTENTIAL.
FT   DISULFID    173    187       BY SIMILARITY.
SQ   SEQUENCE   457 AA;  53183 MW;  1571332B CRC32;
```

```
  Query Match             48.7%;  Score 661;  DB 1;  Length 457;
  Best Local Similarity   57.9%;  Pred. No. 3.5e-48;
  Matches  110;  Conservative   44;  Mismatches   36;  Indels    0;  Gaps    0;

Qy      70 EASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDE 129
           :|:::|||::| |||:|||| || ||| : |:| |||:||:|:: ||||||| |:|||||
Db      48 DATQILNSLLKNYDNKLRPDIGIKPTFIDVDIYVNSIGPVSVIQMEYTIDIFFAQTWYDR 107

Qy     130 RLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
           || :| | ::| || |:||::|||||||||||||   | || |||::||: |||||||:|:
Db     108 RLRFNSTLKALTLNTNMVSRIWIPDTFFRNSKRADSHWITTPNQLLRIWNDGKVLYTLRL 167

Qy     190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
           ||:| | | :  ||||:|||| ||| ||  |::|:|  : :|:::: :|:|:|||||
Db     168 TIEAECLLQLQNFPMDTHSCPLVFSSYGYPREEIVYRWRRYSIEVSDQRTWRLYQFDFTG 227

Qy     250 VSNKTEIITT 259
           : | :|:: |
Db     228 LRNTSEVLRT 237
```

```
RESULT   3
GAC3_MOUSE
ID   GAC3_MOUSE     STANDARD;      PRT;   467 AA.
AC   P27681;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C C57; TISSUE=BRAIN;
RX   MEDLINE; 91285135.
RA   WILSON-SHAW D., ROBINSON M., ALALJEV B., SIEGEL R.E., SIKELA J.M.;
RT   "A novel gamma subunit of the GABAA receptor identified using the
RT   polymerase chain reaction.";
RL   FEBS Lett. 284:211-215(1991).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
```

```
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC    -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC    -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC        SITE.
CC    -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC    ---------------------------------------------------------------------
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC    the European Bioinformatics Institute. There are no restrictions on its
CC    use by non-profit institutions as long as its content is in no way
CC    modified and this statement is not removed. Usage by and for commercial
CC    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC    or send an email to license@isb-sib.ch).
CC    ---------------------------------------------------------------------
DR    EMBL; X59300; CAA41988.1; -.
DR    PIR; S16915; S16915.
DR    MGD; MGI:95624; GABRG3.
DR    PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR    PFAM; PF00065; neur_chan; 1.
KW    Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW    Multigene family; Transmembrane.
FT    SIGNAL       1     17       POTENTIAL.
FT    CHAIN       18    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3
FT                                SUBUNIT.
FT    DOMAIN      18    254       EXTRACELLULAR (PROBABLE).
FT    TRANSMEM   255    277       PROBABLE.
FT    TRANSMEM   281    303       PROBABLE.
FT    TRANSMEM   315    337       PROBABLE.
FT    DOMAIN     338    443       CYTOPLASMIC (PROBABLE).
FT    TRANSMEM   444    467       PROBABLE.
FT    CARBOHYD   110    110       POTENTIAL.
FT    CARBOHYD   228    228       POTENTIAL.
FT    DISULFID   171    185       BY SIMILARITY.
SQ    SEQUENCE   467 AA;  54303 MW;  A332B008 CRC32;


  Query Match             46.5%;  Score 631;  DB 1;  Length 467;
  Best Local Similarity   46.6%;  Pred. No. 1.2e-45;
  Matches  124;  Conservative   46;  Mismatches   58;  Indels   38;  Gaps    4;

Qy       1 MLSKVLPVLLGILLILQS-------RVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEE 53
           | :|:|     :|| | |       |||  : |::: |::  |  |:||
Db       1 MAAKLL-----LLLCLFSGLHARSRRVE--EDENEDSPSNQKWVLAPKPQD--------- 45

Qy      54 TKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILD 113
                     :|: ||| :|  || |||| || ||||: |:| |||:||:| ::
Db      45 ---------------TDATLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSIN 89

Qy     114 MEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
           ||| ||| |:||| | || :| | ::| || |:|  :|||| |||||    | || |||
Db      90 MEYQIDIFFAQTWTDSRLRFNSTMKTLTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQ 149

Qy     174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLE 233
           ::||: |||:|||:|:||:| | | :  ||||:|:|||:|||: ||: ||||:|    :|
Db     150 LLRIWNDGKILYTLRLTINAECQLQLHNFPMDAHACPLTFSSYGYPKEEMIYRWRKNSVE 209

Qy     234 INEKNSWKLFQFDFTGVSNKTEIITT 259
             :: ||:|:|||| |: | |||:||
Db     210 AADQKSWRLYQFDFMGLRNTTEIVTT 235


RESULT   4
GAC2_CHICK
ID    GAC2_CHICK     STANDARD;      PRT;   474 AA.
AC    P21548;
DT    01-MAY-1991 (Rel. 18, Created)
DT    01-MAY-1991 (Rel. 18, Last sequence update)
DT    15-JUL-1999 (Rel. 38, Last annotation update)
DE    GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE    RECEPTOR).
GN    GABRG2.
OS    Gallus gallus (Chicken).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC    Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=COMMERCIAL RHODE ISLAND CROSS; TISSUE=BRAIN;
RX    MEDLINE; 91088318.
RA    GLENCORSE T.A., BATESON A.N., DARLISON M.G.;
RT    "Sequence of the chicken GABAA receptor gamma 2-subunit cDNA.";
RL    Nucleic Acids Res. 18:7157-7157(1990).
CC    -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC        VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC        GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC        CHANNEL.
CC    -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC        RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC    -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC    -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC        SITE.
CC    -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC    ---------------------------------------------------------------------
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC    the European Bioinformatics Institute. There are no restrictions on its
CC    use by non-profit institutions as long as its content is in no way
CC    modified and this statement is not removed. Usage by and for commercial
CC    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC    or send an email to license@isb-sib.ch).
CC    ---------------------------------------------------------------------
DR    EMBL; X54944; CAA38704.1; -.
DR    PIR; S13086; S13086.
DR    PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR    PFAM; PF00065; neur_chan; 1.
KW    Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW    Multigene family; Transmembrane; Phosphorylation.
FT    SIGNAL       1     38       POTENTIAL.
FT    CHAIN       39    474       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                                SUBUNIT.
FT    DOMAIN      39    272       EXTRACELLULAR (PROBABLE).
FT    TRANSMEM   273    295       PROBABLE.
FT    TRANSMEM   299    321       PROBABLE.
FT    TRANSMEM   333    355       PROBABLE.
FT    DOMAIN     356    450       CYTOPLASMIC (PROBABLE).
FT    TRANSMEM   451    474       PROBABLE.
FT    CARBOHYD    51     51       POTENTIAL.
FT    CARBOHYD   128    128       POTENTIAL.
FT    CARBOHYD   246    246       POTENTIAL.
FT    CARBOHYD   266    266       POTENTIAL.
FT    DISULFID   189    203       BY SIMILARITY.
FT    MOD_RES    411    411       PHOSPHORYLATION.
FT    DOMAIN     376    383       INSERTION, SIMILAR TO HUMAN GAMMA-2
FT                                SEQUENCE WHICH IS PROPOSED TO BE CAUSED
FT                                BY ALTERNATIVE SPLICING.
SQ    SEQUENCE   474 AA;  54969 MW;  F3975109 CRC32;


  Query Match             45.8%;  Score 622;  DB 1;  Length 474;
  Best Local Similarity   55.8%;  Pred. No. 6.8e-45;
  Matches  106;  Conservative   39;  Mismatches   45;  Indels    0;  Gaps    0;

Qy      70 EASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDE 129
           : : ||| :|  ||:|||| || ||||:  :: |||:|||:: ::|||||||| |:|||||
Db      64 DVTLILNGLLEGYDNKLRPDIGVKPTVIHTDMYVNSIGPVNAINMEYTIDIFFAQTWYDR 123

Qy     130 RLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
           || :| | : | || |:| ::||||||||||:   | || ||:|:||: ||:||||:|:
Db     124 RLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVLYTLRL 183

Qy     190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
           |||| | | :  ||||:|||| ||| || |:||:|:   :|: :  ||:|:|| |||
Db     184 TIDAECQLQLHNFPMDAHSCPLEFSSYGYPREEIIYQWKRSSVEVGDTRSWRLYQFSFTG 243

Qy     250 VSNKTEIITT 259
           : | ||:: |
Db     244 LRNTTEVVKT 253
```

```
RESULT   5
GAC2_MOUSE
ID   GAC2_MOUSE     STANDARD;      PRT;   474 AA.
AC   P22723;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91108470.
RA   KOFUJI P., WANG J.B., MOSS S.J., HUGANIR R.L., BURT D.R.;
RT   "Generation of two forms of the gamma-aminobutyric acidA receptor
RT   gamma 2-subunit in mice by alternative splicing.";
RL   J. Neurochem. 56:713-715(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   SIKELA J.M., SHAW W.D., KHAN A.S., LIN L.-H., LEIDENHEIMER G.,
RA   SIEGEL R.E.;
RL   Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: ALTERNATIVE RNA SPLICING DIRECTS EXPRESSION
CC       OF TWO FORMS OF GAMMA2 SUBUNIT (2S AND 2L), ONE (2L) CONTAINS A
CC       PROTEIN KINASE C PHOSPHORYLATION SITE.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M86572; AAB59635.1; -.
DR   EMBL; M62374; AAA37653.1; -.
DR   PIR; JH0317; JH0317.
DR   PIR; JH0316; JH0316.
DR   MGD; MGI:95623; GABRG2.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane; Phosphorylation;
KW   Alternative splicing.
FT   SIGNAL       1     38       POTENTIAL.
FT   CHAIN       39    474       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                               SUBUNIT.
FT   DOMAIN      39    272       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM   273    295       PROBABLE.
FT   TRANSMEM   299    321       PROBABLE.
FT   TRANSMEM   333    355       PROBABLE.
FT   DOMAIN     356    450       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM   451    474       PROBABLE.
FT   CARBOHYD    51     51       POTENTIAL.
FT   CARBOHYD   128    128       POTENTIAL.
FT   CARBOHYD   246    246       POTENTIAL.
FT   DISULFID   189    203       BY SIMILARITY.
FT   MOD_RES    381    381       PHOSPHORYLATION (BY PKC) (PROBABLE).
FT   VARSPLIC   376    383       MISSING (IN ISOFORM GAMMA-2S).
FT   CONFLICT    49     49       T -> A (IN REF. 2).
FT   CONFLICT   414    414       Q -> E (IN REF. 2).
FT   CONFLICT   443    443       M -> I (IN REF. 2).
SQ   SEQUENCE   474 AA;  55145 MW;  A3049225 CRC32;


  Query Match             45.8%;  Score 621;  DB 1;  Length 474;
  Best Local Similarity   52.7%;  Pred. No. 8.2e-45;
  Matches  108;  Conservative   41;  Mismatches   54;  Indels    2;  Gaps    1;

Qy      57 TETETGSRVGKLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDM 114
           |  :|     |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|
Db      49 TSNKTWVLTPKVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINM 108

Qy     115 EYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQM 174
           |||||| |:||||| || :| | : | || |:| ::||||||||||:   | || ||:|
Db     109 EYTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRM 168

Qy     175 VRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEI 234
           :||: ||:||||:|:|||| | | :  |||| ||||| ||||: ||  |::|:|:   :|:
Db     169 LRIWNDGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEV 228

Qy     235 NEKNSWKLFQFDFTGVSNKTEIITT 259
           :  ||:|:|| | |: | ||:: |
Db     229 GDTRSWRLYQFSFVGLRNTTEVVKT 253


RESULT   6
GAC2_BOVIN
ID   GAC2_BOVIN     STANDARD;      PRT;   475 AA.
AC   P22300;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC   Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN CORTEX;
RX   MEDLINE; 91088632.
RA   WHITING P.J., MCKERNAN R.M., IVERSEN L.L.;
RT   "Another mechanism for creating diversity in gamma-aminobutyrate type
RT   A receptors: RNA splicing directs expression of two forms of gamma 2
RT   phosphorylation site.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:9966-9970(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: ALTERNATIVE RNA SPLICING DIRECTS EXPRESSION
CC       OF TWO FORMS OF GAMMA-2 SUBUNITS (2S AND 2L), ONE (2L) CONTAINS A
CC       PROTEIN KINASE C PHOSPHORYLATION SITE.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
```

```
DR   EMBL; M55563; AAA30531.1; -.
DR   PIR; A39272; A39272.
DR   PIR; B39272; B39272.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane; Phosphorylation;
KW   Alternative splicing.
FT   SIGNAL        1     39       POTENTIAL.
FT   CHAIN        40    475       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                                 SUBUNIT.
FT   DOMAIN       40    273       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    274    296       PROBABLE.
FT   TRANSMEM    300    322       PROBABLE.
FT   TRANSMEM    334    356       PROBABLE.
FT   DOMAIN      357    451       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    452    475       PROBABLE.
FT   CARBOHYD     52     52       POTENTIAL.
FT   CARBOHYD    129    129       POTENTIAL.
FT   CARBOHYD    247    247       POTENTIAL.
FT   DISULFID    190    204       BY SIMILARITY.
FT   MOD_RES     382    382       PHOSPHORYLATION (BY PKC) (PROBABLE).
FT   VARSPLIC    377    384       MISSING (IN ISOFORM GAMMA-2S).
FT   VARIANT     230    230       S -> G.
SQ   SEQUENCE   475 AA;  55264 MW;  EEBD5FCE CRC32;


  Query Match             45.5%;  Score 618;  DB 1;  Length 475;
  Best Local Similarity   54.4%;  Pred. No. 1.5e-44;
  Matches  106;  Conservative   40;  Mismatches   47;  Indels    2;  Gaps    1;

Qy      67 KLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
           |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|||||||  | |
Db      60 KVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFGQ 119

Qy     125 TWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVL 184
           |||| || :| | : | || |:| ::||||||||||:   | || ||:|:||: ||:||
Db     120 TWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVL 179

Qy     185 YTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQ 244
           ||:|:|||| | | :  |||| ||||| |||: ||  |::|:|:  :|:::  ||:|:|
Db     180 YTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEVSDTRSWRLYQ 239

Qy     245 FDFTGVSNKTEIITT 259
           | | |: | ||:: |
Db     240 FSFVGLRNTTEVVKT 254


RESULT   7
GAC2_RAT
ID   GAC2_RAT       STANDARD;      PRT;   466 AA.
AC   P18508;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 90380375.
RA   SHIVERS B.D., KILLISCH I., SPRENGEL R., SONTHEIMER H., KOEHLER M.,
RA   SCHOFIELD P.R., SEEBURG P.H.;
RT   "Two novel GABAA receptor subunits exist in distinct neuronal
RT   subpopulations.";
RL   Neuron 3:327-337(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90331051.
RA   MALHERBE P., SIGEL E., BAUR R., PERSOHN E., RICHARDS J.G., MOHLER H.;
RT   "Functional characteristics and sites of gene expression of the alpha
RT   1, beta 1, gamma 2-isoform of the rat GABAA receptor.";
RL   J. Neurosci. 10:2330-2337(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L08497; AAC42036.1; -.
DR   PIR; A37164; A37164.
DR   PIR; JQ0077; JQ0077.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     38       POTENTIAL.
FT   CHAIN        39    466       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                                 SUBUNIT.
FT   DOMAIN       39    272       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    273    295       PROBABLE.
FT   TRANSMEM    299    321       PROBABLE.
FT   TRANSMEM    333    355       PROBABLE.
FT   DOMAIN      356    442       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    443    465       PROBABLE.
FT   CARBOHYD     51     51       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    246    246       POTENTIAL.
FT   DISULFID    189    203       BY SIMILARITY.
FT   CONFLICT     22     22       M -> I (IN REF. 2).
SQ   SEQUENCE   466 AA;  54077 MW;  EDDEFFEF CRC32;


  Query Match             45.5%;  Score 618;  DB 1;  Length 466;
  Best Local Similarity   54.4%;  Pred. No. 1.4e-44;
  Matches  106;  Conservative   40;  Mismatches   47;  Indels    2;  Gaps    1;

Qy      67 KLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
           |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|||||||  |:|
Db      59 KVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFAQ 118

Qy     125 TWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVL 184
           |||| || :| | : | || |:| ::||||||||||:   | || ||:|:||: ||:||
Db     119 TWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVL 178

Qy     185 YTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQ 244
           ||:|:|||| | | :  |||| ||||| |||: ||  |::|:|:  :|: :  ||:|:|
Db     179 YTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQ 238

Qy     245 FDFTGVSNKTEIITT 259
           | | |: | ||:: |
Db     239 FSFVGLRNTTEVVKT 253


RESULT   8
GAC3_RAT
ID   GAC3_RAT       STANDARD;      PRT;   467 AA.
AC   P28473;
DT   01-DEC-1992 (Rel. 24, Created)
```

```
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 92159063.
RA   HERB A., WISDEN W., LUEDDENS H., PUIA G., VICINI S., SEEBURG P.H.;
RT   "The third gamma subunit of the gamma-aminobutyric acid type A
RT   receptor family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:1433-1437(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZUR-SIV; TISSUE=BRAIN;
RX   MEDLINE; 92070559.
RA   KNOFLACH F., RHYNER T., VILLA M., KELLENBERGER S., DRESCHER U.,
RA   MALHERBE P., SIGEL E., MOEHLER H.;
RT   "The gamma 3-subunit of the GABAA-receptor confers sensitivity to
RT   benzodiazepine receptor ligands.";
RL   FEBS Lett. 293:191-194(1991).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M81142; AAA41181.1; -.
DR   EMBL; X63324; CAA44930.1; -.
DR   PIR; S19317; S19317.
DR   PIR; A40221; A40221.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL       1     17       POTENTIAL.
FT   CHAIN       18    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3
FT                               SUBUNIT.
FT   DOMAIN      18    254       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM   255    277       PROBABLE.
FT   TRANSMEM   281    303       PROBABLE.
FT   TRANSMEM   315    337       PROBABLE.
FT   DOMAIN     338    443       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM   444    467       PROBABLE.
FT   CARBOHYD   110    110       POTENTIAL.
FT   CARBOHYD   228    228       POTENTIAL.
FT   DISULFID   171    185       BY SIMILARITY!
FT   CONFLICT   416    416       S -> T (IN REF. 2).
SQ   SEQUENCE   467 AA;  54292 MW;  B7263D44 CRC32;


  Query Match             45.5%;  Score 618;  DB 1;  Length 467;
  Best Local Similarity   46.6%;  Pred. No. 1.4e-44;
  Matches  124;  Conservative   45;  Mismatches   59;  Indels   38;  Gaps    5;

Qy       1 MLSKVLPVLLGILLILQS-------RVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEE 53
           | :|:|     :|| | |       |||  : :|::  |::  |  |
Db       1 MAAKLL-----LLLCLFSGLHARSRRVE--EDDSEDSPSNQKWVLAP------------ 41

Qy      54 TKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILD 113
           || :|          : : ||| :|  || |||| || |||: |:| |||:||:| ::
Db      41 -KSQDT----------DVTLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSIN 89

Qy     114 MEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQ 173
           ||| ||| |:||| | || :| | : | || |:|  :|||| |||||    | || |||
Db      90 MEYQIDIFFAQTWTDSRLRFNSTMKILTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQ 149

Qy     174 MVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLE 233
           ::||: |||:|||:|:||:| | | :  ||||:|:|||:|||: ||: ||||:|    :|
Db     150 LLRIWNDGKILYTLRLTINAECQLQLHNFPMDAHACPLTFSSYGYPKEEMIYRWRKNSVE 209

Qy     234 INEKNSWKLFQFDFTGVSNKTEIITT 259
           :: ||:|:|||| |: | |||:||
Db     210 AADQKSWRLYQFDFMGLRNTTEIVTT 235


RESULT   9
GAC3_HUMAN
ID   GAC3_HUMAN     STANDARD;      PRT;   467 AA.
AC   Q99928;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=FETAL BRAIN;
RX   MEDLINE; 96360042.
RA   HADINGHAM K.L., WAFFORD K.A., THOMPSON S.A., PALMER K.J.,
RA   WHITING P.J.;
RT   "Expression and pharmacology of human GABAA receptors containing
RT   gamma 3 subunits.";
RL   Eur. J. Pharmacol. 291:301-309(1995).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S82769; AAB39369.1; -.
DR   MIM; 600233; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL       1     17       POTENTIAL.
FT   CHAIN       18    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3
FT                               SUBUNIT.
FT   DOMAIN      18    254       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM   255    277       PROBABLE.
FT   TRANSMEM   281    303       PROBABLE.
```

```
FT   TRANSMEM     315    337       PROBABLE.
FT   DOMAIN       338    443       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM     444    467       PROBABLE.
FT   CARBOHYD     110    110       POTENTIAL.
FT   CARBOHYD     228    228       POTENTIAL.
FT   DISULFID     171    185       BY SIMILARITY.
SQ   SEQUENCE   467 AA;  54284 MW;  EAB28EEC CRC32;


  Query Match             45.2%;  Score 613;  DB 1;  Length 467;
  Best Local Similarity   49.0%;  Pred. No. 3.8e-44;
  Matches  124;  Conservative   35;  Mismatches   74;  Indels   20;  Gaps    3;

Qy       7 PVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETETGSRVG 66
           | || :|| | | :          | || |           ||       || :|
Db       3 PKLL-LLLCLFSGL---------HARSRKVEEDEYEDSSSNQKWVLAPKSQDT------- 46

Qy      67 KLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTW 126
             : : ||| :|  || |||| || ||||: |:| |||:||:| ::||| ||| |:|||
Db      46 ---DVTLILNKLLREYDKKLRPDIGIKPTVIDVDIYVNSIGPVSSINMEYQIDIFFAQTW 102

Qy     127 YDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYT 186
           | || :| | : | || |:|  :|||| |||||    | || |||::||: |||:|||
Db     103 TDSRLRFNSTMKILTLNSNMVGLIWIPDTIFRNSKTAEAHWITTPNQLLRIWNDGKILYT 162

Qy     187 IRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFD 246
           :|:||:| | | :  |||| ||||| ||||: ||: |||:|    :|  :: ||:|:|:|||
Db     163 LRLTINAECQLQLHNFPMDEHSCPLIFSSYGYPKEEMIYRWRKNSVEAADQKSWRLYQFD 222

Qy     247 FTGVSNKTEIITT 259
           | |: | ||||:||
Db     223 FMGLRNTTEIVTT 235


RESULT  10
GAC2_HUMAN
ID   GAC2_HUMAN     STANDARD;      PRT;   467 AA.
AC   P18507;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 89181956.
RA   PRITCHETT D.B., SONTHEIMER H., SHIVERS B.D., YMER S., KETTENMANN H.,
RA   SCHOFIELD P.R., SEEBURG P.H.;
RT   "Importance of a novel GABAA receptor subunit for benzodiazepine
RT   pharmacology.";
RL   Nature 338:582-585(1989).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X15376; CAA33437.1; -.
DR   PIR; S03905; S03905.
DR   MIM; 137164; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     39       POTENTIAL.
FT   CHAIN        40    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                                SUBUNIT.
FT   DOMAIN       40    273       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    274    296       PROBABLE.
FT   TRANSMEM    300    322       PROBABLE.
FT   TRANSMEM    334    356       PROBABLE.
FT   DOMAIN      357    443       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    444    466       PROBABLE.
FT   CARBOHYD     52     52       POTENTIAL.
FT   CARBOHYD    129    129       POTENTIAL.
FT   CARBOHYD    247    247       POTENTIAL.
FT   DISULFID    190    204       BY SIMILARITY.
SQ   SEQUENCE   467 AA;  54178 MW;  E78E8090 CRC32;


  Query Match             44.8%;  Score 608;  DB 1;  Length 467;
  Best Local Similarity   53.3%;  Pred. No. 1e-43;
  Matches  104;  Conservative   41;  Mismatches   48;  Indels    2;  Gaps    1;

Qy      67 KLPE--ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQ 124
             |:||   : ||| :|  ||:|||| || |||::  :: |||:||:: ::|||||| |:|
Db      60 KVPEGDVTVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMEYTIDIFFAQ 119

Qy     125 TWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVL 184
             ||| || :| | : | || |:| ::|||||||||||:   | || ||:|:||: ||:||
Db     120 MWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRNSKKADAHWITTPNRMLRIWNDGRVL 179

Qy     185 YTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQ 244
             |::|:|||| | | :  |||| ||||| |||: ||  |::|:|:   :|: :  ||:|:|
Db     180 YSLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQ 239

Qy     245 FDFTGVSNKTEIITT 259
           | | |: | ||:: |
Db     240 FSFVGLRNTTEVVKT 254


RESULT  11
GAC1_RAT
ID   GAC1_RAT       STANDARD;      PRT;   465 AA.
AC   P23574;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 91006020.
RA   YMER S., DRAGUHN A., WISDEN W., WERNER P., KEINAENEN K.,
RA   SCHOFIELD P.R., SPRENGEL R., PRITCHETT D.B., SEEBURG P.H.;
RT   "Structural and functional characterization of the gamma 1 subunit of
RT   GABAA/benzodiazepine receptors.";
RL   EMBO J. 9:3261-3267(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
```

```
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X57514; CAA40739.1; -.
DR   PIR; S12056; S12056.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36    465       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1
FT                                 SUBUNIT.
FT   DOMAIN       36    272       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    273    294       PROBABLE.
FT   TRANSMEM    299    320       PROBABLE.
FT   TRANSMEM    332    354       PROBABLE.
FT   DOMAIN      355    444       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    445    465       PROBABLE.
FT   CARBOHYD     50     50       POTENTIAL.
FT   CARBOHYD    127    127       POTENTIAL.
FT   CARBOHYD    245    245       POTENTIAL.
FT   DISULFID    188    202       BY SIMILARITY.
SQ   SEQUENCE   465 AA;  53550 MW;  963AF632 CRC32;


  Query Match             44.1%;  Score 598;  DB 1;  Length 465;
  Best Local Similarity   53.7%;  Pred. No. 6.8e-43;
  Matches  102;  Conservative   44;  Mismatches   44;  Indels    0;  Gaps    0;

Qy      70 EASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDE 129
           : ::|||::|  ||:|||| || :|||:  :: |||:||:  ::||||||||||:|||:|
Db      63 DITQILNSLLQGYDNKLRPDIGVRPTVIETDVYVNSIGPVDPINMEYTIDIIFAQTWFDS 122

Qy     130 RLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRM 189
           || :| | : |:|| |:| ::||||||||||:::  | || ||:::||: ||:||||:|:
Db     123 RLKFNSTMKVLMLNSNMVGKIWIPDTFFRNSRKSDAHWITTPNRLLRIWSDGRVLYTLRL 182

Qy     190 TIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWENFKLEINEKNSWKLFQFDFTG 249
           ||:| | | :  |||| ||||| ||||: ||:||: |||:   :|: :   |:|:|| | |
Db     183 TINAECYLQLHNFPMDEHSCPLEFSSYGYPKNEIEYKWKKPSVEVADPKYWRLYQFAFVG 242

Qy     250 VSNKTEIITT 259
           : | |||  |
Db     243 LRNSTEISHT 252


RESULT  12
GAA6_HUMAN
ID   GAA6_HUMAN     STANDARD;      PRT;   453 AA.
AC   Q16445;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRA6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=CEREBELLUM;
RX   MEDLINE; 96226062.
RA   HADINGHAM K.L., GARRETT E.M., WAFFORD K.A., BAIN C., HEAVENS R.P.,
RA   SIRINATHSINGHJI D.J., WHITING P.J.;
RT   "Cloning of cDNAs encoding the human gamma-aminobutyric acid type A
RT   receptor alpha 6 subunit and characterization of the pharmacology of
RT   alpha 6-containing receptors.";
RL   Mol. Pharmacol. 49:253-259(1996).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S81944; AAB36480.1; -.
DR   MIM; 137143; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    453       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6
FT                                 SUBUNIT.
FT   DOMAIN       20    242       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    243    264       PROBABLE.
FT   TRANSMEM    269    290       PROBABLE.
FT   TRANSMEM    301    324       PROBABLE.
FT   DOMAIN      325    419       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    420    441       PROBABLE.
FT   CARBOHYD     31     31       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    141    141       POTENTIAL.
FT   DISULFID    156    170       BY SIMILARITY.
SQ   SEQUENCE   453 AA;  51034 MW;  4FE3C480 CRC32;


  Query Match             35.7%;  Score 485;  DB 1;  Length 453;
  Best Local Similarity   44.6%;  Pred. No. 2e-33;
  Matches   91;  Conservative   44;  Mismatches   57;  Indels   12;  Gaps    3;

Qy      65 VGKL--------PEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEY 116
           :|||          ||||: :|  ||::|||| |   | |  :| | | ||:| ::|||
Db      18 LGKLEVEGNFYSENVSRILDNLLEGYDNRLRPGFGGAVTEVKTDIYVTSFGPVSDVEMEY 77

Qy     117 TIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVR 176
           |:|: | ||| |||| :    | | ||  :||::| ||||||| |::  | :| ||:: |
Db      78 TMDVFFRQTWTDERLKFGGPTEILSLNNLMVSKIWTPDTFFRNGKKSIAHNMTTPNKLFR 137

Qy     177 IYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLE 233
           | ::| :|||:|:||:| | : :: |||| |:||| | |::||::|:|| |:    : :|
Db     138 IMQNGTILYTMRLTINADCPMRLVNFPMDGHACPLKFGSYAYPKSEIIYTWKKGPLYSVE 197

Qy     234 INEKNSWKLFQFDFTGVSNKTEII 257
           : |::|  | |:|  | :  :| |
Db     198 VPEESS-SLLQYDLIGQTVSSETI 220


RESULT  13
GAA6_RAT
ID   GAA6_RAT       STANDARD;      PRT;   453 AA.
AC   P30191;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
```

```
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRA6 OR GABRA-6.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 90348963.
RA   LUEDDENS H., PRITCHETT D., KHLER M., KILLISCH I., KEINAENEN K.,
RA   MONYER H., SPRENGEL R., SEEBURG P.H.;
RT   "Cerebellar GABAA receptor selective for a behavioural alcohol
RT   antagonist.";
RL   Nature 346:648-651(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: ONLY FOUND IN CEREBELLAR GRANULE CELLS.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L08495; AAC42034.1; -.
DR   EMBL; X55742; CAA39273.1; -.
DR   PIR; S11087; S11087.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    453       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6
FT                                SUBUNIT.
FT   DOMAIN       20    242       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    243    264       PROBABLE.
FT   TRANSMEM    269    290       PROBABLE.
FT   TRANSMEM    301    324       PROBABLE.
FT   DOMAIN      325    419       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    420    441       PROBABLE.
FT   CARBOHYD     31     31       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    141    141       POTENTIAL.
FT   DISULFID    156    170       BY SIMILARITY.
SQ   SEQUENCE   453 AA;  51184 MW;  0ED8616E CRC32;


  Query Match             35.4%;  Score 480;  DB 1;  Length 453;
  Best Local Similarity   46.0%;  Pred. No. 5.2e-33;
  Matches   87;  Conservative   43;  Mismatches   55;  Indels    4;  Gaps    2;

Qy      72 SRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTIDIIFSQTWYDERL 131
           ||||: :|  ||::|||| |   | |  :| | | ||:| ::|||||:|: | ||| ||||
Db      33 SRILDNLLEGYDNRLRPGFGGAVTEVKTDIYVTSFGPVSDVEMEYTMDVFFRQTWTDERL 92

Qy     132 CYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIYKDGKVLYTIRMTI 191
           :    | | ||  :||::| ||||||| |::  | :| ||:: |:  :| :|||:|:||
Db      93 KFKGPAEILSLNNLMVSKIWTPDTFFRNGKKSIAHNMTTPNKLFRLMHNGTILYTMRLTI 152

Qy     192 DAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKWEN---FKLEINEKNSWKLFQFDFT 248
           :| | : :: |||| |:||| | |::||::|:|| |:    : :|: |::|  | |:|
Db     153 NADCPMRLVNFPMDGHACPLKFGSYAYPKSEIIYTWKKGPLYSVEVPEESS-SLLQYDLI 211
```

```
Qy     249 GVSNKTEII 257
           | :  :| |
Db     212 GQTVSSETI 220


RESULT  14
GAA4_HUMAN
ID   GAA4_HUMAN     STANDARD;      PRT;   554 AA.
AC   P48169;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRA4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN CORTEX;
RA   YANG W., DREWE J.A., LAN N.C.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U30461; AAB52519.1; -.
DR   MIM; 137141; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36    554       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4
FT                                SUBUNIT.
FT   DOMAIN       36    258       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    259    280       PROBABLE.
FT   TRANSMEM    285    306       PROBABLE.
FT   TRANSMEM    318    340       PROBABLE.
FT   DOMAIN      341    523       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    524    543       PROBABLE.
FT   CARBOHYD     47     47       POTENTIAL.
FT   CARBOHYD    144    144       POTENTIAL.
FT   CARBOHYD    157    157       POTENTIAL.
FT   DISULFID    172    186       BY SIMILARITY.
SQ   SEQUENCE   554 AA;  61640 MW;  49E8E56A CRC32;


  Query Match             35.2%;  Score 477.5;  DB 1;  Length 554;
  Best Local Similarity   43.8%;  Pred. No. 1.1e-32;
  Matches   95;  Conservative   41;  Mismatches   64;  Indels   17;  Gaps    4;

Qy      44 PLENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIAV 103
           | :||   ||   ||  |           |||:::|  ||::|||| |   | |  :| |
Db      34 PGQNQ--KEEKLCTENFT----------RILDSLLDGYDNRLRPGFGGPVTEVKTDIYV 80

Qy     104 NSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRT 163
           | ||:| ::|||||:|: | ||| |:|| |:   | | ||  :|:::| |||||||  |::
Db      81 TSFGPVSDVEMEYTMDVFFRQTWIDKRLKYDGPIEILRLNNMMVTKVWTPDTFFRNGKKS 140
```

```
Qy     164 HEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEM 223
           | :| ||:: || ::| :|||:|:|| | | : :: |||| |:||| | |::||::||
Db     141 VSHNMTAPNKLFRIMRNGTILYTMRLTISAECPMRLVDFPMDGHACPLKFGSYAYPKSEM 200

Qy     224 IYKW---ENFKLEINEKNSWKLFQFDFTGVSNKTEII 257
           || |       :|:  | |  | |:|  | :  :| |
Db     201 IYTWTKGPEKSVEV-PKESSSLVQYDLIGQTVSSETI 236


RESULT  15
GAA4_RAT
ID   GAA4_RAT       STANDARD;      PRT;   552 AA.
AC   P28471;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRA4.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92008629.
RA   WISDEN W., HERB A., WIELAND H., KEINAENEN K., LUEDDENS H.,
RA   SEEBURG P.H.;
RT   "Cloning, pharmacological characteristics and expression pattern of
RT   the rat GABAA receptor alpha 4 subunit.";
RL   FEBS Lett. 289:227-230(1991).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L08493; AAC42032.1; -.
DR   EMBL; S55933; AAB19902.1; -.
DR   PIR; S17551; S17551.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36    552       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4
FT                                 SUBUNIT.
FT   DOMAIN       36    258       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    259    280       PROBABLE.
FT   TRANSMEM    285    306       PROBABLE.
FT   TRANSMEM    318    340       PROBABLE.
FT   DOMAIN      341    521       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    522    541       PROBABLE.
FT   CARBOHYD     47     47       POTENTIAL.
FT   CARBOHYD    144    144       POTENTIAL.
FT   CARBOHYD    157    157       POTENTIAL.
FT   DISULFID    172    186       BY SIMILARITY.
SQ   SEQUENCE   552 AA;  60951 MW;  62956C8F CRC32;


  Query Match             34.9%;  Score 473;  DB 1;  Length 552;
  Best Local Similarity   38.5%;  Pred. No. 2.6e-32;

  Matches  101;  Conservative   45;  Mismatches   74;  Indels   42;  Gaps    5;

Qy       1 MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQPLENQLLSEETKSTETE 60
           : | |   || :| :     | |   ||:|
Db      12 LCSGVSLALLHVLCLATCLNESPGQNSKDE---------------------------- 42

Qy      61 TGSRVGKL-PE-ASRILNTILSNYDHKLRPGIGEKPTVVTVEIAVNSLGPLSILDMEYTI 118
               || ||  :|||:::|  ||::|||| |   | |  :| | | ||:| ::||||:
Db      42 ------KLCPENFTRILDSLLDGYDNRLRPGFGGPVTEVKTDIYVTSFGPVSDVEMEYTM 95

Qy     119 DIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNSKRTHEHEITMPNQMVRIY 178
           |: | ||| |:|| |:   | | ||  :|:::| ||||||| |::  | :| ||:: ||
Db      96 DVFFRQTWIDKRLKYDGPIEILRLNNMMVTKVWTPDTFFRNGKKSVSHNMTAPNKLFRIM 155

Qy     179 KDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSYPENEMIYKW---ENFKLEIN 235
           ::| :|||:|:|| | | : :: |||| |:||| | |::||::|||| |       :|:
Db     156 RNGTILYTMRLTISAECPMRLVDFPMDGHACPLKFGSYAYPKSEMIYTWTKGPEKSVEV- 215

Qy     236 EKNSWKLFQFDFTGVSNKTEII 257
           | |  | |:|  | :  :| |
Db     215 PKESSSLVQYDLIGQTVSSETI 236


Search completed: March 11, 2000, 06:26:41
Job time: 44 sec
```

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2000, 10:50:04 ; Search time 439.26 Seconds
(without alignments)
56.822 Million cell updates/sec

Title: US-09-030-832-42_COPY_247_488
Perfect score: 1302
Sequence: 1 FTGVSNKTEIITTPVGDFMV.....QQGRLCIHVYRLDNYSRVVF 242

Scoring table: BLOSUM62

Searched: 659037 seqs, 103139215 residues

Database : Pending_Patents_AA:*

Word size : 0

Number of hits that pass the threshold : 659037
1: /cgn2_6/ptodata/2/paa/PCTUS9_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US084A_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US084B_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep:*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep:*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep:*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep:*
19: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*
20: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
21: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
22: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
23: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
24: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1302	100.0	506	14	US-09-030-832-42	Sequence 42, Appl
2	1209	92.9	242	12	US-08-888-012-2	Sequence 2, Appli
3	1209	92.9	242	14	US-09-030-832-2	Sequence 2, Appli
4	467.5	35.9	467	11	US-08-716-396-8	Sequence 8, Appli
5	337	25.9	554	12	US-08-809-802-8	Sequence 8, Appli
6	329	25.3	453	2	US-07-971-767-18	Sequence 18, Appl
7	329	25.3	453	6	US-08-341-610-4	Sequence 4, Appli
8	317.5	24.4	462	2	US-07-971-767-16	Sequence 16, Appl
9	317.5	24.4	462	6	US-08-341-610-2	Sequence 2, Appli
10	312	24.0	492	2	US-07-971-767-14	Sequence 14, Appl
11	312	24.0	492	6	US-08-341-610-10	Sequence 10, Appl
12	302	23.2	451	2	US-07-971-767-12	Sequence 12, Appl
13	302	23.2	451	6	US-08-341-610-8	Sequence 8, Appli
14	298.5	22.9	919	19	US-60-164-769-15096	Sequence 15096, A
15	298.5	22.9	496	19	US-60-167-216-505	Sequence 505, App
16	298.5	22.9	496	19	US-60-173-383-27057	Sequence 27057, A
17	298.5	22.9	496	19	US-60-173-464-21214	Sequence 21214, A
18	284	21.8	474	2	US-07-971-767-20	Sequence 20, Appl
19	284	21.8	474	6	US-08-341-610-6	Sequence 6, Appli
20	282.5	21.7	437	19	US-60-164-769-2660	Sequence 2660, Ap
21	282.5	21.7	387	19	US-60-173-383-35869	Sequence 35869, A
22	282.5	21.7	387	19	US-60-173-464-27455	Sequence 27455, A
23	269.5	20.7	638	14	US-09-083-194A-8	Sequence 8, Appli
24	268.5	20.6	452	12	US-08-809-802-12	Sequence 12, Appl
25	267.5	20.5	1431	19	US-60-161-932-1074	Sequence 1074, Ap
26	267.5	20.5	1431	19	US-60-164-769-7494	Sequence 7494, Ap
27	267.5	20.5	485	19	US-60-167-216-423	Sequence 423, App
28	267.5	20.5	485	19	US-60-173-383-17300	Sequence 17300, A
29	267.5	20.5	485	19	US-60-173-464-13598	Sequence 13598, A
30	267	20.5	250	19	US-60-140-804-913	Sequence 913, App
31	265	20.4	101	19	US-60-137-521-95	Sequence 95, Appl
32	264	20.3	632	14	US-09-083-194A-2	Sequence 2, Appli
33	262.5	20.2	165	16	US-09-270-767-33201	Sequence 33201, A
34	262.5	20.2	165	16	US-09-270-767-48418	Sequence 48418, A
35	260	20.0	133	19	US-60-142-843-282	Sequence 282, App
36	258	19.8	496	1	PCT-US98-08563-2	Sequence 2, Appli
37	258	19.8	467	1	PCT-US98-08563-3	Sequence 3, Appli
38	258	19.8	496	14	US-09-002-361-2	Sequence 2, Appli
39	258	19.8	467	14	US-09-002-361-3	Sequence 3, Appli
40	257.5	19.8	438	19	US-60-164-769-414	Sequence 414, App
41	257.5	19.8	683	19	US-60-167-245-592	Sequence 592, App
42	257.5	19.8	683	19	US-60-173-383-17399	Sequence 17399, A
43	257.5	19.8	683	19	US-60-173-464-13676	Sequence 13676, A
44	251	19.3	637	2	US-07-770-881D-1	Sequence 1, Appli
45	251	19.3	606	6	US-08-333-956A-1	Sequence 1, Appli

ALIGNMENTS

```
RESULT 1
US-09-030-832-42
; Sequence 42, Application US/09030832
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/030,832
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/888,012
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950001/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  506 amino acids
```

```
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-030-832-42


  Query Match           100.0%;  Score 1302;  DB 14;  Length 506;
  Best Local Similarity   100.0%;  Pred. No. 6e-126;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 306

Qy     61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 366

Qy    121 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 426

Qy    181 QPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 QPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 486

Qy    241 VF 242
          ||
Db    487 VF 488


RESULT   2
US-08-888-012-2
; Sequence 2, Application US/08888012
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  ET2: An Alternative Transcript of the GABA-A
;    TITLE OF INVENTION:  Receptor n Subunit
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,012
;      FILING DATE:  Herewith
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950000/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  242 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-888-012-2


  Query Match           92.9%;  Score 1209;  DB 12;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 1e-116;
  Matches  224;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     19 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 78
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60

Qy     79 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 120

Qy    139 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 198
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 RAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKL 180

Qy    199 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVF 242
          |||||||||||||||||||||||||||||||||||||||||||||
Db    181 ACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVF 224


RESULT   3
US-09-030-832-2
; Sequence 2, Application US/09030832
;  GENERAL INFORMATION:
;    APPLICANT:  Hanna, Michael C.
;    APPLICANT:  Kirkness, Ewen F.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/030,832
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/888,012
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0950001/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  242 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-030-832-2


  Query Match           92.9%;  Score 1209;  DB 14;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 1e-116;
  Matches  224;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     19 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 78
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLG 60

Qy     79 TFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINS 138
```

```
                                                
```

```
; Sequence 18, Application US/07971767
;  GENERAL INFORMATION:
;    APPLICANT:  Hadingham, Karen L.
;    APPLICANT:  Le Bourdelles, Beatrice
;    APPLICANT:  Whiting, Paul J.
;    APPLICANT:  Wingrove, Peter B.
;    TITLE OF INVENTION:  GABA-A RECEPTOR SUBUNITS (ALPHA-2,
;    TITLE OF INVENTION:  ALPHA-3, ALPHA-5, ALPHA-6, BETA-2) AND TRANSFECTED CELLS
;    TITLE OF INVENTION:  EXPRESSING THEM
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robert J. North
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,767
;      FILING DATE:  19930202
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  North, Robert J.
;      REGISTRATION NUMBER:  27,366
;      REFERENCE/DOCKET NUMBER:  T-1109
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908 594-7262
;      TELEFAX:  908 594-4720
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  453 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-971-767-18


  Query Match             25.3%;  Score 329;  DB 2;  Length 453;
  Best Local Similarity   31.8%;  Pred. No. 1.5e-25;
  Matches   83;  Conservative   40;  Mismatches   70;  Indels   68;  Gaps    7;

Qy       3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
           |  :  :| | :  |::::||::|:: |: ||   | | |  :| :|| ||||| || ||
Db     212 GQTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPA 271

Qy      63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
           || ||||:|||||||   :| : |:||| ||:|::||:|| | | ||:||| :|:    |
Db     272 RTVLGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQ 331

Qy     123 TK------AHASPK--------------LRHPRINSRAHARTRARSRACARQHQEAFVC 161
           |:        |:|                : ||  :|: | : |  | :
Db     332 TQKAKRKAQFAAPPTVTISKATEPLEAEIVLHP--DSKYHLKKRITSLS----------L 379

Qy     162 QIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGST 221
            ||::      |      : |    :|  |  |                      |  | |
Db     380 PIVSS-----SEANKVLTRAPILQSTPVTPPPL--------------------PPAFGGT 414

Qy     222 WQQGRLCIHVYRLDNYSRVVF 242
                   ::| |||::|
Db     415 ----------SKIDQYSRILF 425


RESULT   7
US-08-341-610-4
; Sequence 4, Application US/08341610
;  GENERAL INFORMATION:
;    APPLICANT:  Karen Hadingham
;    APPLICANT:  Paul John Whiting
;    TITLE OF INVENTION:  Stably transfected cell lines expressing GABA-A receptors
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jack L. Tribble
;      STREET:  126 E. Lincoln Avenue, P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/341,610
;      FILING DATE:  17-NOV-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tribble, Jack L.
;      REGISTRATION NUMBER:  32,633
;      REFERENCE/DOCKET NUMBER:  T-1220Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)594-5321
;      TELEFAX:  (908)594-4720
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  453 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-341-610-4


  Query Match             25.3%;  Score 329;  DB 6;  Length 453;
  Best Local Similarity   31.8%;  Pred. No. 1.5e-25;
  Matches   83;  Conservative   40;  Mismatches   70;  Indels   68;  Gaps    7;

Qy       3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
           |  :  :| | :  |::::||::|:: |: ||   | | |  :| :|| ||||| || ||
Db     212 GQTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPA 271

Qy      63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
           || ||||:|||||||   :| : |:||| ||:|::||:|| | | ||:||| :|:    |
Db     272 RTVLGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQ 331

Qy     123 TK------AHASPK--------------LRHPRINSRAHARTRARSRACARQHQEAFVC 161
           |:        |:|                : ||  :|: | : |  | :
Db     332 TQKAKRKAQFAAPPTVTISKATEPLEAEIVLHP--DSKYHLKKRITSLS----------L 379

Qy     162 QIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGST 221
            ||::      |      : |    :|  |  |                      |  | |
Db     380 PIVSS-----SEANKVLTRAPILQSTPVTPPPL--------------------PPAFGGT 414

Qy     222 WQQGRLCIHVYRLDNYSRVVF 242
                   ::| |||::|
Db     415 ----------SKIDQYSRILF 425


RESULT   8
US-07-971-767-16
; Sequence 16, Application US/07971767
;  GENERAL INFORMATION:
;    APPLICANT:  Hadingham, Karen L.
;    APPLICANT:  Le Bourdelles, Beatrice
;    APPLICANT:  Whiting, Paul J.
;    APPLICANT:  Wingrove, Peter B.
;    TITLE OF INVENTION:  GABA-A RECEPTOR SUBUNITS (ALPHA-2,
;    TITLE OF INVENTION:  ALPHA-3, ALPHA-5, ALPHA-6, BETA-2) AND TRANSFECTED CELLS
;    TITLE OF INVENTION:  EXPRESSING THEM
```

```
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robert J. North
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,767
;      FILING DATE:  19930202
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  North, Robert J.
;      REGISTRATION NUMBER:  27,366
;      REFERENCE/DOCKET NUMBER:  T-1109
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908 594-7262
;      TELEFAX:  908 594-4720
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  462 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-971-767-16


  Query Match             24.4%;  Score 317.5;  DB 2;  Length 462;
  Best Local Similarity   30.5%;  Pred. No. 2.4e-24;
  Matches   74;  Conservative   43;  Mismatches   75;  Indels   51;  Gaps    5;

Qy       8 TEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLG 67
           || |:|  |:: :||  |:: |: ||   | |:|  :| :|| |||:  || ||||  |
Db     234 TENISTSTGEYTIMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFG 293

Qy      68 ITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL-----IYNQ 122
           :|:|||||||   :| : |:|:| ||:|:::||:|: | | ||:||| :|:       ::
Db     294 VTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGWAWDG 353

Qy     123 TKAHASPKLRHPR---INSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSA 179
            ||  : |::  |   :|   :| |  :                            |:
Db     354 KKALEAAKIKKKREVILNKSTNAFTTGKM----------------------SHPPNIPK 390

Qy     180 QQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSR 239
           :|     :| |  :  |                 |   |  | :  :    : ::|  ||
Db     391 EQ-----TPAGTSNTTS--------------VSVKPSEEKTSESKKTYNSISKIDKMSR 430

Qy     240 VVF 242
           :||
Db     431 IVF 433


RESULT  9
US-08-341-610-2
; Sequence 2, Application US/08341610
;  GENERAL INFORMATION:
;    APPLICANT:  Karen Hadingham
;    APPLICANT:  Paul John Whiting
;    TITLE OF INVENTION:  Stably transfected cell lines expressing GABA-A receptors
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jack L. Tribble
;      STREET:  126 E. Lincoln Avenue, P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/341,610
;      FILING DATE:  17-NOV-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tribble, Jack L.
;      REGISTRATION NUMBER:  32,633
;      REFERENCE/DOCKET NUMBER:  T-1220Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)594-5321
;      TELEFAX:  (908)594-4720
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  462 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-341-610-2


  Query Match             24.4%;  Score 317.5;  DB 6;  Length 462;
  Best Local Similarity   30.5%;  Pred. No. 2.4e-24;
  Matches   74;  Conservative   43;  Mismatches   75;  Indels   51;  Gaps    5;

Qy       8 TEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLG 67
           || |:|  |:: :||  |:: |: ||   | |:|  :| :|| |||:  || ||||  |
Db     234 TENISTSTGEYTIMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFG 293

Qy      68 ITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL-----IYNQ 122
           :|:|||||||   :| : |:|:| ||:|:::||:|: | | ||:||| :|:       ::
Db     294 VTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGWAWDG 353

Qy     123 TKAHASPKLRHPR---INSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSA 179
            ||  : |::  |   :|   :| |  :                            |:
Db     354 KKALEAAKIKKKREVILNKSTNAFTTGKM----------------------SHPPNIPK 390

Qy     180 QQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSR 239
           :|     :| |  :  |                 |   |  | :  :    : ::|  ||
Db     391 EQ-----TPAGTSNTTS--------------VSVKPSEEKTSESKKTYNSISKIDKMSR 430

Qy     240 VVF 242
           :||
Db     431 IVF 433


RESULT  10
US-07-971-767-14
; Sequence 14, Application US/07971767
;  GENERAL INFORMATION:
;    APPLICANT:  Hadingham, Karen L.
;    APPLICANT:  Le Bourdelles, Beatrice
;    APPLICANT:  Whiting, Paul J.
;    APPLICANT:  Wingrove, Peter B.
;    TITLE OF INVENTION:  GABA-A RECEPTOR SUBUNITS (ALPHA-2,
;    TITLE OF INVENTION:  ALPHA-3, ALPHA-5, ALPHA-6, BETA-2) AND TRANSFECTED CELLS
;    TITLE OF INVENTION:  EXPRESSING THEM
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robert J. North
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
```

```
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,767
;      FILING DATE:  19930202
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  North, Robert J.
;      REGISTRATION NUMBER:  27,366
;      REFERENCE/DOCKET NUMBER:  T-1109
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908 594-7262
;      TELEFAX:  908 594-4720
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  492 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-971-767-14


  Query Match             24.0%;  Score 312;  DB 2;  Length 492;
  Best Local Similarity   50.0%;  Pred. No. 9.7e-24;
  Matches   55;  Conservative   25;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      8 TEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLG 67
          ||||  :  |:::|||  |:: |: ||   | |:|  :| :|| ||||:  || ||||  |
Db    252 TEIIRSSTGEYVVMTTHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFG 311

Qy     68 ITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNF 117
          :|:|||||||   :| : |:|:| ||:|::||:|: | | ||:||| :|:
Db    312 VTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNY 361


RESULT  11
US-08-341-610-10
; Sequence 10, Application US/08341610
;  GENERAL INFORMATION:
;    APPLICANT:  Karen Hadingham
;    APPLICANT:  Paul John Whiting
;    TITLE OF INVENTION:  Stably transfected cell lines expressing GABA-A receptors
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jack L. Tribble
;      STREET:  126 E. Lincoln Avenue, P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/341,610
;      FILING DATE:  17-NOV-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tribble, Jack L.
;      REGISTRATION NUMBER:  32,633
;      REFERENCE/DOCKET NUMBER:  T-1220Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)594-5321
;      TELEFAX:  (908)594-4720
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  492 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-341-610-10


  Query Match             24.0%;  Score 312;  DB 6;  Length 492;
  Best Local Similarity   50.0%;  Pred. No. 9.7e-24;
  Matches   55;  Conservative   25;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      8 TEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLG 67
          ||||  :  |:::|||  |:: |: ||   | |:|  :| :|| ||||:  || ||||  |
Db    252 TEIIRSSTGEYVVMTTHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFG 311

Qy     68 ITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNF 117
          :|:|||||||   :| : |:|:| ||:|::||:|: | | ||:||| :|:
Db    312 VTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNY 361


RESULT  12
US-07-971-767-12
; Sequence 12, Application US/07971767
;  GENERAL INFORMATION:
;    APPLICANT:  Hadingham, Karen L.
;    APPLICANT:  Le Bourdelles, Beatrice
;    APPLICANT:  Whiting, Paul J.
;    APPLICANT:  Wingrove, Peter B.
;    TITLE OF INVENTION:  GABA-A RECEPTOR SUBUNITS (ALPHA-2,
;    TITLE OF INVENTION:  ALPHA-3, ALPHA-5, ALPHA-6, BETA-2) AND TRANSFECTED CELLS
;    TITLE OF INVENTION:  EXPRESSING THEM
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robert J. North
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/971,767
;      FILING DATE:  19930202
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  North, Robert J.
;      REGISTRATION NUMBER:  27,366
;      REFERENCE/DOCKET NUMBER:  T-1109
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908 594-7262
;      TELEFAX:  908 594-4720
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  451 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-971-767-12


  Query Match             23.2%;  Score 302;  DB 2;  Length 451;
  Best Local Similarity   47.8%;  Pred. No. 9.4e-23;
  Matches   55;  Conservative   24;  Mismatches   36;  Indels    0;  Gaps    0;

Qy      3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
            | |   | | :  |:: |||  |:: |: ||   | |:|  :| :|| ||||:  || ||
```

```
Db    222 GQSIGKETIKSSTGEYTVMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPA 281

Qy     63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNF 117
          ||  |:|:|||||||   :| : |:|:| ||:|::||:|: | | ||:||| :|:
Db    282 RTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNY 336


RESULT 13
US-08-341-610-8
; Sequence 8, Application US/08341610
;  GENERAL INFORMATION:
;    APPLICANT:  Karen Hadingham
;    APPLICANT:  Paul John Whiting
;    TITLE OF INVENTION:  Stably transfected cell lines expressing GABA-A receptors
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jack L. Tribble
;      STREET:  126 E. Lincoln Avenue, P.O. Box 2000
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/341,610
;      FILING DATE:  17-NOV-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Tribble, Jack L.
;      REGISTRATION NUMBER:  32,633
;      REFERENCE/DOCKET NUMBER:  T-1220Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)594-5321
;      TELEFAX:  (908)594-4720
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  451 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-341-610-8


  Query Match             23.2%;  Score 302;  DB 6;  Length 451;
  Best Local Similarity   47.8%;  Pred. No. 9.4e-23;
  Matches   55;  Conservative   24;  Mismatches   36;  Indels    0;  Gaps    0;

Qy      3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
          | |   | | :  |:: |||  |:: |: ||   | |:|  :| :|| ||||:  || ||
Db    222 GQSIGKETIKSSTGEYTVMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPA 281

Qy     63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNF 117
          ||  |:|:|||||||   :| : |:|:| ||:|::||:|: | | ||:||| :|:
Db    282 RTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNY 336


RESULT 14
US-60-164-769-15096
; Sequence 15096, Application US/60164769
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
;  TITLE OF INVENTION: Acid Sequences, Systems Containin the Nucleic Acid Sequences
;  TITLE OF INVENTION: and Uses Thereof
;  FILE REFERENCE: CL000144
;  CURRENT APPLICATION NUMBER: US/60/164,769
;  CURRENT FILING DATE: 1999-11-12
;  NUMBER OF SEQ ID NOS: 27328
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15096
;   LENGTH: 919
;   TYPE: PRT
;   ORGANISM: Drosophila
US-60-164-769-15096


  Query Match             22.9%;  Score 298.5;  DB 19;  Length 919;
  Best Local Similarity   39.9%;  Pred. No. 5e-22;
  Matches   59;  Conservative   30;  Mismatches   54;  Indels    5;  Gaps    2;

Qy      5 SNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPART 64
          ::: | : |  | :  ::: | : |  ||  || |:|| :  |||||||||  |:  ||
Db    655 NDRKERLAT--GVYQRLSLSFKLQRNIGYFVFQTYLPSILIVMLSWVSFWINHEATSARV 712

Qy     65 SLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTK 124
          :||||:||||||: |  | : ||:||: |:| |: :|||| | ||||:| :|:  : :
Db    713 ALGITTVLTMTTISTGVRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWGK-- 771

Qy    125 AHASPKLRHPRINSRAHARTRARSRACA 152
            |  |::  :            ||  |:
Db    771 -RAKKKIKKVKECCPGKIGKSERSETCS 797


RESULT 15
US-60-167-216-505
; Sequence 505, Application US/60167216
; GENERAL INFORMATION:
;  APPLICANT: Li, Peter W.D.
;  TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL000150
;  CURRENT APPLICATION NUMBER: US/60/167,216
;  CURRENT FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 593
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 505
;   LENGTH: 496
;   TYPE: PRT
;   ORGANISM: Drosophila
US-60-167-216-505


  Query Match             22.9%;  Score 298.5;  DB 19;  Length 496;
  Best Local Similarity   39.9%;  Pred. No. 2.4e-22;
  Matches   59;  Conservative   30;  Mismatches   54;  Indels    5;  Gaps    2;

Qy      5 SNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPART 64
          ::: | : |  | :  ::: | : |  ||  || |:|| :  |||||||||  |:  ||
Db    232 NDRKERLAT--GVYQRLSLSFKLQRNIGYFVFQTYLPSILIVMLSWVSFWINHEATSARV 289

Qy     65 SLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTK 124
          :||||:||||||: |  | : ||:||: |:| |: :|||| | ||||:| :|:  : :
Db    290 ALGITTVLTMTTISTGVRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWGK-- 348

Qy    125 AHASPKLRHPRINSRAHARTRARSRACA 152
            |  |::  :            ||  |:
Db    348 -RAKKKIKKVKECCPGKIGKSERSETCS 374


Search completed: March 10, 2000, 10:50:05
Job time: 3508 sec
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2000, 08:51:54 ; Search time 47.6 Seconds
(without alignments)
120.421 Million cell updates/sec

Title: US-09-030-832-42_COPY_247_488
Perfect score: 1302
Sequence: 1 FTGVSNKTEIITTPVGDFMV.....QQGRLCIHVYRLDNYSRVVF 242

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database : A_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 188963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1302	100.0	506	1	W59048	GABA-A receptor ep
2	1302	100.0	474	1	W59049	Variant of GABA-A
3	1302	100.0	506	1	W61045	Human GABA recepto
4	461.5	35.4	467	1	R83968	GABA-A receptor ga
5	337	25.9	554	1	R97298	Human GABA-A recep
6	329	25.3	453	1	R31187	GABA-A receptor al
7	329	25.3	453	1	R59865	Human GABA recepto
8	317.5	24.4	462	1	R31186	GABA-A receptor al
9	317.5	24.4	462	1	R59864	Human GABA recepto
10	312	24.0	492	1	R31185	GABA-A receptor al
11	312	24.0	492	1	R59863	Human GABA recepto
12	302	23.2	451	1	R31184	GABA-A receptor al
13	302	23.2	451	1	R59862	Human GABA recepto
14	298.5	22.9	496	1	R89336	GABA receptor subu
15	298.5	22.9	496	1	W86161	Insect GABA recept
16	284	21.8	474	1	R31188	GABA-A receptor be
17	284	21.8	474	1	R59866	Human GABA recepto
18	268.5	20.6	452	1	R97299	Human GABA-A recep
19	264	20.3	627	1	W85597	Human GABA-A recep
20	258	19.8	496	1	W81633	GABA-gated chlorid
21	258	19.8	467	1	W81634	GABA-gated chlorid
22	258	19.8	561	1	W97413	Lucilia cuprina GA
23	257.5	19.8	686	1	W86162	Insect GABA recept
24	256	19.7	627	1	W85596	Human GABA-A recep
25	251	19.3	637	1	R34035	Sequence of a GABA
26	247.5	19.0	488	1	W69285	GABA gated chlorid
27	246	18.9	440	1	R93118	Human GABA-A recep
28	246	18.9	440	1	W26464	Human GABA-A recep
29	245	18.8	222	1	W81637	GABA-gated chlorid
30	244.5	18.8	488	1	W69286	GABA gated chlorid
31	244.5	18.8	481	1	W81635	GABA-gated chlorid
32	244.5	18.8	459	1	W81636	GABA-gated chlorid
33	241	18.5	456	1	W05246	Drosophila glutama
34	234.5	18.0	510	1	R88360	Caenorhabditis ele
35	226.5	17.4	455	1	W97860	Cat flea glutamate
36	207	15.9	487	1	R88361	Caenorhabditis ele
37	150	11.5	57	1	R89337	GABA receptor subu
38	118	9.1	50	1	W05247	Glutamate-gated ch
39	90	6.9	459	1	P96202	Human muscarinic a
40	88	6.8	479	1	R60695	Fragment of the mu
41	83.5	6.4	404	1	W31344	Human G-protein co
42	83.5	6.4	404	1	W34984	Human G-protein co
43	83.5	6.4	404	1	W59035	Human G-protein co
44	80	6.1	898	1	W31853	Mycobacterium tube
45	80	6.1	430	1	W57403	Human MAD-related

ALIGNMENTS

RESULT 1
W59048
ID W59048 standard; Protein; 506 AA.
AC W59048;
DT 25-SEP-1998 (first entry)
DE GABA-A receptor epsilon sub-unit related protein.
KW GABA-A receptor; diagnosis; therapy; drug screening.
OS Mammalia.
PN DE19644501-A1.
PD 30-APR-1998.
PF 25-OCT-1996; 044501.
PR 25-OCT-1996; DE-044501.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR WPI; 98-252096/23.
DR N-PSDB; V11776.
PT Protein related to GABA-A receptor sub-unit epsilon - useful for
PT diagnosis, therapy or drug screening
PS Example 1; Fig 1; 12pp; German.
CC The GABA-A receptor sub-unit epsilon related protein is used for the
CC diagnosis and/or therapy of related disorders. It can also be used to
CC screen for substances that modulate the activity of the protein.
SQ Sequence 506 AA;

Query Match 100.0%; Score 1302; DB 1; Length 506;
Best Local Similarity 100.0%; Pred. No. 3.3e-119;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 306

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 366

Qy     121 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 426

Qy     181 QPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     427 QPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 486

Qy     241 VF 242
           ||
Db     487 VF 488
```

RESULT 2
W59049
ID W59049 standard; Protein; 474 AA.
AC W59049;
DT 25-SEP-1998 (first entry)
DE Variant of GABA-A receptor epsilon sub-unit related protein.
KW GABA-A receptor; diagnosis; therapy; drug screening.
OS Mammalia.
PN DE19644501-A1.
PD 30-APR-1998.
PF 25-OCT-1996; 044501.
PR 25-OCT-1996; DE-044501.

```
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PI   Bilke K, Gaul R, Kioschis P, Poustka A, Wilke K;
DR   WPI; 98-252096/23.
DR   N-PSDB; V11777.
PT   Protein related to GABA-A receptor sub-unit epsilon - useful for
PT   diagnosis, therapy or drug screening
PS   Disclosure; Fig 2; 12pp; German.
CC   The GABA-A receptor sub-unit epsilon related protein is used for the
CC   diagnosis and/or therapy of related disorders.  It can also be used to
CC   screen for substances that modulate the activity of the protein.
SQ   Sequence   474 AA;

  Query Match             100.0%;  Score 1302;  DB 1;  Length 474;
  Best Local Similarity   100.0%;  Pred. No. 3e-119;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     215 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 274

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     275 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 334

Qy     121 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     335 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 394

Qy     181 QPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     395 QPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 454

Qy     241 VF 242
           ||
Db     455 VF 456


RESULT   3
W61045
ID   W61045 standard; Protein; 506 AA.
AC   W61045;
DT   12-OCT-1998  (first entry)
DE   Human GABA receptor epsilon subunit.
KW   GABA receptor; gamma-amino butyric acid receptor; human;
KW   appetite; cognition.
OS   Homo sapiens.
PN   WO9823742-A1.
PD   04-JUN-1998.
PF   18-NOV-1997; G03159.
PR   03-OCT-1997; GB-020995.
PR   25-NOV-1996; GB-024442.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Whiting PJ;
DR   WPI; 98-322722/28.
DR   N-PSDB; V36319.
PT   New isolated GABA receptor subunit, epsilon - used to develop
PT   products for the screening and design of drugs, e.g. for modulating
PT   appetite behaviours, hormonal interactions and cognition
PS   Claim 15; Fig 1; 37pp; English.
CC   This polypeptide comprises a novel class of subunit, classified as
CC   as epsilon, within the human GABA receptor gene family.  Its amino
CC   acid sequence was deduced from a cDNA clone (see V36319) isolated
CC   from a human brain cDNA library.  A stably co-transfected eukaryotic
CC   cell line capable of expressing the GABA epsilon receptor subunit,
CC   at least one alpha receptor subunit and at least one beta receptor
CC   subunit is claimed.  A recombinant expression vector, and protein
CC   and membrane preparations of the GABA receptor obtained from the
CC   co-transfected cells are also claimed.  The new GABA-A receptor
CC   epsilon subunit and products can be used in the screening and
CC   design of drugs which act upon the GABA receptor.  The ligands or
CC   drug candidates identified may be used as therapeutic agents, e.g.
CC   for the modulation of appetite behaviours, hormonal interactions
CC   and cognition.  They can also be used for the study of structure,
CC   pharmacology and function of the various GABA receptor subtypes.
SQ   Sequence   506 AA;

  Query Match             100.0%;  Score 1302;  DB 1;  Length 506;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-119;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 306

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 366

Qy     121 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 426

Qy     181 QPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     427 QPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 486

Qy     241 VF 242
           ||
Db     487 VF 488


RESULT   4
R83968
ID   R83968 standard; Protein; 467 AA.
AC   R83968;
DT   02-FEB-1996  (first entry)
DE   GABA-A receptor gamma-3 subunit.
KW   GABA-A receptor; gamma-aminobutyric acid receptor; gamma-3 subunit.
OS   Homo sapiens.
PN   WO9529234-A1.
PD   02-NOV-1995.
PF   12-APR-1995; G00834.
PR   22-APR-1994; GB-008064.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Whiting PJ;
DR   WPI; 95-382983/49.
DR   N-PSDB; T02334.
PT   New cell line expressing human GABA-A receptor sub-units - useful in
PT   drug screening and design
PS   Disclosure; Page 21-23; 30pp; English.
CC   A cDNA clone isolated from a human foetal brain cDNA library
CC   encoded the GABA-A receptor gamma-3 subunit (R83968).
CC   The cDNA can be expressed in eukaryotic (pref. rodent fibroblast)
CC   cell lines to produce recombinant gamma-3 subunit or hybrid
CC   GABA-A receptors having novel subunit compositions.
SQ   Sequence   467 AA;

  Query Match             35.4%;  Score 461.5;  DB 1;  Length 467;
  Best Local Similarity   37.7%;  Pred. No. 2.8e-37;
  Matches   98;  Conservative   43;  Mismatches   68;  Indels   51;  Gaps    6;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           | |: | |||:||  ||::||||:| :| | ||   | |:|  :| :|||||||| ::
Db     223 FMGLRNTTEIVTTSAGDYVVMTIYFELSTRMGYFTIQTYIPCILTVVLSWVSFWIKKDAT 282

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           ||||:||||:||||||| | :||: |||||:||:| :: :||:| | ||:|:| ||:  |
Db     283 PARTALGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEYATLNY--Y 340

Qy     121 NQTKAHASPK----LRHP--------RINSRAHARTRARSRACARQHQEAFVCQIVTTEG 168
           :  :   : |    | ||         ||: :| :
Db     341 SSCRKPTTTKKTTSLLHPDSSRWIPERISLQAPSNY---------------------- 377
```

```
Qy    169 SDGEERPSCSAQQPPSPGSPEGPRSLC---SKLACCEWC---KRFKKYFCMVPDCEGSTW 222
Db    377 -------SLLDMRPPPPAMITLNNSVYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSW 429

Qy    223 QQGRLCIHVYRLDNYSRVVF 242
Db    430 RKGRIHIDILELDSYSRVFF 449
```

RESULT 5
R97298
ID R97298 standard; Protein; 554 AA.
AC R97298;
DT 06-JAN-1997 (first entry)
DE Human GABA-A receptor alpha 4 subunit.
KW GABA-A receptor; gamma-aminobutyric acid; alpha-4 subunit.
OS Homo sapiens.
PN WO9610637-A1.
PD 11-APR-1996.
PF 29-SEP-1995; G02323.
PR 01-OCT-1994; GB-020010.
PA (MERI) MERCK SHARP & DOHME LTD.
PI Le Bourdelles B, Whiting PJ;
DR WPI; 96-209359/21.
DR N-PSDB; T28988.
PT DNA encoding alpha-4 and delta subunit(s) of the human GABAa
PT receptor - also stably co-transfected eukaryotic cells expressing
PT receptors contg. these subunit(s), used for screening and designing
PT drugs
PS Example 1; Fig 2; 45pp; English.
CC The amino acid sequence (R97298) of the alpha-4 subunit of the
CC human GABA-A receptor was deduced from a cDNA clone (T28988)
CC isolated from a human brain thalamus cDNA library. The alpha-4
CC subunit can be produced in transfected host cells, partic. rodent
CC fibroblasts. Co-transfected host cells capable of expressing the
CC alpha-4, delta (see also R97299) and beta subunits can be used to
CC screen or design drugs that act on GABA-A receptors, e.g.
CC benzodiazepines, barbiturates, beta-carbolines and neurosteroids.
CC Construction of recombinant receptors contg. the alpha-4 and
CC delta subunits becomes possible for the first time.
SQ Sequence 554 AA;

Query Match 25.9%; Score 337; DB 1; Length 554;
Best Local Similarity 38.4%; Pred. No. 4.8e-25;
Matches 78; Conservative 37; Mismatches 66; Indels 22; Gaps 6;

```
Qy      3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
Db    228 GQTVSSETIKSITGEYIVMTVYFHLRRKMGYFMIQTYIPCIMTVILSQVSFWINKESVPA 287

Qy     63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
Db    288 RTVFGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNIQ 347

Qy    123 ------------TKAHASP--KLRHPRI---NSRAHARTRARSRACARQHQEAFVCQIVT 165
Db    348 MEKAKRKTSKPPQEVPAAPVQREKHPEAPLQNTNANLNMRKRTNALV--HSESDVGN--R 403

Qy    166 TEGSDGEERPSCSAQQPPSPGSP 188
Db    404 TEVGNHSSKSSTVVQE-SSKGTP 425
```

RESULT 6
R31187
ID R31187 standard; Protein; 453 AA.
AC R31187;
DT 10-MAY-1993 (first entry)
DE GABA-A receptor alpha-6 subunit.
KW Primer; human; alpha-6; subunit; gamma-amino butyric acid; GABA; -A;
KW receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW ligand; alpha; beta; gamma; delta.
OS Homo sapiens.
PN WO9222652-A.
PD 23-DEC-1992.
PF 09-JUN-1992; G01031.
PR 11-JUN-1991; GB-012504.
PA (MERI) MERCK SHARP & DOHME LTD.
PI Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR WPI; 93-018138/02.
DR N-PSDB; Q33130.
PT Stably transfected eukaryotic cell line - expresses human GABA-A
PT receptor comprising alpha, beta and gamma sub-units, useful for
PT medicament prepn.
PS Disclosure; Fig 5; 43pp; English.
CC This sequence represents the human alpha-6 subunit of gamma-amino
CC butyric acid (GABA)-A receptor. Rat alpha-6 cDNA was used as a probe
CC and a human alpha-6 cDNA clone was isolated from a cerebellum cDNA
CC library. No full length cDNA's were isolated. To obtain a full length
CC cDNA 3 clones were joined together using convenient restriction sites.
CC GABA-A receptor comprises a multimeric protein of molecular size
CC 230-370 kD with specific binding sites for various drugs including
CC benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC agonist ligand GABA. The receptor is composed of several distinct
CC types of subunit, which are divided into four classes (alpha, beta,
CC gamma and delta) based on sequence homology. To date six types of
CC alpha, three types of beta, two types of gamma and one type of delta
CC subunit have been identified. It has been found that in addition to
CC an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC required to confer benzodiazipine sensitivity. The benzodiazepine
CC pharmacology of the receptor is largely dependent on the identity of
CC the alpha and gamma subunits present. Receptors containing a delta
CC subunit do not appear to bind benzodiazepines.
SQ Sequence 453 AA;

Query Match 25.3%; Score 329; DB 1; Length 453;
Best Local Similarity 31.8%; Pred. No. 2.3e-24;
Matches 83; Conservative 40; Mismatches 70; Indels 68; Gaps 7;

```
Qy      3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
Db    212 GQTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPA 271

Qy     63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
Db    272 RTVLGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQ 331

Qy    123 TK------AHASPK--------------LRHPRINSRAHARTRARSRACARQHQEAFVC 161
Db    332 TQKAKRKAQFAAPPTVTISKATEPLEAEIVLHP--DSKYHLKKRITSLS----------L 379

Qy    162 QIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGST 221
Db    380 PIVSS-----SEANKVLTRAPILQSTPVTPPPL------------------PPAFGGT 414

Qy    222 WQQGRLCIHVYRLDNYSRVVF 242
Db    415 ----------SKIDQYSRILF 425
```

RESULT 7
R59865
ID R59865 standard; Protein; 453 AA.
AC R59865;
DT 20-MAR-1995 (first entry)
DE Human GABA receptor alpha6 subunit DNA.
KW GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW central nervous system.
OS Homo sapiens.
PN WO9413799-A.
PD 23-JUN-1994.
PF 07-DEC-1993; G02506.
PR 10-DEC-1992; GB-025776.

```
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   N-PSDB; Q69142.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.5; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   453 AA;


  Query Match             25.3%;  Score 329;  DB 1;  Length 453;
  Best Local Similarity   31.8%;  Pred. No. 2.3e-24;
  Matches   83;  Conservative   40;  Mismatches   70;  Indels   68;  Gaps    7;

Qy       3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
           | :  :| | :  |::::||::|:: |: ||   | | |  :| :|| ||||| || ||
Db     212 GQTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPA 271

Qy      63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
           || ||||:|||||||   :| : |:||| ||:|::||:|| | | ||:||| :|:    |
Db     272 RTVLGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQ 331

Qy     123 TK------AHASPK--------------LRHPRINSRAHARTRARSRACARQHQEAFVC 161
           |:        |:|                : ||  :|: | : |  | :
Db     332 TQKAKRKAQFAAPPTVTISKATEPLEAEIVLHP--DSKYHLKKRITSLS----------L 379

Qy     162 QIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGST 221
             ||::      |      : |    :|  |  |                  |   | |
Db     380 PIVSS-----SEANKVLTRAPILQSTPVTPPPL------------------PPAFGGT 414

Qy     222 WQQGRLCIHVYRLDNYSRVVF 242
                     ::| |||::|
Db     415 ----------SKIDQYSRILF 425


RESULT   8
R31186
ID   R31186 standard; Protein; 462 AA.
AC   R31186;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-5 subunit.
KW   Primer; human; alpha-5; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta.
OS   Homo sapiens.
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   N-PSDB; Q33129.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Disclosure; Fig 4; 43pp; English.
CC   This sequence represents the human alpha-5 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Rat alpha-5 cDNA was used as a probe
CC   and a human alpha-5 cDNA clone was isolated from a hippocampal cDNA
CC   library.  GABA-A receptor comprises a multimeric protein of molecular
CC   size 230-370 kD with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   462 AA;


  Query Match             24.4%;  Score 317.5;  DB 1;  Length 462;
  Best Local Similarity   30.5%;  Pred. No. 3.1e-23;
  Matches   74;  Conservative   43;  Mismatches   75;  Indels   51;  Gaps    5;

Qy       8 TEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLG 67
           || |:|  |:: :||  |:: |: ||   | |:|  :| :|| ||||:  || ||||  |
Db     234 TENISTSTGEYTIMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFG 293

Qy      68 ITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL-----IYNQ 122
           :|:|||||||   :| : |:|:| ||:|::||:|: | | ||:||| :|:       ::
Db     294 VTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGWAWDG 353

Qy     123 TKAHASPKLRHPR---INSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSA 179
           ||  : |::  |   :|   :| |  :                              |:
Db     354 KKALEAAKIKKKREVILNKSTNAFTTGKM----------------------SHPPNIPK 390

Qy     180 QQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSR 239
           :|     :| |  :  |                 |   |  | :  :    : ::|  ||
Db     391 EQ-----TPAGTSNTTS--------------VSVKPSEEKTSESKKTYNSISKIDKMSR 430

Qy     240 VVF 242
           :||
Db     431 IVF 433


RESULT   9
R59864
ID   R59864 standard; Protein; 462 AA.
AC   R59864;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha5 subunit.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   N-PSDB; Q69141.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.4; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   462 AA;


  Query Match             24.4%;  Score 317.5;  DB 1;  Length 462;
  Best Local Similarity   30.5%;  Pred. No. 3.1e-23;
  Matches   74;  Conservative   43;  Mismatches   75;  Indels   51;  Gaps    5;

Qy       8 TEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLG 67
           || |:|  |:: :||  |:: |: ||   | |:|  :| :|| ||||:  || ||||  |
Db     234 TENISTSTGEYTIMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFG 293

Qy      68 ITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL-----IYNQ 122
```

```
          :|:|||||||   :| : |:|:| ||:|::||:|: | | ||:||| :|:       ::
Db    294 VTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGWAWDG 353

Qy    123 TKAHASPKLRHPR---INSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSA 179
           ||  : |::  |   :|   :| |  :                            |:
Db    354 KKALEAAKIKKKREVILNKSTNAFTTGKM----------------------SHPPNIPK 390

Qy    180 QQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSR 239
          :|     :| |  :  |                 |   |  | :  :    : ::|  ||
Db    391 EQ-----TPAGTSNTTS--------------VSVKPSEEKTSESKKTYNSISKIDKMSR 430

Qy    240 VVF 242
          :||
Db    431 IVF 433


RESULT  10
R31185
ID   R31185 standard; Protein; 492 AA.
AC   R31185;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-3 subunit.
KW   Primer; human; alpha-3; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta.
OS   Homo sapiens.
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   N-PSDB; Q33128.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Disclosure; Fig 3; 43pp; English.
CC   This sequence represents the human alpha-3 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Bovine alpha-3 cDNA was used as a
CC   probe and an alpha-3 cDNA clone was isolated from a human foetal
CC   brain cDNA library, which was missing approx. 100 bp of the 5' end.
CC   This missing fragment was isolated by PCR.  The two fragments were
CC   ligated together to give a full length alpha-3 cDNA.    GABA-A
CC   receptor comprises a multimeric protein of molecular size 230-370 kD
CC   with specific binding sites for various drugs including
CC   benzodiazepines, barbiturates, and beta-carbolines, in addition to the
CC   agonist ligand GABA.  The receptor is composed of several distinct
CC   types of subunit, which are divided into four classes (alpha, beta,
CC   gamma and delta) based on sequence homology.  To date six types of
CC   alpha, three types of beta, two types of gamma and one type of delta
CC   subunit have been identified.  It has been found that in addition to
CC   an alpha and a beta subunit, either gamma-1 or gamma-2 is also
CC   required to confer benzodiazipine sensitivity.  The benzodiazepine
CC   pharmacology of the receptor is largely dependent on the identity of
CC   the alpha and gamma subunits present.  Receptors containing a delta
CC   subunit do not appear to bind benzodiazepines.
SQ   Sequence   492 AA;


  Query Match             24.0%;  Score 312;  DB 1;  Length 492;
  Best Local Similarity   50.0%;  Pred. No. 1.1e-22;
  Matches   55;  Conservative   25;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      8 TEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLG 67
          ||||  :  |:::|||  |:: |: ||   | |:|  :| :|| ||||:  || ||||  |
Db    252 TEIIRSSTGEYVVMTTHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFG 311

Qy     68 ITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNF 117
          :|:|||||||   :| : |:|:| ||:|::||:|: | | ||:||| :|:
Db    312 VTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNY 361


RESULT  11
R59863
ID   R59863 standard; Protein; 492 AA.
AC   R59863;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha3 subunit.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   N-PSDB; Q69140.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.3; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   492 AA;


  Query Match             24.0%;  Score 312;  DB 1;  Length 492;
  Best Local Similarity   50.0%;  Pred. No. 1.1e-22;
  Matches   55;  Conservative   25;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      8 TEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLG 67
          ||||  :  |:::|||  |:: |: ||   | |:|  :| :|| ||||:  || ||||  |
Db    252 TEIIRSSTGEYVVMTTHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFG 311

Qy     68 ITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNF 117
          :|:|||||||   :| : |:|:| ||:|::||:|: | | ||:||| :|:
Db    312 VTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNY 361


RESULT  12
R31184
ID   R31184 standard; Protein; 451 AA.
AC   R31184;
DT   10-MAY-1993  (first entry)
DE   GABA-A receptor alpha-2 subunit.
KW   Primer; human; alpha-3; subunit; gamma-amino butyric acid; GABA; -A;
KW   receptor; bovine; probe; PCR; polymerase chain reaction; multimeric;
KW   binding site; benzodiazepine; barbiturate; beta-carboline; agonist;
KW   ligand; alpha; beta; gamma; delta.
OS   Homo sapiens.
PN   WO9222652-A.
PD   23-DEC-1992.
PF   09-JUN-1992; G01031.
PR   11-JUN-1991; GB-012504.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL, Le Bourdelles B, Whiting PJ, Wingrove PB;
DR   WPI; 93-018138/02.
DR   N-PSDB; Q33127.
PT   Stably transfected eukaryotic cell line - expresses human GABA-A
PT   receptor comprising alpha, beta and gamma sub-units, useful for
PT   medicament prepn.
PS   Disclosure; Fig 2; 43pp; English.
CC   This sequence represents the human alpha-2 subunit of gamma-amino
CC   butyric acid (GABA)-A receptor.  Bovine alpha-2 cDNA was used as a
CC   probe and an alpha-2 cDNA clone was isolated from a human foetal
CC   brain cDNA library. GABA-A receptor comprises a multimeric protein
CC   of molecular size 230-270 kD with specific binding sites for various
CC   drugs including benzodiazepines, barbiturates, and beta-carbolines,
CC   in addition to the agonist ligand GABA.  The receptor is composed of
```

```
CC   several distinct types of subunit, which are divided into four classes
CC   (alpha, beta, gamma and delta) based on sequence homology.  To date
CC   six types of alpha, three types of beta, two types of gamma and one
CC   type of delta subunit have been identified.  It has been found that
CC   in addition to an alpha and a beta subunit, either gamma-1 or gamma-2
CC   is also required to confer benzodiazipine sensitivity.  The benzo-
CC   diazepine pharmacology of the receptor is largely dependent on the
CC   identity of the alpha and gamma subunits present.  Receptors
CC   containing a delta subunit do not appear to bind benzodiazepines.
SQ   Sequence   451 AA;


  Query Match             23.2%;  Score 302;  DB 1;  Length 451;
  Best Local Similarity   47.8%;  Pred. No. 9.6e-22;
  Matches   55;  Conservative   24;  Mismatches   36;  Indels    0;  Gaps    0;

Qy       3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
           | |   | | :  |:: |||  |:: |: ||   | |:|  :| :|| |||:  || ||
Db     222 GQSIGKETIKSSTGEYTVMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPA 281

Qy      63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNF 117
           ||  |:|:|||||||   :| : |:|:| ||:|::||:|: | | ||:||| :|:
Db     282 RTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNY 336


RESULT  13
R59862
ID   R59862 standard; Protein; 451 AA.
AC   R59862;
DT   20-MAR-1995  (first entry)
DE   Human GABA receptor alpha2 subunit.
KW   GABA receptor; gamma-aminobutyric acid; neurotransmitter;
KW   central nervous system.
OS   Homo sapiens.
PN   WO9413799-A.
PD   23-JUN-1994.
PF   07-DEC-1993; G02506.
PR   10-DEC-1992; GB-025776.
PR   07-SEP-1993; GB-018528.
PA   (MERI ) MERCK SHARP & DOHME LTD.
PI   Hadingham KL,  Whiting PJ;
DR   WPI; 94-234213/28.
DR   N-PSDB; Q69139.
PT   Cell lines expressing GABA-A receptors - used for screening for
PT   and designing medicaments which act on the GABA-A receptors
PS   Disclosure; Fig.2; 79pp; English.
CC   This receptor may be expressed in mammal cell lines which may be
CC   used for screening for and designing medicaments which act on the
CC   human GABAA receptor.  The cells expressing this subunit are ideal
CC   systems for the study of the structure, pharmacology and function
CC   of the receptor subtype.
SQ   Sequence   451 AA;


  Query Match             23.2%;  Score 302;  DB 1;  Length 451;
  Best Local Similarity   47.8%;  Pred. No. 9.6e-22;
  Matches   55;  Conservative   24;  Mismatches   36;  Indels    0;  Gaps    0;

Qy       3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
           | |   | | :  |:: |||  |:: |: ||   | |:|  :| :|| |||:  || ||
Db     222 GQSIGKETIKSSTGEYTVMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPA 281

Qy      63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNF 117
           ||  |:|:|||||||   :| : |:|:| ||:|::||:|: | | ||:||| :|:
Db     282 RTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNY 336


RESULT  14
R89336
ID   R89336 standard; Protein; 496 AA.
AC   R89336;
DT   13-APR-1996  (first entry)
DE   GABA receptor subunit.
KW   Gamma-aminobutyric acid receptor; GABA receptor; subunit; LCCH3;
KW   ligand-gated chloride channel; polymerase chain reaction; PCR;
KW   probe; hybridisation; primer; cloning; pupa; signature motif;
KW   transmembrane domain; extracellular domain; intracellular domain;
KW   disulphide bond; loop; vector; insecticide; pesticide; screening.
OS   Drosophila melanogaster.
FH   Key             Location/Qualifiers
FT   peptide         1. .20
FT                   /note= "Signal peptide"
FT   domain          21. .258
FT                   /note= "Extracellular domain"
FT   modified_site   39
FT                   /note= "N-glycosylation site"
FT   disulfide_bond  176. .190
FT                   /note= "Forms loop in extracellular domain"
FT   modified_site   189
FT                   /note= "N-glycosylation site"
FT   domain          259. .280
FT                   /note= "Transmembrane domain M1"
FT   domain          285. .306
FT                   /note= "Transmembrane domain M2"
FT   peptide         294. .301
FT                   /note= "Signature motif (R89338)"
FT   domain          318. .342
FT                   /note= "Transmembrane domain M3"
FT   peptide         326. .331
FT                   /note= "Conserved motif (R89339)"
FT   domain          343. .472
FT                   /note= "Intracellular domain"
FT   modified_site   388
FT                   /note= "Phosphorylation site"
FT   modified_site   454
FT                   /note= "Phosphorylation site"
FT   domain          473. .494
FT                   /note= "Transmembrane domain M4"
PN   US5487976-A.
PD   30-JAN-1996.
PF   15-OCT-1993; 137614.
PR   15-OCT-1993; US-137614.
PA   (CORR ) CORNELL RES FOUND INC.
PI   Henderson JE,  Knipple DC,  Soderlund DM;
DR   WPI; 96-105226/11.
DR   N-PSDB; Q99330.
PT   DNA molecule encoding gamma-aminobutyric acid receptor subunit  -
PT   used to screen for insect, e.g. Drosophila melanogaster, control
PT   pesticides
PS   Claim 1; Column 23-26; 37pp; English.
CC   The sequence represents a Drosophila melanogaster GABA receptor
CC   subunit with homology to the ligand-gated chloride channel family,
CC   designated LCCH3.  A cDNA encoding the receptor has been isolated by
CC   polymerase chain reaction (PCR)-based homology probing, along with
CC   a gene encoding LCCH2 (R89337), using primers Q99333-35 (based on
CC   conserved signature motif R89338) and probe Q99336 (based on
CC   conserved motif R89339), followed by screening of a pupa cDNA
CC   library.  The protein (mol.wt. 54,442) has several typical features
CC   of ligand-gated chloride channel subunits, including 4 hydrophobic
CC   domains capable of forming transmembrane helices, a large
CC   intracellular domain, and cysteine residues forming a
CC   disulphide-bridged loop structure in the extracellular domain.  DNA
CC   encoding the protein may be expressed in heterologous cells using a
CC   vector, for screening of insecticides by evaluating their
CC   specificity for the GABA receptor.
SQ   Sequence   496 AA;


  Query Match             22.9%;  Score 298.5;  DB 1;  Length 496;
  Best Local Similarity   39.9%;  Pred. No. 2.4e-21;
  Matches   59;  Conservative   30;  Mismatches   54;  Indels    5;  Gaps    2;

Qy       5 SNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPART 64
           ::: | : |  | :  ::: | : |  ||  || |:|| :  |||||||||  |:  ||
Db     232 NDRKERLAT--GVYQRLSLSFKLQRNIGYFVFQTYLPSILIVMLSWVSFWINHEATSARV 289
```

```
Qy      65 SLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTK 124
           :||||:||||||: |  | : ||:||: |:| |: :|||| | ||||:| :|:  : :
Db     290 ALGITTVLTMTTISTGVRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWGK-- 348

Qy     125 AHASPKLRHPRINSRAHARTRARSRACA 152
             |  |::  :          ||  |:
Db     348 -RAKKKIKKVKECCPGKIGKSERSETCS 374


RESULT  15
W86161
ID   W86161 standard; Protein; 496 AA.
AC   W86161;
DT   04-MAR-1999  (first entry)
DE   Insect GABA receptor subunit LCCH3.
KW   GABA; gamma-aminobutyric acid receptor; LCCH3; GABA recognition site;
KW   Grd; insecticide; insect; pharmacological; screening.
OS   Drosophila sp.
PN   US5854002-A.
PD   29-DEC-1998.
PF   17-DEC-1996; 768301.
PR   17-DEC-1996; US-768301.
PA   (RHON ) RHONE-POULENC INC.
PI   Gant DB, Tomalski MD;
DR   WPI; 99-094901/08.
DR   N-PSDB; V84685.
PT   Host cells that express LCCH3 and Grd subunits of insect
PT   gamma-aminobutyric acid receptor - comprises separate vectors or a
PT   single vector, used for screening compounds for insecticidal
PT   activity
PS   Claim 1; Columns 17-20; 27pp; English.
CC   This represents an insect gamma-aminobutyric acid (GABA) receptor subunit
CC   LCCH3. The invention provides host cells comprising (i) two expression
CC   vectors, one containing a sequence encoding the GABA receptor subunit
CC   LCCH3 and the other containing a sequence encoding the GABA receptor Grd
CC   subunit, with the sequences under control of separate promoters; or (ii)
CC   a single expression vector containing both GABA receptor subunits LCCH3
CC   and Grd linked to one or more regulatory elements. Membrane preparation
CC   from these cells are used to screen compounds for their ability to bind
CC   to the GABA recognition site of an insect GABA receptor, specifically to
CC   identify new insecticides. Co-expression of LCCH3 and Grd generates a
CC   GABA recognition site in the host cell membrane that has pharmacological
CC   properties very similar to those of the native receptor. The cells and
CC   membrane preparations are suitable for high throughput screening.
SQ   Sequence   496 AA;


  Query Match            22.9%;  Score 298.5;  DB 1;  Length 496;
  Best Local Similarity   39.9%;  Pred. No. 2.4e-21;
  Matches   59;  Conservative   30;  Mismatches   54;  Indels    5;  Gaps    2;

Qy       5 SNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPART 64
           ::: | : |  | :  ::: | : |  ||  || |:|| :  |||||||||  |:  ||
Db     232 NDRKERLAT--GVYQRLSLSFKLQRNIGYFVFQTYLPSILIVMLSWVSFWINHEATSARV 289

Qy      65 SLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTK 124
           :||||:||||||: |  | : ||:||: |:| |: :|||| | ||||:| :|:  : :
Db     290 ALGITTVLTMTTISTGVRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWGK-- 348

Qy     125 AHASPKLRHPRINSRAHARTRARSRACA 152
             |  |::  :          ||  |:
Db     348 -RAKKKIKKVKECCPGKIGKSERSETCS 374


Search completed: March 10, 2000, 08:51:55
Job time: 5288 sec
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:01:24 ; Search time 34.6 Seconds
(without alignments)
93.006 Million cell updates/sec

Title: US-09-030-832-42_COPY_247_488
Perfect score: 1302
Sequence: 1 FTGVSNKTEIITTPVGDFMV.....QQGRLCIHVYRLDNYSRVVF 242

Scoring table: BLOSUM62

Searched: 133990 seqs, 13297546 residues

Database : Issued_Patents_AA:*

Word size : 0

Number of hits that pass the threshold : 133990
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/PCTUS9_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	450	34.6	467	1	US-08-459-100A-3	Sequence 3, Appli
2	329	25.3	453	1	US-08-417-330A-18	Sequence 18, Appl
3	318	24.4	617	1	US-08-137-614A-24	Sequence 24, Appl
4	317.5	24.4	462	1	US-08-417-330A-16	Sequence 16, Appl
5	312	24.0	492	1	US-08-417-330A-14	Sequence 14, Appl
6	302	23.2	451	1	US-08-417-330A-12	Sequence 12, Appl
7	298.5	22.9	496	1	US-08-137-614A-2	Sequence 2, Appli
8	298.5	22.9	496	2	US-08-768-301-2	Sequence 2, Appli
9	294	22.6	617	1	US-08-137-614A-25	Sequence 25, Appl
10	294	22.6	474	1	US-08-459-100A-4	Sequence 4, Appli
11	284	21.8	474	1	US-08-417-330A-20	Sequence 20, Appl
12	257.5	19.8	686	2	US-08-768-301-4	Sequence 4, Appli
13	254	19.5	637	3	US-08-072-064-4	Sequence 4, Appli
14	253	19.4	637	3	US-08-072-064-6	Sequence 6, Appli
15	251	19.3	617	1	US-08-137-614A-26	Sequence 26, Appl
16	251	19.3	637	3	US-08-072-064-1	Sequence 1, Appli
17	251	19.3	637	4	PCT-US92-08558-1	Sequence 1, Appli
18	250	19.2	637	3	US-08-072-064-8	Sequence 8, Appli
19	247.5	19.0	488	1	US-08-554-659-2	Sequence 2, Appli
20	246	18.9	440	1	US-08-459-100A-2	Sequence 2, Appli
21	246	18.9	440	4	PCT-US94-09589-2	Sequence 2, Appli
22	244.5	18.8	488	1	US-08-554-659-4	Sequence 4, Appli
23	241	18.5	456	1	US-08-435-933-6	Sequence 6, Appli
24	241	18.5	456	4	PCT-US96-06035-6	Sequence 6, Appli
25	234.5	18.0	510	1	US-08-249-112-3	Sequence 3, Appli
26	234.5	18.0	510	4	PCT-US95-06556-3	Sequence 3, Appli
27	207	15.9	487	1	US-08-249-112-4	Sequence 4, Appli
28	207	15.9	487	4	PCT-US95-06556-4	Sequence 4, Appli
29	198	15.2	57	1	US-08-137-614A-21	Sequence 21, Appl
30	174	13.4	57	1	US-08-137-614A-19	Sequence 19, Appl
31	171	13.1	57	1	US-08-137-614A-17	Sequence 17, Appl
32	167	12.8	57	1	US-08-137-614A-23	Sequence 23, Appl
33	166	12.7	57	1	US-08-137-614A-18	Sequence 18, Appl
34	161	12.4	57	1	US-08-137-614A-22	Sequence 22, Appl
35	158	12.1	57	1	US-08-137-614A-20	Sequence 20, Appl
36	150	11.5	57	1	US-08-137-614A-16	Sequence 16, Appl
37	137	10.5	52	1	US-08-137-614A-15	Sequence 15, Appl
38	122	9.4	56	4	PCT-US92-08558-7	Sequence 7, Appli
39	118	9.1	50	1	US-08-435-933-3	Sequence 3, Appli
40	118	9.1	50	4	PCT-US96-06035-3	Sequence 3, Appli
41	88	6.8	479	1	US-08-313-553-7	Sequence 7, Appli
42	88	6.8	479	3	US-08-767-993-7	Sequence 7, Appli
43	87	6.7	53	4	PCT-US92-08558-12	Sequence 12, Appl
44	84	6.5	56	4	PCT-US92-08558-5	Sequence 5, Appli
45	83.5	6.4	404	1	US-08-696-770-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-459-100A-3
; Sequence 3, Application US/08459100A
; Patent No. 5654172
; GENERAL INFORMATION:
; APPLICANT: Li, ET AL.
; TITLE OF INVENTION: GABAA Receptor Epsilon Subunit
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,100A
; FILING DATE: June 2, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09589
; FILING DATE: 26 AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-325
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-459-100A-3

Query Match 34.6%; Score 450; DB 1; Length 467;
Best Local Similarity 34.3%; Pred. No. 2e-36;
Matches 85; Conservative 53; Mismatches 64; Indels 46; Gaps 5;

```
Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           | |: | ||:: |  ||:::||:::|::||| ||   | |:| ::  :||||||||  ::
Db     242 FVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAV 301

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           |||||||||:|||||| | :||: |:|||:||:| ::::||:| | ||:|:  |:: :
Db     302 PARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVS 361
```

```
Qy    121 NQTKAHASPKLRH---PRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEER 174
          |:  :    | :    | |: |  : |   : |     |  :  : |          ||::
Db    362 NRKPSKDKDKKKKNPAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD- 414

Qy    175 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 234
            |::                          :||   ||    |: ||: | : ::
Db    414 --CAS-----------------------------FFCCFEDCRTGAWRHGRIHIRIAKM 441

Qy    235 DNYSRVVF 242
            |:|:|: |
Db    442 DSYARIFF 449


RESULT   2
US-08-417-330A-18
; Sequence 18, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  453 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-18


  Query Match             25.3%;  Score 329;  DB 1;  Length 453;
  Best Local Similarity   31.8%;  Pred. No. 1.3e-24;
  Matches   83;  Conservative   40;  Mismatches   70;  Indels   68;  Gaps    7;

Qy      3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
            | :  :| | :  |::::||::|:: |: ||   | | |  :| :|| ||||| || ||
Db    212 GQTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPA 271

Qy     63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
          || ||||:|||||||   :| : |:||| ||:|::||:|| | | ||:||| :|:    |
Db    272 RTVLGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQ 331

Qy    123 TK------AHASPK--------------LRHPRINSRAHARTRARSRACARQHQEAFVC 161
            |:        |:|                : ||  :|: | : |  | :
Db    332 TQKAKRKAQFAAPPTVTISKATEPLEAEIVLHP--DSKYHLKKRITSLS----------L 379

Qy    162 QIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGST 221
            ||::      |      : |    :|  |  |                      |   | |
Db    380 PIVSS-----SEANKVLTRAPILQSTPVTPPPL-------------------PPAFGGT 414

Qy    222 WQQGRLCIHVYRLDNYSRVVF 242
                    ::| |||::|
Db    415 ----------SKIDQYSRILF 425


RESULT   3
US-08-137-614A-24
; Sequence 24, Application US/08137614A
; Patent No. 5487976
;  GENERAL INFORMATION:
;    APPLICANT:  Soderlund, David M.
;    APPLICANT:  Knipple, Douglas C.
;    APPLICANT:  Henderson, Joseph E.
;    TITLE OF INVENTION:  Gene Encoding An Insect
;    TITLE OF INVENTION:  Gamma-Aminobutyric Acid (GABA) Receptor Subunit
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,614A
;      FILING DATE:  15-OCT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716)263-1636
;      TELEFAX:  (716)263-1600
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  617 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-137-614A-24


  Query Match             24.4%;  Score 318;  DB 1;  Length 617;
  Best Local Similarity   44.4%;  Pred. No. 2.3e-23;
  Matches   64;  Conservative   25;  Mismatches   45;  Indels   10;  Gaps    3;

Qy      6 NKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTS 65
          || | ::|  ||:  ::: | : |  ||  || |:|| :  |||||||||  |:  || :
Db    254 NKIEELST--GDYQRLSLIFQLQRNIGYFIFQTYLPSILIVMLSWVSFWINHEATSARVA 311

Qy     66 LGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKA 125
          ||||:||||||:    | : ||:||: |:| |: :|||| | ||||:| :|:  :
Db    312 LGITTVLTMTTISNGVRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWG---- 368

Qy    126 HASPKLRHPRINSRAHARTRARSR 149
            |  : :|  ||   |  | |
```

```
Db    368 -ARAKRKAKRLRERA---TSVRKR 387


RESULT   4
US-08-417-330A-16
; Sequence 16, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  462 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-16


  Query Match             24.4%;  Score 317.5;  DB 1;  Length 462;
  Best Local Similarity   30.5%;  Pred. No. 1.8e-23;
  Matches   74;  Conservative   43;  Mismatches   75;  Indels   51;  Gaps    5;

Qy      8 TEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLG 67
          || |:|  |:: :||  |:: |: ||   | |:|  :| :|| ||||:  || ||||  |
Db    234 TENISTSTGEYTIMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFG 293

Qy     68 ITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFL-----IYNQ 122
          :|:|||||||   :| : |:|:| ||:|::||:|: | | ||:||| :|:       ::
Db    294 VTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGWAWDG 353

Qy    123 TKAHASPKLRHPR---INSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSA 179
           ||  : |::  |   :|   :| |  :                          |:
Db    354 KKALEAAKIKKKREVILNKSTNAFTTGKM----------------------SHPPNIPK 390

Qy    180 QQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSR 239
          :|     :| |  :  |                 |   | | :  :    : ::|  ||
Db    391 EQ-----TPAGTSNTTS--------------VSVKPSEEKTSESKKTYNSISKIDKMSR 430

Qy    240 VVF 242
          :||
Db    431 IVF 433


RESULT   5
US-08-417-330A-14
; Sequence 14, Application US/08417330A
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  492 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-14


  Query Match             24.0%;  Score 312;  DB 1;  Length 492;
  Best Local Similarity   50.0%;  Pred. No. 6.8e-23;
  Matches   55;  Conservative   25;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      8 TEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLG 67
          |||| :  |:::|||  |:: |: ||   | |:|  :| :|| ||||:  || ||||  |
Db    252 TEIIRSSTGEYVVMTTHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPARTVFG 311

Qy     68 ITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNF 117
          :|:|||||||   :| : |:|:| ||:|::||:|: | | ||:||| :|:
Db    312 VTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNY 361


RESULT   6
US-08-417-330A-12
; Sequence 12, Application US/08417330A
```

```
; Patent No. 5719057
;  GENERAL INFORMATION:
;    APPLICANT:  HADINGHAM, KAREN
;    APPLICANT:  LE BOURDELLES, BEATRICE
;    APPLICANT:  WHITING, PAUL
;    APPLICANT:  WINGROVE, PETER
;    TITLE OF INVENTION:  STABLY TRANSFECTED CELL LINE EXPRESSING
;    TITLE OF INVENTION:  GABA-A RECEPTOR AND NOVEL CLONED
;    TITLE OF INVENTION:  GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/417,330A
;      FILING DATE:  05-APR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  T1109IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  451 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-417-330A-12


  Query Match             23.2%;  Score 302;  DB 1;  Length 451;
  Best Local Similarity   47.8%;  Pred. No. 5.8e-22;
  Matches   55;  Conservative   24;  Mismatches   36;  Indels    0;  Gaps    0;

Qy       3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
           | |   | | :  |:: |||  |:: |: ||   | |:|  :| :|| |||| :  || ||
Db     222 GQSIGKETIKSSTGEYTVMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVPA 281

Qy      63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNF 117
           ||  |:|:|||||||   :| : |:|:| ||:|::||:|: | | ||:||| :|:
Db     282 RTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNY 336


RESULT   7
US-08-137-614A-2
; Sequence 2, Application US/08137614A
; Patent No. 5487976
;  GENERAL INFORMATION:
;    APPLICANT:  Soderlund, David M.
;    APPLICANT:  Knipple, Douglas C.
;    APPLICANT:  Henderson, Joseph E.
;    TITLE OF INVENTION:  Gene Encoding An Insect
;    TITLE OF INVENTION:  Gamma-Aminobutyric Acid (GABA) Receptor Subunit
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,614A
;      FILING DATE:  15-OCT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716)263-1636
;      TELEFAX:  (716)263-1600
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  496 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-137-614A-2


  Query Match             22.9%;  Score 298.5;  DB 1;  Length 496;
  Best Local Similarity   39.9%;  Pred. No. 1.4e-21;
  Matches   59;  Conservative   30;  Mismatches   54;  Indels    5;  Gaps    2;

Qy       5 SNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPART 64
           ::: | : |  | :  ::: | : |  ||  || |:|| :  |||||||||  |:  ||
Db     232 NDRKERLAT--GVYQRLSLSFKLQRNIGYFVFQTYLPSILIVMLSWVSFWINHEATSARV 289

Qy      65 SLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTK 124
           :||||:||||||: |  | : ||:||: |:| |: :|||| | ||||:| :|:  : :
Db     290 ALGITTVLTMTTISTGVRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWGK-- 348

Qy     125 AHASPKLRHPRINSRAHARTRARSRACA 152
             |  |::  :          ||  |:
Db     348 -RAKKKIKKVKECCPGKIGKSERSETCS 374


RESULT   8
US-08-768-301-2
; Sequence 2, Application US/08768301
; Patent No. 5854002
;  GENERAL INFORMATION:
;    APPLICANT:  Tomalski, Michael D.
;    APPLICANT:  Gant, Daniel B.
;    TITLE OF INVENTION:  METHOD OF IDENTIFYING COMPOUNDS THAT BIND
;    TITLE OF INVENTION:  TO THE INSECT GABA RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brumbaugh, Graves, Donohue & Raymond
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  10112-0228
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/768,301
;      FILING DATE:
```

```
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacLeod, Janet M
;      REGISTRATION NUMBER:  35,263
;      REFERENCE/DOCKET NUMBER:  A30693
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-408-2500
;      TELEFAX:  212-765-2519
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  496 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
US-08-768-301-2


  Query Match             22.9%;  Score 298.5;  DB 2;  Length 496;
  Best Local Similarity   39.9%;  Pred. No. 1.4e-21;
  Matches   59;  Conservative   30;  Mismatches   54;  Indels    5;  Gaps    2;

Qy       5 SNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPART 64
           ::: | : |  | :  ::: | : |  ||  || |:|| :  |||||||||  |:  ||
Db     232 NDRKERLAT--GVYQRLSLSFKLQRNIGYFVFQTYLPSILIVMLSWVSFWINHEATSARV 289

Qy      65 SLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTK 124
           :||||:||||||: |  | : ||:||: |:| |: :|||| | ||||:| :|:  : :
Db     290 ALGITTVLTMTTISTGVRSSLPRISYVKAIDIYLVMCFVFVFAALLEYAAVNYTYWGK-- 348

Qy     125 AHASPKLRHPRINSRAHARTRARSRACA 152
             |  |::  :           ||  |:
Db     348 -RAKKKIKKVKECCPGKIGKSERSETCS 374


RESULT  9
US-08-137-614A-25
; Sequence 25, Application US/08137614A
; Patent No. 5487976
;  GENERAL INFORMATION:
;    APPLICANT:  Soderlund, David M.
;    APPLICANT:  Knipple, Douglas C.
;    APPLICANT:  Henderson, Joseph E.
;    TITLE OF INVENTION:  Gene Encoding An Insect
;    TITLE OF INVENTION:  Gamma-Aminobutyric Acid (GABA) Receptor Subunit
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,614A
;      FILING DATE:  15-OCT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716)263-1636
;      TELEFAX:  (716)263-1600
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  617 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-137-614A-25


  Query Match             22.6%;  Score 294;  DB 1;  Length 617;
  Best Local Similarity   38.9%;  Pred. No. 5.2e-21;
  Matches   58;  Conservative   30;  Mismatches   47;  Indels   14;  Gaps    2;

Qy       4 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 63
             || | |  |   | :  ::: | : |  ||   | |:||:: |:||||||||  ::: ||
Db     253 VSKKVEFTT---GAYPRLSLSFRLKRNIGYFILQTYMPSTLITILSWVSFWINYDASAAR 309

Qy      64 TSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ- 123
             :||||:||||||: |  |:  |:: |: |:| |:  |||| | ||||:| :|:: : :
Db     310 VALGITTVLTMTTISTHLRETLPKIPYVKAIDIYLMGCFVFVFLALLEYAFVNYIFFGKG 369

Qy     123 ----------TKAHASPKLRHPRINSRAH 141
                       |:  ||   ::   ||
Db     370 PQKKGASKQDQSANEKNKLEMNKVQVDAH 398


RESULT  10
US-08-459-100A-4
; Sequence 4, Application US/08459100A
; Patent No. 5654172
;  GENERAL INFORMATION:
;    APPLICANT:  Li, ET AL.
;    TITLE OF INVENTION:  GABAA Receptor Epsilon Subunit
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,100A
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09589
;      FILING DATE:  26 AUG 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-325
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  474 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-459-100A-4
```

```
  Query Match           22.6%;  Score 294;  DB 1;  Length 474;
  Best Local Similarity  38.9%;  Pred. No. 3.8e-21;
  Matches   58;  Conservative   30;  Mismatches   47;  Indels   14;  Gaps    2;

Qy       4 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 63
           || | |  |   | :  ::: | : |  ||   | |:||:: |:||||||||  ::: ||
Db     219 VSKKVEFTT---GAYPRLSLSFRLKRNIGYFILQTYMPSTLITILSWVSFWINYDASAAR 275

Qy      64 TSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ- 123
           :||||:||||||: |  |:  |:: |: |:| |:  |||| | ||||:| :|:: : :
Db     276 VALGITTVLTMTTISTHLRETLPKIPYVKAIDIYLMGCFVFVFLALLEYAFVNYIFFGKG 335

Qy     123 ----------TKAHASPKLRHPRINSRAH 141
                    |:   ||   ::   ||
Db     336 PQKKGASKQDQSANEKNKLEMNKVQVDAH 364
```

RESULT 11
US-08-417-330A-20
; Sequence 20, Application US/08417330A
; Patent No. 5719057
; GENERAL INFORMATION:
; APPLICANT: HADINGHAM, KAREN
; APPLICANT: LE BOURDELLES, BEATRICE
; APPLICANT: WHITING, PAUL
; APPLICANT: WINGROVE, PETER
; TITLE OF INVENTION: STABLY TRANSFECTED CELL LINE EXPRESSING
; TITLE OF INVENTION: GABA-A RECEPTOR AND NOVEL CLONED
; TITLE OF INVENTION: GABA-RECEPTOR SUBUNIT cDNA SEQUENCES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,330A
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: T1109IA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3905
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 474 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-417-330A-20

```
  Query Match           21.8%;  Score 284;  DB 1;  Length 474;
  Best Local Similarity  42.6%;  Pred. No. 3.6e-20;
  Matches   49;  Conservative   29;  Mismatches   37;  Indels    0;  Gaps    0;

Qy       8 TEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLG 67
           |: :   | :  ::: | : |  ||   | |:|| : |:||||||||  ::: || :||
Db     219 TKKVVFSTGSYPRLSLSFKLKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALG 278

Qy      68 ITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
           ||:|||||: |  |:  |:: |: |:| |:  |||| | ||||:|::|:: : :
Db     279 ITTVLTMTTINTHLRETLPKIPYVKAIDMYLMGCFVFVFMALLEYALVNYIFFGR 333
```

RESULT 12
US-08-768-301-4
; Sequence 4, Application US/08768301
; Patent No. 5854002
; GENERAL INFORMATION:
; APPLICANT: Tomalski, Michael D.
; APPLICANT: Gant, Daniel B.
; TITLE OF INVENTION: METHOD OF IDENTIFYING COMPOUNDS THAT BIND
; TITLE OF INVENTION: TO THE INSECT GABA RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/768,301
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLeod, Janet M
; REGISTRATION NUMBER: 35,263
; REFERENCE/DOCKET NUMBER: A30693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2500
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 686 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-768-301-4

```
  Query Match           19.8%;  Score 257.5;  DB 2;  Length 686;
  Best Local Similarity  29.4%;  Pred. No. 2.2e-17;
  Matches   60;  Conservative   30;  Mismatches   63;  Indels   51;  Gaps    3;

Qy       2 TGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAP 61
           ||:|    : |    :: :: : |:: |  |    | | |  :  :|||||||:  |:
Db     362 TGLSGTITLETNHPSEYSMLMVNFHLQRHMGNFLIQVYGPCCLLVVLSWVSFWLNREATA 421

Qy      62 ARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYN 121
             | |||||:|||| ||  :| : |:||| |||||:: : | | |  :|:|||:
Db     422 DRVSLGITTVLTMTFLGLEARTDLPKVSYPTALDFFVFLSFGFIFATILQFAVV------ 476
```

```
Qy    122 QTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERP------ 176
                          |  |:  |  |       |: : : :|  : |  |
Db    476 ------------------HYYTKYGSGEC------YFIIEELDSESGESETEPLTSDFR 510

Qy    176 -------------SCSAQQPPSP 185
                        |:   || |
Db    511 GSTESKIYEVIPLSMCAISMPPPP 534


RESULT  13
US-08-072-064-4
; Sequence 4, Application US/08072064
; Patent No. 6008046
;  GENERAL INFORMATION:
;    APPLICANT:  FFRENCH-CONSTANT, RICHARD H.
;    APPLICANT:  JACKSON, MEYER B.
;    TITLE OF INVENTION:  DRUG AND PESTICIDE SCREENING
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER G. CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/072,064
;      FILING DATE:  19930602
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 770,881
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  OPHD-00574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  637 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-072-064-4


  Query Match           19.5%;  Score 254;  DB 3;  Length 637;
  Best Local Similarity   28.1%;  Pred. No. 4.5e-17;
  Matches   59;  Conservative   39;  Mismatches   68;  Indels   44;  Gaps    6;

Qy      3 GVSNKTEI-------------ITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTML 48
          |:|:: |:             |    |::  :       |  ||   | |:|| :  ::
Db    256 GMSSEVELPQFRVLGHRQRATEINLTTGNYSRLACEIQFVRSMGYYLIQIYIPSGLIVVI 315

Qy     49 SWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCA 108
          ||||||:   : ||| |||:|:|||||||| : :    |::||: ::| |:  ||| | :
Db    316 SWVSFWLNRNATPARVSLGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTCFVMVFAS 375

Qy    109 LLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEG 168
          |||:| : ::                 ||  |   |  |  :   :: |:         :|
Db    376 LLEYATVGYMA-------------KRIQMRKQ-RFMAIQKIAEQKKQQ--------LDG 412

Qy    169 SDGEE---RPSCSAQQP----PSPGSPEGP 191
          :: ::    |: :   |      || | ||
Db    413 ANQQQANPNPNANVGGPGGVGVGPGGPGGP 442
```

```
RESULT  14
US-08-072-064-6
; Sequence 6, Application US/08072064
; Patent No. 6008046
;  GENERAL INFORMATION:
;    APPLICANT:  FFRENCH-CONSTANT, RICHARD H.
;    APPLICANT:  JACKSON, MEYER B.
;    TITLE OF INVENTION:  DRUG AND PESTICIDE SCREENING
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETER G. CARROLL
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/072,064
;      FILING DATE:  19930602
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 770,881
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARROLL, PETER G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  OPHD-00574
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/705-8410
;      TELEFAX:  415/397-8338
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  637 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-072-064-6


  Query Match           19.4%;  Score 253;  DB 3;  Length 637;
  Best Local Similarity   28.1%;  Pred. No. 5.6e-17;
  Matches   59;  Conservative   39;  Mismatches   68;  Indels   44;  Gaps    6;

Qy      3 GVSNKTEI-------------ITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTML 48
          |:|:: |:             |    |::  :       |  ||   | |:|| :  ::
Db    256 GMSSEVELPQFRVLGHRQRATEINLTTGNYSRLACEIQFVRSMGYYLIQIYIPSGLIVVI 315

Qy     49 SWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCA 108
          ||||||:   : ||| |||:|:|||||||| : :    |::||: ::| |:  ||| | :
Db    316 SWVSFWLNRNATPARVSLGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTCFVMVFAS 375

Qy    109 LLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEG 168
          |||:| : ::                 ||  |   |  |  :   :: |:         :|
Db    376 LLEYATVGYMA-------------KRIQIRKQ-RFMAIQKIAEQKKQQ--------LDG 412

Qy    169 SDGEE---RPSCSAQQP----PSPGSPEGP 191
          :: ::    |: :   |      || | ||
Db    413 ANQQQANPNPNANVGGPGGVGVGPGGPGGP 442


RESULT  15
US-08-137-614A-26
; Sequence 26, Application US/08137614A
; Patent No. 5487976
;  GENERAL INFORMATION:
;    APPLICANT:  Soderlund, David M.
;    APPLICANT:  Knipple, Douglas C.
```

```
;    APPLICANT:  Henderson, Joseph E.
;    TITLE OF INVENTION:  Gene Encoding An Insect
;    TITLE OF INVENTION:  Gamma-Aminobutyric Acid (GABA) Receptor Subunit
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,614A
;      FILING DATE:  15-OCT-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716)263-1636
;      TELEFAX:  (716)263-1600
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  617 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-137-614A-26


  Query Match           19.3%;  Score 251;  DB 1;  Length 617;
  Best Local Similarity  27.6%;  Pred. No. 8.5e-17;
  Matches   58;  Conservative   40;  Mismatches   68;  Indels   44;  Gaps    6;

Qy       3 GVSNKTEI--------------ITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTML 48
           |:|:: |:               |    |::  :       |  ||   | |:|| :  ::
Db     235 GMSSEVELPQFRVLGHRQRATEINLTTGNYSRLACEIQFVRSMGYYLIQIYIPSGLIVVI 294

Qy      49 SWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCA 108
           ||||||:   : ||| :||:|:|||||||| : :    |::||: ::| |:  |||  | :
Db     295 SWVSFWLNRNATPARVALGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTCFVMVFAS 354

Qy     109 LLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEG 168
           |||:| : ::              ||  |   |  |  :   :: |:         :|
Db     355 LLEYATVGYMA--------------KRIQMRKQ-RFMAIQKIAEQKKQQ--------LDG 391

Qy     169 SDGEE---RPSCSAQQP----PSPGSPEGP 191
           :: ::    |: :   |      || | ||
Db     392 ANQQQANPNPNANVGGPGGVGVGPGGPGGP 421


Search completed: March 11, 2000, 06:01:25
Job time: 1114 sec
```

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:06:26 ; Search time 52.39 Seconds
(without alignments)
217.885 Million cell updates/sec

Title: US-09-030-832-42_COPY_247_488
Perfect score: 1302
Sequence: 1 FTGVSNKTEIITTPVGDFMV.....QQGRLCIHVYRLDNYSRVVF 242

Scoring table: BLOSUM62

Searched: 142080 seqs, 47169319 residues

Database : PIR_62:*

Word size : 0

Number of hits that pass the threshold : 142080
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	525.5	40.4	457	2	S38296	gamma-aminobutyric
2	461.5	35.4	467	2	S16915	gamma-aminobutyric
3	461	35.4	474	2	S13086	gamma-aminobutyric
4	460.5	35.4	467	2	S19317	gamma-aminobutyric
5	452.5	34.8	464	2	JH0824	gamma-aminobutyric
6	451	34.6	474	2	JH0317	gamma-aminobutyric
7	450	34.6	467	2	S03905	gamma-aminobutyric
8	450	34.6	466	2	JQ0077	gamma-aminobutyric
9	450	34.6	466	2	JH0316	gamma-aminobutyric
10	447	34.3	475	2	B39272	gamma-aminobutyric
11	444	34.1	465	2	S12056	gamma-aminobutyric
12	341	26.2	552	2	S17551	gamma-aminobutyric
13	336	25.8	453	2	S11087	gamma-aminobutyric
14	336	25.8	554	2	G01928	gamma-aminobutyric
15	330	25.3	556	2	S06838	gamma-aminobutyric
16	329	25.3	443	2	S11396	gamma-aminobutyric
17	319	24.5	464	2	B34130	gamma-aminobutyric
18	318	24.4	499	2	S17785	gamma-aminobutyric
19	317.5	24.4	462	2	A48933	gamma-aminobutyric
20	312	24.0	492	2	I77911	gamma-aminobutyric
21	309	23.7	492	1	CHBOA3	gamma-aminobutyric
22	309	23.7	493	2	A34130	gamma-aminobutyric
23	303.5	23.3	455	1	CHCHA1	gamma-aminobutyric
24	303.5	23.3	452	2	S12381	glycine receptor a
25	302	23.2	451	1	ACBOG2	gamma-aminobutyric
26	302	23.2	451	2	JH0370	gamma-aminobutyric
27	302	23.2	451	2	I57947	gamma-aminobutyric
28	301	23.1	456	2	A60652	gamma-aminobutyric
29	301	23.1	455	2	JQ0158	gamma-aminobutyric
30	301	23.1	456	2	A27142	gamma-aminobutyric
31	301	23.1	455	2	A39062	gamma-aminobutyric
32	300	23.0	451	2	C49970	glycine receptor a
33	300	23.0	449	2	S12382	glycine receptor a
34	299	23.0	457	2	S20662	glycine receptor a
35	298.5	22.9	452	2	S14816	glycine receptor a
36	298.5	22.9	452	2	S18836	glycine receptor a
37	298.5	22.9	496	2	JN0603	gamma-aminobutyric
38	297.5	22.8	451	2	B49970	glycine receptor a
39	296.5	22.8	488	2	JH0359	gamma-aminobutyric
40	295	22.7	473	2	A55275	gamma-aminobutyric
41	294	22.6	474	2	B60039	gamma-aminobutyric
42	294	22.6	474	2	A40336	gamma-aminobutyric
43	294	22.6	474	2	B27142	gamma-aminobutyric
44	293	22.5	464	2	A23682	glycine receptor a
45	292	22.4	473	2	S04466	gamma-aminobutyric

ALIGNMENTS

RESULT 1
S38296
gamma-aminobutyric acid receptor A gamma-4 chain precursor - chicken
N;Alternate names: GABA(A) receptor gamma-4 chain
C;Species: Gallus gallus (chicken)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S38296
R;Harvey, R.J.; Kim, H.C.; Darlison, M.G.
FEBS Lett. 331, 211-216, 1993
A;Title: Molecular cloning reveals the existence of a fourth gamma subunit of the ver
A;Reference number: S38296; MUID:93387470
A;Accession: S38296
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-457 <HAR>
A;Cross-references: EMBL:X73533; NID:g414021; PIDN:CAA51939.1; PID:g414022
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein

Query Match 40.4%; Score 525.5; DB 2; Length 457;
Best Local Similarity 41.1%; Pred. No. 9.8e-40;
Matches 106; Conservative 39; Mismatches 54; Indels 59; Gaps 5;

```
Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           |||: | :|:: |  |::|||||: |::||| || | | |:|  :| :|||||||||| :|
Db     225 FTGLRNTSEVLRTGAGEYMVMTVSFDLSRRMGYFAIQTYIPCILTVVLSWVSFWIKRDST 284

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           |||||||||:|||||||  | |||: ||||||||:| ::::||:| | ||:|:| ||:|:
Db     285 PARTSLGITTVLTMTTLSTISRKHLPRVSYITAMDLFVSVCFIFVFAALMEYATLNYLVG 344

Qy     121 NQTK-AHASPKLRHP--------------RINSRAHARTRARSRACARQHQEAFVCQIV 164
           |:    |:| | | |                ||:  |
Db     345 NKKPLEHSSRKARLPPAGAQVMPSFTAININININMH---------------------- 382

Qy     165 TTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQ 224
                     |     :   ||||           | |  |  :::|| : ||:   |::
Db     382 --------WPPEIEEDEDDDPGSP----------CLEG-KECERFFCCIEDCQTGMWRE 421

Qy     225 GRLCIHVYRLDNYSRVVF 242
           ||: ||: |||:|||| |
Db     422 GRVRIHISRLDSYSRVFF 439
```

RESULT 2
S16915
gamma-aminobutyric acid/benzodiazepine receptor gamma-3 chain precursor - mouse
N;Alternate names: GABA(A) receptor gamma-3 chain
C;Species: Mus musculus (house mouse)
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 20-Aug-1999
C;Accession: S16915; S15469
R;Wilson-Shaw, D.; Robinson, M.; Gambarana, C.; Siegel, R.E.; Sikela, J.M.
FEBS Lett. 284, 211-215, 1991
A;Title: A novel gamma subunit of the GABA(A) receptor identified using the polymeras
A;Reference number: S16915; MUID:91285135
A;Accession: S16915
A;Molecule type: mRNA

```
A;Residues: 1-467 <WIL>
A;Cross-references: EMBL:X59300; NID:g51121; PIDN:CAA41988.1; PID:g51122
C;Superfamily: acetylcholine receptor
C;Keywords: disulfide bond; glycoprotein; ion channel; neurotransmitter receptor; transm
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-467/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-3 chain #status
F;255-277/Domain: transmembrane #status predicted <TM1>
F;281-303/Domain: transmembrane #status predicted <TM2>
F;315-337/Domain: transmembrane #status predicted <TM3>
F;444-467/Domain: transmembrane #status predicted <TM4>
F;110,228/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;171-185/Disulfide bonds: #status predicted


  Query Match             35.4%;  Score 461.5;  DB 2;  Length 467;
  Best Local Similarity   39.5%;  Pred. No. 5.4e-34;
  Matches   98;  Conservative   43;  Mismatches   80;  Indels   27;  Gaps    5;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           | |: | |||:||  ||::||||:| :||| ||   | |:|  :| :|||||||| ::
Db     223 FMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFWIKKDAT 282

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           ||||:||||:||||||| | :||: |||||:||:| :: :||:| | ||:|:| ||:  |
Db     283 PARTTLGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEYATLNY--Y 340

Qy     121 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 180
           :  :    | :|  : :      ||      : |    :                |
Db     341 SSCR---KPTIRKKKTSLLHPDSTRWIPDRISLQAPSNY---------------SLLDM 381

Qy     181 QPPSPGSPEGPRSLC---SKLACCEWC---KRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 234
           :|| |       |:     :  |   |   | : :||   :|:  :|::||: | |  |
Db     382 RPPPPVMITLNNSMYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSWRRGRIHIDVSEL 441

Qy     235 DNYSRVVF 242
           |:|||| |
Db     442 DSYSRVFF 449


RESULT   3
S13086
gamma-aminobutyric acid/benzodiazepine receptor A gamma-2 chain precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S13086
R;Glencorse, T.A.; Bateson, A.N.; Darlison, M.G.
Nucleic Acids Res. 18, 7157, 1990
A;Title: Sequence of the chicken GABA(A) receptor gamma-2-subunit cDNA.
A;Reference number: S13086; MUID:91088318
A;Accession: S13086
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <GLE>
A;Cross-references: EMBL:X54944; NID:g62896; PIDN:CAA38704.1; PID:g62897
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; phosphoprotein; transmembrane protein


  Query Match             35.4%;  Score 461;  DB 2;  Length 474;
  Best Local Similarity   35.2%;  Pred. No. 6e-34;
  Matches   90;  Conservative   51;  Mismatches   61;  Indels   54;  Gaps    6;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           |||: | ||:: |  ||:||:::||:||| ||   | |:| ::  :||||||||  ::
Db     241 FTGLRNTTEVVKTTSGDYVVMSVYFNLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAV 300

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           |||||||||:|||||| | :||: |:||||:||:| ::::||:| | ||:|:  |:: :
Db     301 PARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVS 360

Qy     121 N------QTKAHASPKLR-----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIVTT 166
           |      : |   :| ||      | |: |  : |   : |     |  :  : |
Db     361 NRKPSKDKDKKKKNPLLRMFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYEC----- 416

Qy     167 EGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGR 226
             ||::   |::                                  :||   ||    |: ||
Db     416 --LDGKD---CAS-----------------------------FFCCFEDCRTGAWRHGR 440

Qy     227 LCIHVYRLDNYSRVVF 242
           : | : ::|:|:|: |
Db     441 IHIRIAKMDSYARIFF 456


RESULT   4
S19317
gamma-aminobutyric acid/benzodiazepine receptor gamma-3 chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: S19317; A40221
R;Knoflach, F.; Rhyner, T.; Villa, M.; Kellenberger, S.; Drescher, U.; Malherbe, P.;
FEBS Lett. 293, 191-194, 1991
A;Title: The gamma3-subunit of the GABA(A)-receptor confers sensitivity to benzodiaze
A;Reference number: S19317; MUID:92070559
A;Accession: S19317
A;Molecule type: mRNA
A;Residues: 1-467 <KNO>
A;Cross-references: EMBL:X63324; NID:g56181; PIDN:CAA44930.1; PID:g56182
R;Herb, A.; Wisden, W.; Luddens, H.; Puia, G.; Vicini, S.; Seeburg, P.H.
Proc. Natl. Acad. Sci. U.S.A. 89, 1433-1437, 1992
A;Title: The third gamma subunit of the gamma-aminobutyric acid type A receptor famil
A;Reference number: A40221; MUID:92159063
A;Accession: A40221
A;Molecule type: mRNA
A;Residues: 1-467 <HER>
A;Note: sequence extracted from NCBI backbone (NCBIP:82491)
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein


  Query Match             35.4%;  Score 460.5;  DB 2;  Length 467;
  Best Local Similarity   39.5%;  Pred. No. 6.6e-34;
  Matches   98;  Conservative   43;  Mismatches   80;  Indels   27;  Gaps    5;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           | |: | |||:||  ||::||||:| :||| ||   | |:|  :| :|||||||| ::
Db     223 FMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFWIKKDAT 282

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           ||||:||||:||||||| | :||: |||||:||:| :: :||:| | ||:|:| ||:  |
Db     283 PARTTLGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEYATLNY--Y 340

Qy     121 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 180
           :  :    | :|  : :      ||      : |    :                |
Db     341 SSCR---KPTIRKKKTSLLHPDSTRWIPDRISLQAPSNY---------------SLLDM 381

Qy     181 QPPSPGSPEGPRSLC---SKLACCEWC---KRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 234
           :|| |       |:     :  |   |   | : :||   :|:  :|::||: | |  |
Db     382 RPPPPVMITLNNSMYWQEFEDTCVYECLDGKDCQTFFCCYEECKSGSWRRGRIHIDVSEL 441

Qy     235 DNYSRVVF 242
           |:|||| |
Db     442 DSYSRVFF 449


RESULT   5
JH0824
gamma-aminobutyric acid A receptor gamma 1 chain precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
C;Accession: JH0824
R;Glencorse, T.A.; Darlison, M.G.; Barnard, E.A.; Bateson, A.N.
J. Neurochem. 61, 2294-2302, 1993
A;Title: Sequence and novel distribution of the chicken homologue of the mammalian ga
A;Reference number: JH0824; MUID:94065817
A;Accession: JH0824
A;Molecule type: mRNA
```

```
A;Residues: 1-464 <GLE>
C;Comment: This protein mediates gamma-aminobutyric acid-induced synaptic inhibition in
C;Superfamily: acetylcholine receptor
C;Keywords: ion channel; neurotransmitter receptor; transmembrane protein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-464/Product: gamma-aminobutyric acid A receptor gamma 1 chain #status predicted <MA
F;269-290/Domain: transmembrane #status predicted <TM1>
F;295-316/Domain: transmembrane #status predicted <TM2>
F;328-349/Domain: transmembrane #status predicted <TM3>
F;441-464/Domain: transmembrane #status predicted <TM4>


  Query Match            34.8%;  Score 452.5;  DB 2;  Length 464;
  Best Local Similarity  35.5%;  Pred. No. 3.4e-33;
  Matches   91;  Conservative   44;  Mismatches   62;  Indels   59;  Gaps    4;

Qy      1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
          | |: | |||  |  ||:::|||||::||| ||   | |:|  :| :||||||||  ::
Db    236 FVGLRNTTEISHTLSGDYIIMTIFFDLSRRMGYFTIQTYIPCILTVVLSWVSFWINKDAV 295

Qy     61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
          |||||||||:|||||| | :||: |:|||:||:| ::::||:| | ||:|:  |::
Db    296 PARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFAALMEYGTLHYFTS 355

Qy    121 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 180
          |:                                        :|  |::: :
Db    356 NR----------------------------------------KGDKGKDKKAKPKP 371

Qy    181 QPPS-----PGSPEGPRSLCSKL---------ACCEWCKRFKKYFCMVPDCEGSTWQQGR 226
            ||     |||   | :  : |           | |  |    :||   ||   :|::||
Db    372 SKPSAIAVRPGSTLIPINNINNLPERDDDYGYECLEG-KDCASFFCCFEDCRTGSWREGR 430

Qy    227 LCIHVYRLDNYSRVVF 242
          : | : ::|:|||: |
Db    431 IHIRIAKIDSYSRIFF 446


RESULT   6
JH0317
gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 13-Sep-1996
C;Accession: JH0317
R;Kofuji, P.; Wang, J.B.; Moss, S.J.; Huganir, R.L.; Burt, D.R.
J. Neurochem. 56, 713-715, 1991
A;Title: Generation of two forms of the gamma-aminobutyric acid A receptor gamma2-subuni
A;Reference number: JH0316; MUID:91108470
A;Accession: JH0317
A;Molecule type: mRNA
A;Residues: 1-474 <KOF>
A;Cross-references: GB:M57522
A;Experimental source: brain
C;Superfamily: acetylcholine receptor
C;Keywords: alternative splicing; glycoprotein; ion channel; neurotransmitter receptor;
F;1-38/Domain: signal sequence #status predicted <SIG>
F;29-375,384-474/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain,
F;39-474/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain, long fo
F;39-272/Domain: extracellular #status predicted <EXT>
F;273-295/Domain: transmembrane #status predicted <TM1>
F;299-321/Domain: transmembrane #status predicted <TM2>
F;333-355/Domain: transmembrane #status predicted <TM3>
F;356-450/Domain: intracellular #status predicted <INT>
F;451-473/Domain: transmembrane #status predicted <TM4>
F;51,128,246/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;381/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted


  Query Match            34.6%;  Score 451;  DB 2;  Length 474;
  Best Local Similarity  34.4%;  Pred. No. 4.8e-33;
  Matches   88;  Conservative   52;  Mismatches   62;  Indels   54;  Gaps    6;

Qy      1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
          | |: | ||:: |  ||::||:::|::||| ||   | |:| ::  :||||||||  ::
Db    241 FVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAV 300

Qy     61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
          |||||||||:|||||| | :||: |:|||:||:| ::::||:| | ||:|:  |:: :
Db    301 PARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVS 360

Qy    121 N------QTKAHASPKLR-----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIVTT 166
          |      : |   :| ||      | |: |  : |   : |     |  :  : |
Db    361 NRKPSKDKDKKKKNPLLRMFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYEC----- 416

Qy    167 EGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGR 226
             ||::   |::                                :||   ||    |: ||
Db    416 --LDGKD---CAS----------------------------FFCCFEDCRTGAWRHGR 440

Qy    227 LCIHVYRLDNYSRVVF 242
          : | : ::|:|:|: |
Db    441 IHIRIAKMDSYARIFF 456


RESULT   7
S03905
gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Aug-1999
C;Accession: S03905
R;Pritchett, D.B.; Sontheimer, H.; Shivers, B.D.; Ymer, S.; Kettenmann, H.; Schofield
Nature 338, 582-585, 1989
A;Title: Importance of a novel GABA(A) receptor subunit for benzodiazepine pharmacolo
A;Reference number: S03905; MUID:89181956
A;Accession: S03905
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-467 <PRI>
A;Cross-references: GB:X15376; NID:g31636; PIDN:CAA33437.1; PID:g31637
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein
F;1-39/Domain: signal sequence #status predicted <SIG>
F;40-467/Product: gamma-aminobutyric acid/benzodiazepine receptor gamma-2 chain #stat


  Query Match            34.6%;  Score 450;  DB 2;  Length 467;
  Best Local Similarity  34.3%;  Pred. No. 5.8e-33;
  Matches   85;  Conservative   53;  Mismatches   64;  Indels   46;  Gaps    5;

Qy      1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
          | |: | ||:: |  ||::||:::|::||| ||   | |:| ::  :||||||||  ::
Db    242 FVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAV 301

Qy     61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
          |||||||||:|||||| | :||: |:|||:||:| ::::||:| | ||:|:  |:: :
Db    302 PARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVS 361

Qy    121 NQTKAHASPKLRH---PRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEER 174
          |:  :    | :    | |: |  : |   : |     |  :  : |        ||::
Db    362 NRKPSKDKDKKKKNPAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD- 414

Qy    175 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 234
            |::                          :||   ||    |: ||: | : ::
Db    414 --CAS----------------------------FFCCFEDCRTGAWRHGRIHIRIAKM 441

Qy    235 DNYSRVVF 242
          |:|:|: |
Db    442 DSYARIFF 449


RESULT   8
JQ0077
gamma-aminobutyric acid receptor A gamma-2 chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Aug-1999
C;Accession: JQ0077; A37164
R;Shivers, B.D.; Killisch, I.; Sprengel, R.; Sontheimer, H.; Koehler, M.; Schofield,
Neuron 3, 327-337, 1989
```

```
A;Title: Two novel GABA-A receptor subunits exist in distinct neuronal subpopulations.
A;Reference number: JQ0076; MUID:90380375
A;Accession: JQ0077
A;Molecule type: mRNA
A;Residues: 1-466 <SHI>
A;Cross-references: GB:L08497; NID:g204217; PIDN:AAC42036.1; PID:g204218
A;Experimental source: brain
R;Malherbe, P.; Sigel, E.; Baur, R.; Persohn, E.; Richards, J.G.; Mohler, H.
J. Neurosci. 10, 2330-2337, 1990
A;Title: Functional characteristics and sites of gene expression of the alpha-1,beta-1,g
A;Reference number: A37164; MUID:90331051
A;Accession: A37164
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-21,'I',23-466 <MAL>
C;Comment: Neurotransmission effected by gamma-aminobutyric acid (GABA) is mediated main
C;Comment: The GABA-A receptor consists of subunits that are structurally related to lig
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F;1-38/Domain: signal sequence #status predicted <SIG>
F;39-466/Product: gamma-aminobutyric acid A receptor gamma-2 chain #status predicted <MA
F;273-295/Domain: transmembrane #status predicted <TM1>
F;299-321/Domain: transmembrane #status predicted <TM2>
F;333-355/Domain: transmembrane #status predicted <TM3>
F;443-465/Domain: transmembrane #status predicted <TM4>
F;51,128,246/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;189-203/Disulfide bonds: #status predicted

  Query Match             34.6%;  Score 450;  DB 2;  Length 466;
  Best Local Similarity   34.3%;  Pred. No. 5.7e-33;
  Matches   85;  Conservative   53;  Mismatches   64;  Indels   46;  Gaps    5;

Qy      1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
          | |: | ||:: |  ||::||:::|::||| ||   | |:| ::  :||||||||  ::
Db    241 FVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAV 300

Qy     61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
          |||||||||:|||||| | :||: |:|||:||:| :::::||:| | ||:|:  |:: :
Db    301 PARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVS 360

Qy    121 NQTKAHASPKLRH---PRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEER 174
          |:  :    | :    | |: |  : |  : |      |  :  : |        ||::
Db    361 NRKPSKDKDKKKKNPAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD- 413

Qy    175 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 234
            |::                          :||   ||    |: ||: | : ::
Db    413 --CAS----------------------------FFCCFEDCRTGAWRHGRIHIRIAKM 440

Qy    235 DNYSRVVF 242
          |:|:|: |
Db    441 DSYARIFF 448


RESULT  9
JH0316
gamma-aminobutyric acid A receptor gamma 2 chain alternatively spliced precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 04-Sep-1998
C;Accession: JH0316
R;Kofuji, P.; Wang, J.B.; Moss, S.J.; Huganir, R.L.; Burt, D.R.
J. Neurochem. 56, 713-715, 1991
A;Title: Generation of two forms of the gamma-aminobutyric acid A receptor gamma2-subuni
A;Reference number: JH0316; MUID:91108470
A;Accession: JH0316
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-466 <KOF>
A;Cross-references: GB:M57522
C;Superfamily: acetylcholine receptor

  Query Match             34.6%;  Score 450;  DB 2;  Length 466;
  Best Local Similarity   34.3%;  Pred. No. 5.7e-33;
  Matches   85;  Conservative   53;  Mismatches   64;  Indels   46;  Gaps    5;

Qy      1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
          | |: | ||:: |  ||::||:::|::||| ||   | |:| ::  :||||||||  ::
Db    241 FVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAV 300

Qy     61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
          |||||||||:|||||| | :||: |:|||:||:| :::::||:| | ||:|:  |:: :
Db    301 PARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVS 360

Qy    121 NQTKAHASPKLRH---PRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEER 174
          |:  :    | :    | |: |  : |  : |      |  :  : |        ||::
Db    361 NRKPSKDKDKKKKNPAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD- 413

Qy    175 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 234
            |::                          :||   ||    |: ||: | : ::
Db    413 --CAS----------------------------FFCCFEDCRTGAWRHGRIHIRIAKM 440

Qy    235 DNYSRVVF 242
          |:|:|: |
Db    441 DSYARIFF 448


RESULT  10
B39272
gamma-aminobutyric acid receptor A gamma-2L chain - bovine
N;Contains: gamma-aminobutyric acid receptor A gamma-2S chain
C;Species: Bos primigenius taurus (cattle)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 30-May-1997
C;Accession: B39272; A39272
R;Whiting, P.; McKernan, R.M.; Iversen, L.L.
Proc. Natl. Acad. Sci. U.S.A. 87, 9966-9970, 1990
A;Title: Another mechanism for creating diversity in gamma-aminobutyrate type A recep
sphorylation site.
A;Reference number: A39272; MUID:91088632
A;Accession: B39272
A;Molecule type: mRNA
A;Residues: 1-475 <WHI>
A;Cross-references: GB:M55563
A;Accession: A39272
A;Molecule type: mRNA
A;Residues: 1-376,385-475 <WH2>
A;Cross-references: GB:M55563
C;Superfamily: acetylcholine receptor
C;Keywords: alternative splicing; neurotransmitter receptor; phosphoprotein; transmem
F;1-475/Product: gamma-aminobutyric acid receptor A gamma-2L chain #status predicted
F;1-376,385-475/Product: gamma-aminobutyric acid receptor A gamma-2S chain #status pr
F;382/Binding site: phosphate (Ser) (covalent) #status predicted

  Query Match             34.3%;  Score 447;  DB 2;  Length 475;
  Best Local Similarity   34.4%;  Pred. No. 1.1e-32;
  Matches   88;  Conservative   51;  Mismatches   63;  Indels   54;  Gaps    6;

Qy      1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
          | |: | ||:: |  ||::|||:: ::||| ||   | |:| ::  :||||||||  ::
Db    242 FVGLRNTTEVVKTTSGDYVVMTVYSDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAV 301

Qy     61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
          |||||||||:|||||| | :||: |:|||:||:| :::::||:| | ||:|:  |:: :
Db    302 PARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVS 361

Qy    121 N------QTKAHASPKLR-----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIVTT 166
          |      : |   :| ||       | |: |  : |   : |      |  :  : |
Db    362 NRKPSKDKDKKKKNPLLRMFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYEC----- 417

Qy    167 EGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGR 226
            ||::   |::                          :||   ||    |: ||
Db    417 --LDGKD---CAS----------------------------FFCCFEDCRTGAWRHGR 441

Qy    227 LCIHVYRLDNYSRVVF 242
          : | : ::|:|:|: |
```

```
Db    442 IHIRIAKMDSYARIFF 457


RESULT  11
S12056
gamma-aminobutyric acid/benzodiazepine receptor gamma-1 chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S12056
R;Ymer, S.; Draguhn, A.; Wisden, W.; Werner, P.; Keinaenen, K.; Schofield, P.R.; Sprenge
EMBO J. 9, 3261-3267, 1990
A;Title: Structural and functional characterization of the gamma(1) subunit of GABA(A)/b
A;Reference number: S12056; MUID:91006020
A;Accession: S12056
A;Molecule type: mRNA
A;Residues: 1-465 <YME>
A;Cross-references: GB:X57514; NID:g56175; PIDN:CAA40739.1; PID:g56176
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein


  Query Match             34.1%;  Score 444;  DB 2;  Length 465;
  Best Local Similarity   35.6%;  Pred. No. 2e-32;
  Matches   90;  Conservative   45;  Mismatches   62;  Indels   56;  Gaps    5;

Qy      1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
          | |: | |||  |  ||:::||||||::||| ||   | |:|  :| :||||||||  ::
Db    240 FVGLRNSTEISHTISGDYIIMTIFFDLSRRMGYFTIQTYIPCILTVVLSWVSFWINKDAV 299

Qy     61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
          |||||||||:|||||| | :||: |:|||:||:| ::::||:| | ||:|:  |::
Db    300 PARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFAALMEYGTLHYFTS 359

Qy    121 N-----------QTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGS 169
          |           ::|   || |       | :     :     | :: :  | :  ||
Db    360 NNKGKTTRDRKLKSKTSVSPGL-------HAGSTLIPMNNISMPQGEDDYGYQCL--EGK 410

Qy    170 DGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCI 229
          |      |:                              :||   ||   :|::||: |
Db    411 D------CAT-----------------------------FFCCFEDCRTGSWREGRIHI 434

Qy    230 HVYRLDNYSRVVF 242
           : ::|:|||: |
Db    435 RIAKIDSYSRIFF 447


RESULT  12
S17551
gamma-aminobutyric acid/benzodiazepine receptor alpha-4 chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S17551
R;Wisden, W.; Herb, A.; Wieland, H.; Keinaenen, K.; Lueddens, H.; Seeburg, P.H.
FEBS Lett. 289, 227-230, 1991
A;Title: Cloning, pharmacological characteristics and expression pattern of the rat GABA
A;Reference number: S17551; MUID:92008629
A;Accession: S17551
A;Molecule type: mRNA
A;Residues: 1-552 <WIS>
A;Cross-references: GB:S55933; NID:g236011; PIDN:AAB19902.1; PID:g236012
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein


  Query Match             26.2%;  Score 341;  DB 2;  Length 552;
  Best Local Similarity   36.4%;  Pred. No. 3.9e-23;
  Matches   76;  Conservative   31;  Mismatches   78;  Indels   24;  Gaps    3;

Qy      3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
          | :  :| | :  |:::|||::|:: |: ||   | |:|  :| :|| ||||  || ||
Db    228 GQTVSSETIKSITGEYIVMTVYFHLRRKMGYFMIQTYIPCIMTVILSQVSFWINKESVPA 287

Qy     63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
          ||  |||:|||||||   :| : |:||| ||:|::||:|| | | ||:||| :|:    |
Db    288 RTVFGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNIQ 347

Qy    123 ------------TKAHASPKLRHPRINS---RAHARTRARSRACARQHQEAFV------- 161
                       :  |:| |:     :     ||    | |  |  | |: |
Db    348 MQKAKKKISKPPPEVPAAPVLKEKHTETSLQNTHANLNMRKRTNALVHSESDVNSRTEVG 407

Qy    161 --CQIVTTEGSDGEERPSCSAQQPPSPGS 187
                |      |  |       |:| |
Db    408 NHSSKTTAAQESSETTPKAHLASSPNPFS 436


RESULT  13
S11087
gamma-aminobutyric acid receptor A, cerebellar - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Feb-1997
C;Accession: S11087
R;Lueddens, H.; Pritchett, D.B.; Koehler, M.; Killisch, I.; Keinaenen, K.; Monyer, H.
Nature 346, 648-651, 1990
A;Title: Cerebellar GABA(A) receptor selective for a behavioural alcohol antagonist.
A;Reference number: S11087; MUID:90348963
A;Accession: S11087
A;Molecule type: mRNA
A;Residues: 1-453 <LUE>
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein


  Query Match             25.8%;  Score 336;  DB 2;  Length 453;
  Best Local Similarity   30.5%;  Pred. No. 9e-23;
  Matches   78;  Conservative   43;  Mismatches   77;  Indels   58;  Gaps    4;

Qy      3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
          | :  :| | :  |::::||::|:: |: ||   | | |  :| :|| |||||  || ||
Db    212 GQTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPA 271

Qy     63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
          ||  |||:|||||||   :| : |:||| ||:|::||:|| | | ||:||| :|:    |
Db    272 RTVFGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQ 331

Qy    123 TKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGS------------ 170
          ::              :   |:| |:      :  |:   :||    |
Db    332 SQ------------KAERQAQTAAKPPVAKSKTTESLEAEIVVHSDSKYHLKKRISSLTL 379

Qy    170 ---DGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGR 226
              |     :: |  | :|  |  |                          :|   |::
Db    380 PIVPSSEASKVLSRTPILPSTPVTPPLL------------------LPAIGGTS----- 416

Qy    227 LCIHVYRLDNYSRVVF 242
              ::| |||::|
Db    416 ------KIDQYSRILF 425


RESULT  14
G01928
gamma-aminobutyric acid receptor A alpha-4 - human
N;Alternate names: GABA(A) receptor alpha-4 chain
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C;Accession: G01928; I38936
R;Yang, W.
submitted to the EMBL Data Library, June 1995
A;Reference number: G08852
A;Accession: G01928
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-554 <YAN>
A;Cross-references: EMBL:U30461; NID:g905392; PIDN:AAB52519.1; PID:g905393
R;McLean, P.J.; Farb, D.H.; Russek, S.J.
Genomics 26, 580-586, 1995
A;Title: Mapping of the alpha 4 subunit gene (GABRA4) to human chromosome 4 defines a
ed from an ancestral cluster.
```

```
A;Reference number: I38936; MUID:95331795
A;Accession: I38936
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-57 <MCL>
A;Cross-references: EMBL:U20166; NID:g924604; PIDN:AAA74743.1; PID:g924605
C;Genetics:
A;Gene: GDB:GABRA4
A;Cross-references: GDB:370881; OMIM:137141
A;Map position: 4p14-4q12
A;Introns: 29/2
A;Note: the list of introns is incomplete
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; neurotransmitter receptor
F;144,157,402,408/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             25.8%;  Score 336;  DB 2;  Length 554;
  Best Local Similarity   38.3%;  Pred. No. 1.1e-22;
  Matches   77;  Conservative   37;  Mismatches   69;  Indels   18;  Gaps    5;

Qy       3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
           |  :  :| | :  |:::|||::|:: |: ||   | |:|  :| :|| ||||| || ||
Db     228 GQTVSSETIKSITGEYIVMTVYFHLRRKMGYFMIQTYIPCIMTVILSQVSFWINKESVPA 287

Qy      63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
           ||  |||:|||||||    :| : |:|||:||:|::||:|| | | ||:||| :|:    |
Db     288 RTVFGITTVLTMTTLSISARHSLPKVSYLTAMDWFIAVCFAFVFSALIEFAAVNYFTNIQ 347

Qy     123 -----------TKAHASP--KLRHPRINSR-AHARTRARSRACARQHQEAFVCQIVTTE 167
                       :  |:|  : :||    :  :|    | |  |  | |: |     ||
Db     348 MEKAKRKTSKPPQEVPAAPVQREKHPEAPLQDTNANLNMRKRTNALVHSESDVGN--RTE 405

Qy     168 GSDGEERPSCSAQQPPSPGSP 188
             :   : |   |:  | |:|
Db     406 VGNHSSKSSTVVQE-SSKGTP 425


RESULT  15
S06838
gamma-aminobutyric acid/benzodiazepine receptor alpha-4 chain precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
C;Accession: S06838
R;Ymer, S.; Draguhn, A.; Koehler, M.; Schofield, P.R.; Seeburg, P.H.
FEBS Lett. 258, 119-122, 1989
A;Title: Sequence and expression of a novel GABA(A) receptor alpha subunit.
A;Reference number: S06838; MUID:90076471
A;Accession: S06838
A;Molecule type: mRNA
A;Residues: 1-556 <YME>
A;Cross-references: EMBL:X61456; NID:g360; PIDN:CAA43696.1; PID:g361
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-556/Product: gamma-aminobutyric acid/benzodiazepine receptor alpha-4 chain #status


  Query Match             25.3%;  Score 330;  DB 2;  Length 556;
  Best Local Similarity   38.4%;  Pred. No. 3.8e-22;
  Matches   81;  Conservative   31;  Mismatches   73;  Indels   26;  Gaps    6;

Qy       3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
           |  :  :| | :  |:::|||::|:: |: ||   | |:|  :| :|| ||||| || ||
Db     228 GQTVSSETIKSITGEYIVMTVYFHLRRKMGYFMIQTYIPCIMTVILSQVSFWINKESVPA 287

Qy      63 RTSLGITSVLTMTTLGTFSRK-NFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYN 121
           ||  |||:|||||||    :|  : |:||| ||:|::||:|| | | ||:||| :|:
Db     288 RTVFGITTVLTMTTLSISARPISLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNV 347

Qy     122 Q--------TKA----HASPKLR--HPRIN-SRAHARTRARSRACARQHQEAFV------ 161
           |        :||     |:| ||  ||       :|    | || |  | |: |
Db     348 QMEKAKRKTSKAPQEISAAPVLREKHPETPLQNTNANLSMRKRANALVHSESDVGSRTDV 407

Qy     161 ----CQIVTTEGSDGEERPSCSAQQPPSPGS 187
                :  |      |  |       |:| |
Db     408 GNHSSKSSTVVQGSSEATPQSYLASSPNPFS 438


Search completed: March 11, 2000, 06:06:27
Job time: 125 sec
```

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:18:28 ; Search time 41.51 Seconds
(without alignments)
404.212 Million cell updates/sec

Title: US-09-030-832-42_COPY_247_488
Perfect score: 1302
Sequence: 1 FTGVSNKTEIITTPVGDFMV.....QQGRLCIHVYRLDNYSRVVF 242

Scoring table: BLOSUM62

Searched: 225878 seqs, 69334122 residues

Database : SPTREMBL_12:*

Word size : 0

Number of hits that pass the threshold : 225878
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1302	100.0	506	4	O15346	O15346 homo sapien
2	1287.5	98.9	505	4	Q99520	Q99520 homo sapien
3	837.5	64.3	384	11	O55209	O55209 rattus norv
4	338	26.0	115	11	O88966	O88966 mus musculu
5	326	25.0	438	13	Q90288	Q90288 carassius a
6	293.5	22.5	453	13	O57430	O57430 fugu rubrip
7	291.5	22.4	444	13	O93430	O93430 brachydanio
8	291	22.4	449	4	O75816	O75816 homo sapien
9	284	21.8	512	4	Q16323	Q16323 homo sapien
10	283	21.7	479	13	Q9YGQ5	Q9ygq5 morone amer
11	282	21.7	430	13	Q90590	Q90590 gallus gall
12	278.5	21.4	499	5	O17555	O17555 caenorhabdi
13	276.5	21.2	545	5	O18276	O18276 caenorhabdi
14	269	20.7	1106	5	Q22637	Q22637 caenorhabdi
15	269	20.7	487	5	Q9Y0I6	Q9y0I6 caenorhabdi
16	267.5	20.5	442	5	Q19358	Q19358 caenorhabdi
17	266	20.4	472	5	Q25035	Q25035 haemonchus
18	261	20.0	473	13	O42157	O42157 morone amer
19	258	19.8	550	5	O17145	O17145 lucilia cup
20	258	19.8	496	5	O18468	O18468 heliothis v
21	257.5	19.8	686	5	Q24352	Q24352 drosophila
22	254	19.5	476	13	Q9YGQ4	Q9ygq4 morone amer
23	253.5	19.5	416	5	Q17367	Q17367 caenorhabdi
24	252.5	19.4	494	5	Q9XZW0	Q9xzw0 heliothis v
25	251	19.3	601	5	P92138	P92138 drosophila
26	251	19.3	365	5	O77249	O77249 apis mellif
27	250.5	19.2	276	5	Q26412	Q26412 blattella g
28	250.5	19.2	475	5	Q9Y0I4	Q9y0I4 caenorhabdi
29	249	19.1	606	5	Q24561	Q24561 drosophila
30	248.5	19.1	533	5	Q16896	Q16896 aedes aegyp
31	248	19.0	437	5	Q08861	Q08861 lymnaea sta
32	247.5	19.0	256	5	Q26409	Q26409 blattella g
33	247.5	19.0	274	5	Q26411	Q26411 blattella g
34	247.5	19.0	657	5	O17547	O17547 caenorhabdi
35	247.5	19.0	478	5	O17548	O17548 caenorhabdi
36	247.5	19.0	478	5	P92023	P92023 caenorhabdi
37	246.5	18.9	444	5	O76472	O76472 musca domes
38	245	18.8	223	5	O18469	O18469 heliothis v
39	244.5	18.8	254	5	Q26410	Q26410 blattella g
40	244.5	18.8	481	5	O18471	O18471 heliothis v
41	244.5	18.8	487	5	Q9Y0I5	Q9y0I5 caenorhabdi
42	243	18.7	430	5	Q17369	Q17369 caenorhabdi
43	242	18.6	77	5	O18470	O18470 heliothis v
44	241.5	18.5	654	5	O01436	O01436 caenorhabdi
45	241	18.5	456	5	Q94900	Q94900 drosophila

ALIGNMENTS

RESULT 1
O15346
ID O15346 PRELIMINARY; PRT; 506 AA.
AC O15346;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE GABA RECEPTOR EPSILON SUBUNIT.
GN GABRE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 97480709.
RA WILKE K., GAUL R., KLAUCK S.M., POUSTKA A.;
RT "A gene in human chromosome band Xq28 (GABRE) defines a putative new
RT subunit class of the GABAA neurotransmitter receptor.";
RL Genomics 45:1-10(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA HANNA M.C., HALES T.G., KIRKNESS E.F.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Y09765; CAA70904.1; -.
DR EMBL; U92283; AAB94645.1; -.
DR EMBL; U92281; AAB94645.1; JOINED.
DR EMBL; U92282; AAB94645.1; JOINED.
DR PFAM; PF00065; neur_chan; 2.
DR PRINTS; PR00253; GABAARECEPTR.
SQ SEQUENCE 506 AA; 57971 MW; 95B5B1C4 CRC32;

Query Match 100.0%; Score 1302; DB 4; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.1e-120;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 306

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 366

Qy     121 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 426
```

```
Qy    181 QPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 QPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 486

Qy    241 VF 242
          ||
Db    487 VF 488
```

```
RESULT   2
Q99520
ID   Q99520      PRELIMINARY;      PRT;   505 AA.
AC   Q99520;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   PUTATIVE GABA-GATED CHLORIDE CHANNEL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97238072.
RA   GARRET M., BASCLES L., BOUE-GRABOT E., SARTOR P., CHARRON G.,
RA   BLOCH B., MARGOLSKEE R.F.;
RT   "An mRNA encoding a putative GABA-gated chloride channel is expressed
RT   in the human cardiac conduction system.";
RL   J. Neurochem. 68:1382-1389(1997).
DR   EMBL; Y07637; CAA68914.1; -.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00253; GABAARECEPTR.
SQ   SEQUENCE   505 AA;  57856 MW;  1E6B104C CRC32;
```

```
  Query Match             98.9%;  Score 1287.5;  DB 4;  Length 505;
  Best Local Similarity   99.6%;  Pred. No. 3e-119;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy      1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    247 FTGVSNKTEIITTP-GDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 305

Qy     61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 365

Qy    121 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 425

Qy    181 QPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 QPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 485

Qy    241 VF 242
          ||
Db    486 VF 487
```

```
RESULT   3
O55209
ID   O55209      PRELIMINARY;      PRT;   384 AA.
AC   O55209;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   GABA-A RECEPTOR EPSILON SUBUNIT (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   HANNA M.C., HALES T.G., KIRKNESS E.F.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U92284; AAB93879.1; -.
DR   PFAM; PF00065; neur_chan; 2.
FT   NON_TER       1      1
SQ   SEQUENCE   384 AA;  45465 MW;  E5D0E1B9 CRC32;
```

```
  Query Match             64.3%;  Score 837.5;  DB 11;  Length 384;
  Best Local Similarity   66.5%;  Pred. No. 5.5e-75;
  Matches  165;  Conservative   24;  Mismatches   46;  Indels   13;  Gaps    4;

Qy      1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
          ||||:||||||:|||||||||| |||||||||:: ||||:|||||||||||||||| |:|
Db    126 FTGVNNKTEIISTPVGDFMVMTFFFNVSRRFGFIVFQNYIPSSVTTMLSWVSFWIKIEAA 185

Qy     61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
          || |:|::|||||| ||||||||||||||:|||||||||||| ||| |||| ||||| |
Db    186 AARASVGVSSVLTMATLGTFSRKNFPRVSYLTALDFYIAICFVLCFCTLLEFTVLNFLTY 245

Qy    121 NQTKAHASPKLRHPRINSRAH------ARTRARSRACARQHQEAFVCQIVTTEGSDGEER 174
          |  :  ||||      ||||:      |||||:|| ||| || |||:||| |  : ||
Db    246 NNIERQASPKFYQFPTNSRANARTRARARTRARARARARQQQEVFVCEIVTYE-ENAEE- 304

Qy    175 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 234
              |  |   |: |   | :   |   :  :|||||| |||::||:||:|||||||
Db    304 ---GYQWSPRSRRPQCPWRRCGRSYVC--FRVLRKYFCMVPGCEGNSWQRGRICIHVYRL 358

Qy    235 DNYSRVVF 242
          |||||||:|
Db    359 DNYSRVLF 366
```

```
RESULT   4
O88966
ID   O88966      PRELIMINARY;      PRT;   115 AA.
AC   O88966;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   GABA-A RECEPTOR EPSILON SUBUNIT (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=AMYGDALA;
RA   GUSTINCICH S., FEIGENSPAN A., SIEGHART W., RAVIOLA E.;
RT   "GABAA receptors of dopaminergic cells of the mouse retina.";
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF090376; AAC35563.1; -.
DR   PFAM; PF00065; neur_chan; 1.
FT   NON_TER       1      1
FT   NON_TER     115    115
SQ   SEQUENCE   115 AA;  13147 MW;  5AD874B8 CRC32;
```

```
  Query Match             26.0%;  Score 338;  DB 11;  Length 115;
  Best Local Similarity   80.8%;  Pred. No. 3e-26;
  Matches   63;  Conservative    8;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
          ||||:||||||:|| ||||||| ||||||||||:: ||||||||||||||||||| |:|
Db     38 FTGVNNKTEIISTPFGDFMVMTFFFNVSRRFGFIVFQNYVPSSVTTMLSWVSFWIKIEAA 97

Qy     61 PARTSLGITSVLTMTTLG 78
          || |:|::|||||| |||
Db     98 AARASVGVSSVLTMATLG 115
```

```
RESULT   5
Q90288
ID   Q90288      PRELIMINARY;      PRT;   438 AA.
```

```
AC   Q90288;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   NEUROTRANSMITTER RECEPTOR ALPHA SUBUNIT PRECURSOR.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC   Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC   Cyprinoidea; Cyprinidae; Cyprininae; Carassius.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 96373714.
RA   BAHN S., HARVEY R.J., DARLISON M.G., WISDEN W.;
RT   "Conservation of gamma-aminobutyric acid type A receptor alpha 6
RT   subunit gene expression in cerebellar granule cells.";
RL   J. Neurochem. 66:1810-1818(1996).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; X94342; CAA64068.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
DR   PRINTS; PR01079; GABAARALPHA.
KW   Signal; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW   Transmembrane.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    483       NEUROTRANSMITTER RECEPTOR ALPHA SUBUNIT.
SQ   SEQUENCE   438 AA;  49982 MW;  ED9DBE5C CRC32;


  Query Match             25.0%;  Score 326;  DB 13;  Length 438;
  Best Local Similarity   33.9%;  Pred. No. 1.8e-24;
  Matches   83;  Conservative   38;  Mismatches   76;  Indels   48;  Gaps    7;

Qy       3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
           | :  :| : :  |:::|||::|:: |: |:   | |:|  :| :|: |||||  || ||
Db     211 GQTVSSERLKSNTGEYIVMTVYFHLQRKMGFFLIQTYIPCIMTVILAQVSFWIDKESVPA 270

Qy      63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
           ||  |||:|||||||   :| : |:||| ||:|::||:|| | | ||:||| :|:    |
Db     271 RTVFGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFSTLQ 330

Qy     123 TKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQP 182
                       |:   |  | |||               ||||         |
Db     331 ----------------ANKELRRASMACAAVR------------SDGE-----LVTNP 355

Qy     183 PSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL-----DNY 237
             ||     |   : ::  :  :|| :     ||      |||     :  |     | |
Db     356 LDPGGVLKKR--LNSVSQRDAPERFSR--APQPDLH----QQGSTVPAINTLTTSIIDKY 407

Qy     238 SRVVF 242
           |||:|
Db     408 SRILF 412


RESULT   6
O57430
ID   O57430      PRELIMINARY;      PRT;   453 AA.
AC   O57430;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GAMMA-AMINOBUTYRIC ACID RECEPTOR BETA SUBUNIT (FRAGMENT).
GN   GABAB RECEPTOR.
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC   Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC   Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   RIBOLDI TUNNICLIFFE G.R., NYAKATURA G., PLATZER M., ELGAR G.S.,
RA   BRENNER S., ROSENTHAL A.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; AF016494; AAB94045.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
FT   NON_TER       1      1
SQ   SEQUENCE   453 AA;  52409 MW;  39C0992B CRC32;


  Query Match             22.5%;  Score 293.5;  DB 13;  Length 453;
  Best Local Similarity   27.1%;  Pred. No. 3e-21;
  Matches   79;  Conservative   41;  Mismatches  103;  Indels   69;  Gaps    6;

Qy       4 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 63
             || :    |   | :  ::: | : |  ||   | |:|| : |:|||||||  ::: ||
Db     161 VSREVRFTT---GSYPRLSLSFRIKRNIGYFILQTYMPSILITILSWVSFWINYDASAAR 217

Qy      64 TSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQT 123
           :||:|:||||||: |  |:  |:: |: |:| |:  |||| | ||||:| :|:: :
Db     218 VALGVTTVLTMTTINTHLRETLPKIPYVKAIDVYLMGCFVFVFLALLEYAFVNYVFFG-- 276

Qy     124 KAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQ---------------------- 163
           :  | |    |:    : | |   :   |  :  |
Db     276 RGPAQQKKLSERVGKSNNERMRYEEKRLREQDSISVPFQTNTFRSFTQRRNLYLEEQRKV 335

Qy     163 --------IVTTEGSDGEERPS----------------CSAQQPPSPGSPEG------- 191
                   ::||   : |  ||                  |  |   |  |
Db     336 GVDPYGNILLTTLEMNNEVMPSDVGSSVSDSRNSVMSFDSSGVQFRKPMVPRDGFSHHSL 395

Qy     191 PRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVF 242
           ||     | |   :|  |    :|:              |  :| :|||:|
Db     396 DRSAMRSRANCRLRRRSSKLKLKIPNLS----------DVSTIDKWSRVIF 436


RESULT   7
O93430
ID   O93430      PRELIMINARY;      PRT;   444 AA.
AC   O93430;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GLYCINE RECEPTOR, ALPHAZ1 SUBUNIT PRECURSOR.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC   Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC   Cyprinoidea; Cyprinidae; Rasborinae; Danio.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   DAVID-WATINE B., GOBLET C., DE SAINT JAN D., FUCILE S., DEVIGNOT V.,
RA   BREGESTOVSKI P., KORN H.;
RT   "A novel alpha subunit of the glycine receptor from zebrafish: primary
RT   structure and functional expression.";
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED ION
CC       CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHLORIDE
CC       CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF
CC       NEURONAL FIRING).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- DOMAIN: THE N-TERMINAL DOMAIN CARRIES STRUCTURAL DETERMINANTS
CC       ESSENTIAL FOR AGONIST AND ANTAGONIST BINDING. TM2 IS THOUGHT TO
CC       FORM THE INNERT WALL OF THE CHLORIDE CHANNEL. THE CYTOPLASMIC LOOP
CC       MAY BE AN IMPORTANT DETERMINANT OF CHANNEL INACTIVATION KINETICS.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; AJ005812; CAA06711.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
```

```
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        26    444       GLYCINE RECEPTOR, ALPHAZ1 SUBUNIT.
FT   DOMAIN       26    242       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    248    268       PROBABLE.
FT   TRANSMEM    277    294       PROBABLE.
FT   TRANSMEM    311    331       PROBABLE.
FT   DOMAIN      343    346       POLY-ARG.
FT   DOMAIN      332    415       CYTOPLASMIC (PROBABLE).
FT   DOMAIN      381    384       POLY-ASN.
FT   TRANSMEM    416    436       PROBABLE.
FT   DISULFID    162    176       BY SIMILARITY.
FT   DISULFID    222    233       BY SIMILARITY.
SQ   SEQUENCE   444 AA;  50765 MW;  3405DED8 CRC32;


  Query Match             22.4%;  Score 291.5;  DB 13;  Length 444;
  Best Local Similarity   29.5%;  Pred. No. 4.6e-21;
  Matches   74;  Conservative   30;  Mismatches   62;  Indels   85;  Gaps    6;

Qy      16 GDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMT 75
           | |   :   |:: |: ||   | |:|| :  :|||||||  ::|||| ||||:|||||
Db     229 GKFTCIEARFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMT 288

Qy      76 TLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPR 135
           |  : || : |:||: |:| ::|:| :| | ||||:| :||:
Db     289 TQSSGSRASLPKVSYVKAIDIWMAVCLLFVFSALLEYAAVNFI----------------- 332

Qy     136 INSRAHARTRARSRACARQHQEAFVCQ-----IVTTEGSDGE-------ERPSC------ 178
                         ||||:|    |     :   |  ||          |:|
Db     332 ---------------ARQHKELLRFQRRRRHLKEDEAGDGRFSFAAYGMGPACLQAKDG 375

Qy     178 ------SAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHV 231
                :  | |   ||          :  :  :| |
Db     376 MAIKGNNNNAPTSTNPPE-----------KTVEEMRKLFIS----------------RA 407

Qy     232 YRLDNYSRVVF 242
             |:|  ||| |
Db     408 KRIDTVSRVAF 418


RESULT   8
O75816
ID   O75816      PRELIMINARY;      PRT;   449 AA.
AC   O75816;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GLYCINE RECEPTOR ALPHA 3 SUBUNIT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 98344067.
RA   NIKOLIC Z., LAUBE B., WEBER R.G., LICHTER P., KIOSCHIS P., POUSTKA A.,
RA   MULHARDT C., BECKER C.M.;
RT   "The human glycine receptor subunit alpha3. Glra3 gene structure,
RT   chromosomal localization, and functional characterization of
RT   alternative transcripts.";
RL   J. Biol. Chem. 273:19708-19714(1998).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; U93917; AAC39917.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   449 AA;  51963 MW;  3170F74B CRC32;


  Query Match             22.4%;  Score 291;  DB 4;  Length 449;
  Best Local Similarity   41.0%;  Pred. No. 5.2e-21;
  Matches   55;  Conservative   31;  Mismatches   40;  Indels    8;  Gaps    1;

Qy      16 GDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMT 75
           | |   : : |:: |: ||   | |:|| :  :|||||||  ::|||| :||||:|||||
Db     238 GKFTCIEVRFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVALGITTVLTMT 297

Qy      76 TLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNF--------LIYNQTKAHA 127
           |  : || : |:|||: |:| ::|:| :| | ||||:| :||        | : : : :
Db     298 TQSSGSRASLPKVSYVKAIDIWMAVCLLFVFSALLEYAAVNFVSRQHKELLRFRRKRKNK 357

Qy     128 SPKLRHPRINSRAH 141
             ::|  | :  |:
Db     358 DDEVRESRFSFTAY 371


RESULT   9
Q16323
ID   Q16323      PRELIMINARY;      PRT;   512 AA.
AC   Q16323;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GABAA RECEPTOR BETA 2 SUBUNIT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95223118.
RA   MCKINLEY D.D., LENNON D.J., CARTER D.B.;
RT   "Cloning, sequence analysis and expression of two forms of mRNA coding
RT   for the human beta 2 subunit of the GABAA receptor.";
RL   Brain Res. Mol. Brain Res. 28:175-179(1995).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; S77553; AAB33982.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
DR   PRINTS; PR01160; GABAARBETA.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   512 AA;  59150 MW;  FF0E2B52 CRC32;


  Query Match             21.8%;  Score 284;  DB 4;  Length 512;
  Best Local Similarity   42.6%;  Pred. No. 2.9e-20;
  Matches   49;  Conservative   29;  Mismatches   37;  Indels    0;  Gaps    0;

Qy       8 TEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLG 67
           |: :    | :  ::: | : |  ||   | |:|| : |:|||||||  ::: || :||
Db     219 TKKVVFSTGSYPRLSLSFKLKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALG 278

Qy      68 ITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
           ||:||||||: |  |:  |:: |: |:| |:  |||| | ||||:|::|:: : :
Db     279 ITTVLTMTTINTHLRETLPKIPYVKAIDMYLMGCFVFVFMALLEYALVNYIFFGR 333


RESULT  10
Q9YGQ5
ID   Q9YGQ5      PRELIMINARY;      PRT;   479 AA.
AC   Q9YGQ5;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-2A SUBUNIT PRECURSOR.
OS   Morone americana (white perch).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC   Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC   Perciformes; Percoidei; Moronidae; Morone.
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RC   TISSUE=RETINA;
RX   MEDLINE; 99022091.
RA   QIAN H., DOWLING J.E., RIPPS H.;
RT   "Molecular and pharmacological properties of GABA-rho subunits from
RT   white perch retina.";
RL   J. Neurobiol. 37:305-320(1998).
DR   EMBL; AF101034; AAD17893.1; -.
KW   Receptor.
SQ   SEQUENCE   479 AA;  55381 MW;  0CEFE4A0 CRC32;


  Query Match             21.7%;  Score 283;  DB 13;  Length 479;
  Best Local Similarity   32.3%;  Pred. No. 3.4e-20;
  Matches   76;  Conservative   39;  Mismatches   78;  Indels   42;  Gaps    7;

Qy      23 IFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSR 82
           | | : |   :   | | |:::  |||||||||   : ||| |||||:||||:|: |
Db     256 INFTLRRHIFFFLLQTYFPATLMVMLSWVSFWIDRRAVPARVSLGITTVLTMSTIITGVN 315

Qy      83 KNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHA 142
           : |||||| |:| |: : ||| | ::|||:| :|:|   | :     |:|
Db     316 ASMPRVSYIKAVDIYLWVSFVFVFLSVLEYAAVNYLSTVQDRRER--KMRE--------- 365

Qy     143 RTRARSRACARQHQEAFVCQIVTT------EGSDGEERPSCSAQQPPSPGSPEGPRSLCS 196
           | |::|  |         | |  |      :|:  |   :  |     |  ||  |  |:
Db     365 RARSQSLPC--------TCGISQTRTMTMLDGTYSEADTNSLAGYTEEPMVPERSRKSCT 416

Qy     197 KLACCEWCKRFKKYFCMVPDC---EGSTWQQGR------LCIHVYRLDNYSRVVF 242
           ::         :|   ||  |   | :| :: :      :  : : :| |||::|
Db     417 EV--------LEKPEHMVVICVSSESTTTKKKKSLRAINIIQNTHAIDKYSRMIF 463


RESULT  11
Q90590
ID   Q90590      PRELIMINARY;      PRT;   430 AA.
AC   Q90590;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   GABA-A RECEPTOR BETA 2 SUBUNIT PRECURSOR (FRAGMENT).
GN   GABARB.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 94087186.
RA   HARVEY R.J., CHINCHETRU M.A., DARLISON M.G.;
RT   "Alternative splicing of a 51-nucleotide exon that encodes a putative
RT   protein kinase C phosphorylation site generates two forms of the
RT   chicken gamma-aminobutyric acidA receptor beta 2 subunit.";
RL   J. Neurochem. 62:10-16(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; X72806; CAA51326.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Signal; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW   Transmembrane.
FT   SIGNAL       1     24       POTENTIAL.
FT   CHAIN       25   >430       GABA-A RECEPTOR BETA 2 SUBUNIT.
FT   NON_TER     430    430
SQ   SEQUENCE   430 AA;  49101 MW;  D21C7CBE CRC32;


  Query Match             21.7%;  Score 282;  DB 13;  Length 430;
  Best Local Similarity   42.6%;  Pred. No. 3.8e-20;
  Matches   49;  Conservative   29;  Mismatches   37;  Indels    0;  Gaps    0;

Qy       8 TEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLG 67
           |: :    | :  ::: | : |  ||   | |:|| : |:||||||||  ::: || :||
Db     219 TKNVVFSTGAYPRLSLSFKLKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALG 278

Qy      68 ITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
           ||:|||||: |  |:  |:: |: |:| |:  |||| | ||||:|::|:: : :
Db     279 ITTVLTMTTINTHLRETLPKIPYVKAIDMYLMGCFVFVFMALLEYALVNYIFFGR 333


RESULT  12
O17555
ID   O17555      PRELIMINARY;      PRT;   499 AA.
AC   O17555; O18279;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   ZC482.5 PROTEIN.
GN   ZC482.5.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC   Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   MCMURRAY A.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94150718.
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA   GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA   JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA   LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA   THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA   WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; Z93397; CAB07722.1; -.
DR   EMBL; Z93372; CAB07722.1; JOINED.
DR   EMBL; Z93372; CAB07549.1; -.
DR   EMBL; Z93397; CAB07549.1; JOINED.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   499 AA;  57553 MW;  34743390 CRC32;


  Query Match             21.4%;  Score 278.5;  DB 5;  Length 499;
  Best Local Similarity   43.8%;  Pred. No. 9.9e-20;
  Matches   53;  Conservative   27;  Mismatches   32;  Indels    9;  Gaps    2;

Qy      15 VGDF-------MVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLG 67
           | ||        |: ::| : |: ||   | | | ::  ::|||||||  |::||| |||
Db     232 VSDFRFSDRNISVLNVYFKLQRQQGYYILQIYTPCTLVVVMSWVSFWINKEASPARVSLG 291

Qy      68 ITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNF--LIYNQTKA 125
           | :||:|:|:|   | : |:||: |||| ||  |||| | |::|:||:|:  ::| : :
Db     292 IMTVLSMSTIGFGLRTDLPKVSHSTALDVYILTCFVFLFAAMVEYAVINYAQIVYIRKQI 351

Qy     126 H 126
           |
Db     352 H 352


RESULT  13
O18276
ID   O18276      PRELIMINARY;      PRT;   545 AA.
AC   O18276;
```

```
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   ZC482.1 PROTEIN.
GN   ZC482.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC   Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   MCMURRAY A.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94150718.
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA   GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA   JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA   LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA   THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA   WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; Z93397; CAB07719.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
DR   PRINTS; PR00252; NRIONCHANNEL.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   545 AA;  61601 MW;  26207FDB CRC32;

  Query Match             21.2%;  Score 276.5;  DB 5;  Length 545;
  Best Local Similarity   32.1%;  Pred. No. 1.7e-19;
  Matches   54;  Conservative   28;  Mismatches   41;  Indels   45;  Gaps    1;

Qy       2 TGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAP 61
           ||   :  |::|  | :  ::: | : |  ||  || |:|  :  |||||||||  |:
Db     194 TGFHTEDSIVSTATGSYQRLSLVFQLRRSVGYFIFQTYLPCVLIVMLSWVSFWINHEATS 253

Qy      62 ARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYI---------------------- 99
           || :||||:||||||: |  |:: ||:||: ::| |:
Db     254 ARVALGITTVLTMTTISTGVRQSLPRISYVKSIDIYLFPTLTNQRQAPPTSKPISDARLR 313

Qy      99 ---------------------AICFVFCFCALLEFAVLNFLIYNQTK 124
                                 :|||| | ||||:| :|:  : : :
Db     314 SLVEERAVLSADWSEFGIFILQVMCFVFVFAALLEYAAVNYSYWGRER 361


RESULT  14
Q22637
ID   Q22637      PRELIMINARY;      PRT;  1106 AA.
AC   Q22637;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   T21C12.1 PROTEIN.
GN   T21C12.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC   Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   WILKINSON J.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94150718.
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA   GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA   JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA   LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA   THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA   WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; Z50016; CAA90318.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 4.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00253; GABAARECEPTR.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane.
SQ   SEQUENCE   1106 AA;  125351 MW;  7F4BD0C6 CRC32;

  Query Match             20.7%;  Score 269;  DB 5;  Length 1106;
  Best Local Similarity   35.2%;  Pred. No. 1.9e-18;
  Matches   51;  Conservative   35;  Mismatches   53;  Indels    6;  Gaps    2;

Qy       4 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 63
           | | |: :::  |::  :  ||   |  |:   | |:|| :  ::||||||:  :: |||
Db     234 VVNHTQKLSS--GEYSRLCWFFLFKRNIGFYIIQIYLPSVLIVVISWVSFWLSRDATPAR 291

Qy      64 TSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQT 123
             :||:|:||||||| | :  : |:|||: ::| :: :||:  ||:|||:| : ::
Db     292 VALGVTTVLTMTTLMTMTNSSMPKVSYVKSIDIFLGVCFMMVFCSLLEYAAVGYISKRMK 351

Qy     124 KAHASPKLRH----PRINSRAHART 144
             |  : |      | : |    ||
Db     352 LVRARKESRMLTPLPHLESLPPKRT 376


RESULT  15
Q9Y0I6
ID   Q9Y0I6      PRELIMINARY;      PRT;  487 AA.
AC   Q9Y0I6;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   IONOTROPIC GABA RECEPTOR SUBUNIT UNC-49A.
GN   UNC-49A.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC   Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   BAMBER B.A., BEG A.A., TWYMAN R.E., JORGENSEN E.M.;
RT   "The Caenorhabditis elegans unc-49 locus encodes multiple subunits of
RT   a heteromultimeric GABA receptor.";
RL   J. Neurosci. 19:0-0(1999).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; AF151640; AAD42382.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW   Transmembrane.
SQ   SEQUENCE   487 AA;  56189 MW;  410A2ADB CRC32;

  Query Match             20.7%;  Score 269;  DB 5;  Length 487;
  Best Local Similarity   35.2%;  Pred. No. 8.3e-19;
  Matches   51;  Conservative   35;  Mismatches   53;  Indels    6;  Gaps    2;
```

```
Qy       4 VSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPAR 63
           | | |: :::  |::  :  ||   |  |:   | |:|| :  ::|||||:  :: |||
Db     222 VVNHTQKLSS--GEYSRLCWFFLFKRNIGFYIIQIYLPSVLIVVISWVSFWLSRDATPAR 279

Qy      64 TSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQT 123
           :||:|:|||||| | :  : |:|||: ::| :: :||:  ||:|||:| : ::
Db     280 VALGVTTVLTMTTLMTMTNSSMPKVSYVKSIDIFLGVCFMMVFCSLLEYAAVGYISKRMK 339

Qy     124 KAHASPKLRH----PRINSRAHART 144
             |  : |     | : |    ||
Db     340 LVRARKESRMLTPLPHLESLPPKRT 364


Search completed: March 11, 2000, 06:18:29
Job time: 57 sec
```

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2000, 06:26:39 ; Search time 22.24 Seconds
(without alignments)
324.968 Million cell updates/sec

Title: US-09-030-832-42_COPY_247_488
Perfect score: 1302
Sequence: 1 FTGVSNKTEIITTPVGDFMV.....QQGRLCIHVYRLDNYSRVVF 242

Scoring table: BLOSUM62

Searched: 82229 seqs, 29864866 residues

Database : SwissProt_38:*

Word size : 0

Number of hits that pass the threshold : 82229

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1302	100.0	506	1	GAE_HUMAN	P78334 homo sapien
2	525.5	40.4	457	1	GAC4_CHICK	P34904 gallus gall
3	467.5	35.9	467	1	GAC3_HUMAN	Q99928 homo sapien
4	461.5	35.4	467	1	GAC3_MOUSE	P27681 mus musculu
5	461.5	35.4	467	1	GAC3_RAT	P28473 rattus norv
6	461	35.4	474	1	GAC2_CHICK	P21548 gallus gall
7	455	34.9	475	1	GAC2_BOVIN	P22300 bos taurus
8	450	34.6	467	1	GAC2_HUMAN	P18507 homo sapien
9	450	34.6	466	1	GAC2_RAT	P18508 rattus norv
10	448	34.4	474	1	GAC2_MOUSE	P22723 mus musculu
11	444	34.1	465	1	GAC1_RAT	P23574 rattus norv
12	348	26.7	465	1	GAA6_CHICK	Q90845 gallus gall
13	341	26.2	552	1	GAA4_RAT	P28471 rattus norv
14	336	25.8	554	1	GAA4_HUMAN	P48169 homo sapien
15	336	25.8	453	1	GAA6_RAT	P30191 rattus norv
16	330	25.3	556	1	GAA4_BOVIN	P20237 bos taurus
17	329	25.3	443	1	GAA6_MOUSE	P16305 mus musculu
18	325	25.0	453	1	GAA6_HUMAN	Q16445 homo sapien
19	319	24.5	464	1	GAA5_RAT	P19969 rattus norv
20	318	24.4	499	1	GAB_LYMST	P26714 lymnaea sta
21	317.5	24.4	462	1	GAA5_HUMAN	P31644 homo sapien
22	312.5	24.0	492	1	GAA3_MOUSE	P26049 mus musculu
23	312	24.0	492	1	GAA3_HUMAN	P34903 homo sapien
24	309	23.7	492	1	GAA3_BOVIN	P10064 bos taurus
25	309	23.7	493	1	GAA3_RAT	P20236 rattus norv
26	303.5	23.3	455	1	GAA1_CHICK	P19150 gallus gall
27	303.5	23.3	452	1	GRA2_HUMAN	P23416 homo sapien
28	303	23.3	449	1	GRA1_MOUSE	Q64018 mus musculu
29	302	23.2	451	1	GAA2_BOVIN	P10063 bos taurus
30	302	23.2	451	1	GAA2_HUMAN	P47869 homo sapien
31	302	23.2	451	1	GAA2_MOUSE	P26048 mus musculu
32	302	23.2	451	1	GAA2_RAT	P23576 rattus norv
33	301	23.1	456	1	GAA1_BOVIN	P08219 bos taurus
34	301	23.1	456	1	GAA1_HUMAN	P14867 homo sapien
35	301	23.1	455	1	GAA1_MOUSE	P18504 mus musculu
36	300	23.0	449	1	GRA1_HUMAN	P23415 homo sapien
37	298.5	22.9	496	1	GAB3_DROME	Q08832 drosophila
38	298.5	22.9	452	1	GRA2_RAT	P22771 rattus norv
39	296.5	22.8	488	1	GAB4_CHICK	P24045 gallus gall
40	295.5	22.7	465	1	GRA3_HUMAN	O75311 homo sapien
41	295	22.7	473	1	GAB3_HUMAN	P28472 homo sapien
42	295	22.7	449	1	GRA1_RAT	P07727 rattus norv
43	294	22.6	474	1	GAB1_BOVIN	P08220 bos taurus
44	294	22.6	474	1	GAB1_HUMAN	P18505 homo sapien
45	294	22.6	474	1	GAB1_RAT	P15431 rattus norv

ALIGNMENTS

```
RESULT   1
GAE_HUMAN
ID   GAE_HUMAN      STANDARD;      PRT;   506 AA.
AC   P78334; O15345;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR EPSILON SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97192095.
RA   DAVIES P.A., HANNA M.C., HALES T.G., KIRKNESS E.F.;
RT   "Insensitivity to anaesthetic agents conferred by a class of GABA(A)
RT   receptor subunit.";
RL   Nature 385:820-823(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97480709.
RA   WILKE K., GAUL R., KLAUCK S.M., POUSTKA A.;
RT   "A gene in human chromosome band Xq28 (GABRE) defines a putative new
RT   subunit class of the GABAA neurotransmitter receptor.";
RL   Genomics 45:1-10(1997).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. ASSOCIATES WITH ALPHA AND BETA
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: FOUND IN MANY TISSUE. HIGHEST LEVELS OF
CC       EXPRESSION IN ADULT HEART AND PLACENTA.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U66661; AAB49284.1; -.
DR   EMBL; Y09763; CAA70903.1; -.
DR   EMBL; Y09764; CAA70903.1; JOINED.
DR   MIM; 300093; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane.
FT   SIGNAL        1      ?       POTENTIAL.
FT   CHAIN         ?    506       GAMMA-AMINOBUTYRIC-ACID RECEPTOR EPSILON
FT                                SUBUNIT.
FT   DOMAIN        ?    253       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    254    274       POTENTIAL.
FT   TRANSMEM    281    301       POTENTIAL.
FT   TRANSMEM    344    364       POTENTIAL.
FT   DOMAIN      365    485       CYTOPLASMIC (PROBABLE).
```

```
FT   TRANSMEM    486    506       POTENTIAL.
FT   CARBOHYD    134    134       POTENTIAL.
FT   CARBOHYD    252    252       POTENTIAL.
FT   DISULFID    195    209       BY SIMILARITY.
FT   CONFLICT    102    102       A -> S (IN REF. 2).
FT   CONFLICT    245    245       F -> L (IN REF. 2).
FT   CONFLICT    471    471       G -> A (IN REF. 2).
FT   CONFLICT    502    502       V -> F (IN REF. 2).
SQ   SEQUENCE   506 AA;  57955 MW;  6BC8394B CRC32;
```

```
  Query Match           100.0%;  Score 1302;  DB 1;  Length 506;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-107;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 306

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 366

Qy     121 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 426

Qy     181 QPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     427 QPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRV 486

Qy     241 VF 242
           ||
Db     487 VF 488
```

```
RESULT   2
GAC4_CHICK
ID   GAC4_CHICK     STANDARD;      PRT;   457 AA.
AC   P34904;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG4.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93387470.
RA   HARVEY R.J., KIM H.-C., DARLISON M.G.;
RT   "Molecular cloning reveals the existence of a fourth gamma subunit of
RT   the vertebrate brain GABAA receptor.";
RL   FEBS Lett. 331:211-216(1993).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: ABUNDANT IN SEVERAL BRAIN REGIONS, INCLUDING
CC       THE ECTOSTRIATUM, NUCLEUS ROTUNDUS AND HYPERSTRIATUM VENTRALE.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X73533; CAA51939.1; -.
DR   PIR; S38296; S38296.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    457       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4
FT                                SUBUNIT.
FT   DOMAIN       22    256       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    257    279       PROBABLE.
FT   TRANSMEM    283    305       PROBABLE.
FT   TRANSMEM    317    339       PROBABLE.
FT   DOMAIN      340    433       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    434    457       PROBABLE.
FT   CARBOHYD     35     35       POTENTIAL.
FT   CARBOHYD    112    112       POTENTIAL.
FT   CARBOHYD    230    230       POTENTIAL.
FT   DISULFID    173    187       BY SIMILARITY.
SQ   SEQUENCE   457 AA;  53183 MW;  1571332B CRC32;
```

```
  Query Match           40.4%;  Score 525.5;  DB 1;  Length 457;
  Best Local Similarity  41.1%;  Pred. No. 2.7e-39;
  Matches  106;  Conservative   39;  Mismatches   54;  Indels   59;  Gaps    5;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           |||: | :|:: |  |:::|||: |::||| || | | |:|  :| :|||||||| :|
Db     225 FTGLRNTSEVLRTGAGEYMVMTVSFDLSRRMGYFAIQTYIPCILTVVLSWVSFWIKRDST 284

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           |||||||||:|||||| | |||: |||||||||:| ::::||:| | ||:|:| ||:|:
Db     285 PARTSLGITTVLTMTTLSTISRKHLPRVSYITAMDLFVSVCFIFVFAALMEYATLNYLVG 344

Qy     121 NQTK-AHASPKLRHP--------------RINSRAHARTRARSRACARQHQEAFVCQIV 164
           |:    |:| | | |                ||:  |
Db     345 NKKPLEHSSRKARLPPAGAQVMPSFTAININNNIMH---------------------- 382

Qy     165 TTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQ 224
                 |     :   ||||          | |  |  :::|| : ||:   |::
Db     382 --------WPPEIEEDEDDDPGSP----------CLEG-KECERFFCCIEDCQTGMWRE 421

Qy     225 GRLCIHVYRLDNYSRVVF 242
           ||: ||: |||:|||| |
Db     422 GRVRIHISRLDSYSRVFF 439
```

```
RESULT   3
GAC3_HUMAN
ID   GAC3_HUMAN     STANDARD;      PRT;   467 AA.
AC   Q99928;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=FETAL BRAIN;
RX   MEDLINE; 96360042.
RA   HADINGHAM K.L., WAFFORD K.A., THOMPSON S.A., PALMER K.J.,
RA   WHITING P.J.;
RT   "Expression and pharmacology of human GABAA receptors containing
RT   gamma 3 subunits.";
RL   Eur. J. Pharmacol. 291:301-309(1995).
```

```
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S82769; AAB39369.1; -.
DR   MIM; 600233; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL       1     17       POTENTIAL.
FT   CHAIN       18    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3
FT                               SUBUNIT.
FT   DOMAIN      18    254       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM   255    277       PROBABLE.
FT   TRANSMEM   281    303       PROBABLE.
FT   TRANSMEM   315    337       PROBABLE.
FT   DOMAIN     338    443       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM   444    467       PROBABLE.
FT   CARBOHYD   110    110       POTENTIAL.
FT   CARBOHYD   228    228       POTENTIAL.
FT   DISULFID   171    185       BY SIMILARITY.
SQ   SEQUENCE   467 AA;  54284 MW;  EAB28EEC CRC32;


  Query Match             35.9%;  Score 467.5;  DB 1;  Length 467;
  Best Local Similarity   38.1%;  Pred. No. 3.6e-34;
  Matches   99;  Conservative   43;  Mismatches   67;  Indels   51;  Gaps    6;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           | |: | |||:||  ||::||||:| :||| ||   | |:|  :| :||||||||| ::
Db     223 FMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFWIKKDAT 282

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           ||||:||||:||||||| | :||: |||||:||:| :: :||:| | ||:|:| ||:  |
Db     283 PARTALGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEYATLNY--Y 340

Qy     121 NQTKAHASPK----LRHP--------RINSRAHARTRARSRACARQHQEAFVCQIVTTEG 168
           :  :   : |    | ||        ||: :| :
Db     341 SSCRKPTTTKKTTSLLHPDSSRWIPERISLQAPSNY---------------------- 377

Qy     169 SDGEERPSCSAQQPPSPGSPEGPRSLC---SKLACCEWC---KRFKKYFCMVPDCEGSTW 222
                 |   :|| |       |:     :  |   |   |  : :||   :|:  :|
Db     377 -------SLLDMRPPPPAMITLNNSVYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSW 429

Qy     223 QQGRLCIHVYRLDNYSRVVF 242
           ::||: | :  ||:|||| |
Db     430 RKGRIHIDILELDSYSRVFF 449


RESULT   4
GAC3_MOUSE
ID   GAC3_MOUSE     STANDARD;      PRT;   467 AA.
AC   P27681;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C C57; TISSUE=BRAIN;
RX   MEDLINE; 91285135.
RA   WILSON-SHAW D., ROBINSON M., ALALJEV B., SIEGEL R.E., SIKELA J.M.;
RT   "A novel gamma subunit of the GABAA receptor identified using the
RT   polymerase chain reaction.";
RL   FEBS Lett. 284:211-215(1991).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X59300; CAA41988.1; -.
DR   PIR; S16915; S16915.
DR   MGD; MGI:95624; GABRG3.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL       1     17       POTENTIAL.
FT   CHAIN       18    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3
FT                               SUBUNIT.
FT   DOMAIN      18    254       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM   255    277       PROBABLE.
FT   TRANSMEM   281    303       PROBABLE.
FT   TRANSMEM   315    337       PROBABLE.
FT   DOMAIN     338    443       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM   444    467       PROBABLE.
FT   CARBOHYD   110    110       POTENTIAL.
FT   CARBOHYD   228    228       POTENTIAL.
FT   DISULFID   171    185       BY SIMILARITY.
SQ   SEQUENCE   467 AA;  54303 MW;  A332B008 CRC32;


  Query Match             35.4%;  Score 461.5;  DB 1;  Length 467;
  Best Local Similarity   39.5%;  Pred. No. 1.2e-33;
  Matches   98;  Conservative   43;  Mismatches   80;  Indels   27;  Gaps    5;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           | |: | |||:||  ||::||||:| :||| ||   | |:|  :| :||||||||| ::
Db     223 FMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFWIKKDAT 282

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           ||||:||||:||||||| | :||: |||||:||:| :: :||:| | ||:|:| ||:  |
Db     283 PARTTLGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEYATLNY--Y 340

Qy     121 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 180
           :  :    | :|  : :      ||      : |   :                    |
Db     341 SSCR---KPTIRKKKTSLLHPDSTRWIPDRISLQAPSNY---------------SLLDM 381

Qy     181 QPPSPGSPEGPRSLC---SKLACCEWC---KRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 234
           :|| |       |:     :  |   |   | : :||   :|:  :|::||: | |  |
Db     382 RPPPPVMITLNNSMYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSWRRGRIHIDVSEL 441
```

```
Qy     235 DNYSRVVF 242
           |:|||| |
Db     442 DSYSRVFF 449


RESULT   5
GAC3_RAT
ID   GAC3_RAT       STANDARD;      PRT;   467 AA.
AC   P28473;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 92159063.
RA   HERB A., WISDEN W., LUEDDENS H., PUIA G., VICINI S., SEEBURG P.H.;
RT   "The third gamma subunit of the gamma-aminobutyric acid type A
RT   receptor family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:1433-1437(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZUR-SIV; TISSUE=BRAIN;
RX   MEDLINE; 92070559.
RA   KNOFLACH F., RHYNER T., VILLA M., KELLENBERGER S., DRESCHER U.,
RA   MALHERBE P., SIGEL E., MOEHLER H.;
RT   "The gamma 3-subunit of the GABAA-receptor confers sensitivity to
RT   benzodiazepine receptor ligands.";
RL   FEBS Lett. 293:191-194(1991).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M81142; AAA41181.1; -.
DR   EMBL; X63324; CAA44930.1; -.
DR   PIR; S19317; S19317.
DR   PIR; A40221; A40221.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN        18    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-3
FT                                 SUBUNIT.
FT   DOMAIN       18    254       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    255    277       PROBABLE.
FT   TRANSMEM    281    303       PROBABLE.
FT   TRANSMEM    315    337       PROBABLE.
FT   DOMAIN      338    443       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    444    467       PROBABLE.
FT   CARBOHYD    110    110       POTENTIAL.
FT   CARBOHYD    228    228       POTENTIAL.
FT   DISULFID    171    185       BY SIMILARITY.
FT   CONFLICT    416    416       S -> T (IN REF. 2).
SQ   SEQUENCE   467 AA;  54292 MW;  B7263D44 CRC32;


  Query Match             35.4%;  Score 461.5;  DB 1;  Length 467;
  Best Local Similarity   39.5%;  Pred. No. 1.2e-33;
  Matches   98;  Conservative   43;  Mismatches   80;  Indels   27;  Gaps    5;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
             | |: | |||:||  ||::||||:| :||| ||   | |:|  :| :|||||||||| ::
Db     223 FMGLRNTTEIVTTSAGDYVVMTIYFELSRRMGYFTIQTYIPCILTVVLSWVSFWIKKDAT 282

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           ||||:||||:||||||| | :||: |||||:||:| :: :||:| | ||:|:| ||:  |
Db     283 PARTTLGITTVLTMTTLSTIARKSLPRVSYVTAMDLFVTVCFLFVFAALMEYATLNY--Y 340

Qy     121 NQTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQ 180
           :  :    | :|  : :      ||      : |   :                |
Db     341 SSCR---KPTIRKKKTSLLHPDSTRWIPDRISLQAPSNY---------------SLLDM 381

Qy     181 QPPSPGSPEGPRSLC---SKLACCEWC---KRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 234
           :|| |       |:     : |  |   | : :||   :|:  :|::||: | |  |
Db     382 RPPPPVMITLNNSMYWQEFEDTCVYECLDGKDCQSFFCCYEECKSGSWRRGRIHIDVSEL 441

Qy     235 DNYSRVVF 242
           |:|||| |
Db     442 DSYSRVFF 449


RESULT   6
GAC2_CHICK
ID   GAC2_CHICK     STANDARD;      PRT;   474 AA.
AC   P21548;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COMMERCIAL RHODE ISLAND CROSS; TISSUE=BRAIN;
RX   MEDLINE; 91088318.
RA   GLENCORSE T.A., BATESON A.N., DARLISON M.G.;
RT   "Sequence of the chicken GABAA receptor gamma 2-subunit cDNA.";
RL   Nucleic Acids Res. 18:7157-7157(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X54944; CAA38704.1; -.
DR   PIR; S13086; S13086.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
```

```
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane; Phosphorylation.
FT   SIGNAL        1     38       POTENTIAL.
FT   CHAIN        39    474       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                                 SUBUNIT.
FT   DOMAIN       39    272       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    273    295       PROBABLE.
FT   TRANSMEM    299    321       PROBABLE.
FT   TRANSMEM    333    355       PROBABLE.
FT   DOMAIN      356    450       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    451    474       PROBABLE.
FT   CARBOHYD     51     51       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    246    246       POTENTIAL.
FT   CARBOHYD    266    266       POTENTIAL.
FT   DISULFID    189    203       BY SIMILARITY.
FT   MOD_RES     411    411       PHOSPHORYLATION.
FT   DOMAIN      376    383       INSERTION, SIMILAR TO HUMAN GAMMA-2
FT                                 SEQUENCE WHICH IS PROPOSED TO BE CAUSED
FT                                 BY ALTERNATIVE SPLICING.
SQ   SEQUENCE   474 AA;  54969 MW;  F3975109 CRC32;


  Query Match             35.4%;  Score 461;  DB 1;  Length 474;
  Best Local Similarity   35.2%;  Pred. No. 1.4e-33;
  Matches   90;  Conservative   51;  Mismatches   61;  Indels   54;  Gaps    6;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           |||: | ||:: |  ||:::||:::||:||| ||   | |:| ::  :||||||||  ::
Db     241 FTGLRNTTEVVKTTSGDYVVMSVYFNLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAV 300

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           |||||||||:|||||| | :||: |:|||:||:| ::::||:| | ||:|:  |:: :
Db     301 PARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVS 360

Qy     121 N------QTKAHASPKLR-----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIVTT 166
           |      : |   :| ||      | |: |  : |   : |     |  :  : |
Db     361 NRKPSKDKDKKKKNPLLRMFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYEC----- 416

Qy     167 EGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGR 226
             ||::   |::                                :||   ||    |: ||
Db     416 --LDGKD---CAS-----------------------------FFCCFEDCRTGAWRHGR 440

Qy     227 LCIHVYRLDNYSRVVF 242
           : | : ::|:|:|: |
Db     441 IHIRIAKMDSYARIFF 456


RESULT   7
GAC2_BOVIN
ID   GAC2_BOVIN     STANDARD;      PRT;   475 AA.
AC   P22300;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC   Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN CORTEX;
RX   MEDLINE; 91088632.
RA   WHITING P.J., MCKERNAN R.M., IVERSEN L.L.;
RT   "Another mechanism for creating diversity in gamma-aminobutyrate type
RT   A receptors: RNA splicing directs expression of two forms of gamma 2
RT   phosphorylation site.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:9966-9970(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: ALTERNATIVE RNA SPLICING DIRECTS EXPRESSION
CC       OF TWO FORMS OF GAMMA-2 SUBUNITS (2S AND 2L), ONE (2L) CONTAINS A
CC       PROTEIN KINASE C PHOSPHORYLATION SITE.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M55563; AAA30531.1; -.
DR   PIR; A39272; A39272.
DR   PIR; B39272; B39272.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane; Phosphorylation;
KW   Alternative splicing.
FT   SIGNAL        1     39       POTENTIAL.
FT   CHAIN        40    475       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                                 SUBUNIT.
FT   DOMAIN       40    273       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    274    296       PROBABLE.
FT   TRANSMEM    300    322       PROBABLE.
FT   TRANSMEM    334    356       PROBABLE.
FT   DOMAIN      357    451       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    452    475       PROBABLE.
FT   CARBOHYD     52     52       POTENTIAL.
FT   CARBOHYD    129    129       POTENTIAL.
FT   CARBOHYD    247    247       POTENTIAL.
FT   DISULFID    190    204       BY SIMILARITY.
FT   MOD_RES     382    382       PHOSPHORYLATION (BY PKC) (PROBABLE).
FT   VARSPLIC    377    384       MISSING (IN ISOFORM GAMMA-2S).
FT   VARIANT     230    230       S -> G.
SQ   SEQUENCE   475 AA;  55264 MW;  EEBD5FCE CRC32;


  Query Match             34.9%;  Score 455;  DB 1;  Length 475;
  Best Local Similarity   34.8%;  Pred. No. 4.7e-33;
  Matches   89;  Conservative   51;  Mismatches   62;  Indels   54;  Gaps    6;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           | |: | ||:: |  ||:::|||:::|:::||| ||   | |:| ::  :|||||||  ::
Db     242 FVGLRNTTEVVKTTSGDYVVMTVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAV 301

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           |||||||||:|||||| | :||: |:|||:||:| ::::||:| | ||:|:  |:: :
Db     302 PARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVS 361

Qy     121 N------QTKAHASPKLR-----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIVTT 166
           |      : |   :| ||      | |: |  : |   : |     |  :  : |
Db     362 NRKPSKDKDKKKKNPLLRMFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYEC----- 417

Qy     167 EGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGR 226
             ||::   |::                                :||   ||    |: ||
Db     417 --LDGKD---CAS-----------------------------FFCCFEDCRTGAWRHGR 441

Qy     227 LCIHVYRLDNYSRVVF 242
           : | : ::|:|:|: |
Db     442 IHIRIAKMDSYARIFF 457
```

```
RESULT   8
GAC2_HUMAN
ID   GAC2_HUMAN     STANDARD;      PRT;   467 AA.
AC   P18507;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 89181956.
RA   PRITCHETT D.B., SONTHEIMER H., SHIVERS B.D., YMER S., KETTENMANN H.,
RA   SCHOFIELD P.R., SEEBURG P.H.;
RT   "Importance of a novel GABAA receptor subunit for benzodiazepine
RT   pharmacology.";
RL   Nature 338:582-585(1989).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X15376; CAA33437.1; -.
DR   PIR; S03905; S03905.
DR   MIM; 137164; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     39       POTENTIAL.
FT   CHAIN        40    467       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                                SUBUNIT.
FT   DOMAIN        40    273       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM     274    296       PROBABLE.
FT   TRANSMEM     300    322       PROBABLE.
FT   TRANSMEM     334    356       PROBABLE.
FT   DOMAIN       357    443       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM     444    466       PROBABLE.
FT   CARBOHYD      52     52       POTENTIAL.
FT   CARBOHYD     129    129       POTENTIAL.
FT   CARBOHYD     247    247       POTENTIAL.
FT   DISULFID     190    204       BY SIMILARITY.
SQ   SEQUENCE   467 AA;  54178 MW;  E78E8090 CRC32;

  Query Match             34.6%;  Score 450;  DB 1;  Length 467;
  Best Local Similarity   34.3%;  Pred. No. 1.3e-32;
  Matches   85;  Conservative   53;  Mismatches   64;  Indels   46;  Gaps    5;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           | |: | ||:: |  ||::||:::|::||| ||   | |:| ::  :||||||||  ::
Db     242 FVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAV 301

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           |||||||||:|||||| | :||: |:|||:||:| ::::||:| | ||:|:  |:: :
Db     302 PARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVS 361

Qy     121 NQTKAHASPKLRH---PRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEER 174
           |:  :   | :    | |: |  : |   : |     |  :  : |        ||::
Db     362 NRKPSKDKDKKKKNPAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD- 414

Qy     175 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 234
           |::                                 :||   ||    |: ||: | : ::
Db     414 --CAS-----------------------------FFCCFEDCRTGAWRHGRIHIRIAKM 441

Qy     235 DNYSRVVF 242
           |:|:|: |
Db     442 DSYARIFF 449


RESULT   9
GAC2_RAT
ID   GAC2_RAT       STANDARD;      PRT;   466 AA.
AC   P18508;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 90380375.
RA   SHIVERS B.D., KILLISCH I., SPRENGEL R., SONTHEIMER H., KOEHLER M.,
RA   SCHOFIELD P.R., SEEBURG P.H.;
RT   "Two novel GABAA receptor subunits exist in distinct neuronal
RT   subpopulations.";
RL   Neuron 3:327-337(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90331051.
RA   MALHERBE P., SIGEL E., BAUR R., PERSOHN E., RICHARDS J.G., MOHLER H.;
RT   "Functional characteristics and sites of gene expression of the alpha
RT   1, beta 1, gamma 2-isoform of the rat GABAA receptor.";
RL   J. Neurosci. 10:2330-2337(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L08497; AAC42036.1; -.
DR   PIR; A37164; A37164.
DR   PIR; JQ0077; JQ0077.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     38       POTENTIAL.
FT   CHAIN        39    466       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
```

```
FT                                SUBUNIT.
FT   DOMAIN       39    272       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    273    295       PROBABLE.
FT   TRANSMEM    299    321       PROBABLE.
FT   TRANSMEM    333    355       PROBABLE.
FT   DOMAIN      356    442       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    443    465       PROBABLE.
FT   CARBOHYD     51     51       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    246    246       POTENTIAL.
FT   DISULFID    189    203       BY SIMILARITY.
FT   CONFLICT     22     22       M -> I (IN REF. 2).
SQ   SEQUENCE   466 AA;  54077 MW;  EDDEFFEF CRC32;


  Query Match             34.6%;  Score 450;  DB 1;  Length 466;
  Best Local Similarity   34.3%;  Pred. No. 1.3e-32;
  Matches   85;  Conservative   53;  Mismatches   64;  Indels   46;  Gaps    5;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           | |: | ||:: |  ||:::|:::|::||| ||   | |:| ::  :|||||||  ::
Db     241 FVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAV 300

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           |||||||||:|||||| | :||: |:|||:||:| ::::||:| | ||:|:  |:: :
Db     301 PARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVS 360

Qy     121 NQTKAHASPKLRH---PRINSRAHARTRARSRAC---ARQHQEAFVCQIVTTEGSDGEER 174
           |:  :   | :   | |: |  : |   : |     |  :  : |        ||::
Db     361 NRKPSKDKDKKKKNPAPTIDIRPRSATIQMNNATHLQERDEEYGYEC-------LDGKD- 413

Qy     175 PSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCIHVYRL 234
             |::                              :||   ||    |: ||: | : ::
Db     413 --CAS------------------------------FFCCFEDCRTGAWRHGRIHIRIAKM 440

Qy     235 DNYSRVVF 242
           |:|:|: |
Db     441 DSYARIFF 448


RESULT  10
GAC2_MOUSE
ID   GAC2_MOUSE     STANDARD;      PRT;   474 AA.
AC   P22723;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91108470.
RA   KOFUJI P., WANG J.B., MOSS S.J., HUGANIR R.L., BURT D.R.;
RT   "Generation of two forms of the gamma-aminobutyric acidA receptor
RT   gamma 2-subunit in mice by alternative splicing.";
RL   J. Neurochem. 56:713-715(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   SIKELA J.M., SHAW W.D., KHAN A.S., LIN L.-H., LEIDENHEIMER G.,
RA   SIEGEL R.E.;
RL   Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: ALTERNATIVE RNA SPLICING DIRECTS EXPRESSION
CC       OF TWO FORMS OF GAMMA2 SUBUNIT (2S AND 2L), ONE (2L) CONTAINS A
CC       PROTEIN KINASE C PHOSPHORYLATION SITE.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M86572; AAB59635.1; -.
DR   EMBL; M62374; AAA37653.1; -.
DR   PIR; JH0317; JH0317.
DR   PIR; JH0316; JH0316.
DR   MGD; MGI:95623; GABRG2.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane; Phosphorylation;
KW   Alternative splicing.
FT   SIGNAL        1     38       POTENTIAL.
FT   CHAIN        39    474       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-2
FT                                SUBUNIT.
FT   DOMAIN       39    272       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    273    295       PROBABLE.
FT   TRANSMEM    299    321       PROBABLE.
FT   TRANSMEM    333    355       PROBABLE.
FT   DOMAIN      356    450       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    451    474       PROBABLE.
FT   CARBOHYD     51     51       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    246    246       POTENTIAL.
FT   DISULFID    189    203       BY SIMILARITY.
FT   MOD_RES     381    381       PHOSPHORYLATION (BY PKC) (PROBABLE).
FT   VARSPLIC    376    383       MISSING (IN ISOFORM GAMMA-2S).
FT   CONFLICT     49     49       T -> A (IN REF. 2).
FT   CONFLICT    414    414       Q -> E (IN REF. 2).
FT   CONFLICT    443    443       M -> I (IN REF. 2).
SQ   SEQUENCE   474 AA;  55145 MW;  A3049225 CRC32;


  Query Match             34.4%;  Score 448;  DB 1;  Length 474;
  Best Local Similarity   34.0%;  Pred. No. 1.9e-32;
  Matches   87;  Conservative   53;  Mismatches   62;  Indels   54;  Gaps    6;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           | |: | ||:: |  ||:::|:::|::||| ||   | |:| ::  :|||||||  ::
Db     241 FVGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLIVVLSWVSFWINKDAV 300

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           |||||||||:|||||| | :||: |:|||:||:| ::::||:| | ||:|:  |:: :
Db     301 PARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFSALVEYGTLHYFVS 360

Qy     121 N------QTKAHASPKLR-----HPRINSRAHARTRARSRAC---ARQHQEAFVCQIVTT 166
           |      : |   :| ||      | |: |  : |   : |     |  :  : |
Db     361 NRKPSKDKDKKKKNPLLRMFSFKAPTIDIRPRSATIQMNNATHLQERDEEYGYQC----- 416

Qy     167 EGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGR 226
             ||::   |::                              :||   ||    |: ||
Db     416 --LDGKD---CAS------------------------------FFCCFEDCRTGAWRHGR 440

Qy     227 LCIHVYRLDNYSRVVF 242
           : : : ::|:|:|: |
Db     441 IHMRIAKMDSYARIFF 456


RESULT  11
GAC1_RAT
ID   GAC1_RAT       STANDARD;      PRT;   465 AA.
```

```
AC   P23574;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRG1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 91006020.
RA   YMER S., DRAGUHN A., WISDEN W., WERNER P., KEINAENEN K.,
RA   SCHOFIELD P.R., SPRENGEL R., PRITCHETT D.B., SEEBURG P.H.;
RT   "Structural and functional characterization of the gamma 1 subunit of
RT   GABAA/benzodiazepine receptors.";
RL   EMBO J. 9:3261-3267(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: THIS SUBUNIT CARRIES THE BENZODIAZEPINE BINDING
CC       SITE.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X57514; CAA40739.1; -.
DR   PIR; S12056; S12056.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Multigene family; Transmembrane.
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36    465       GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1
FT                                 SUBUNIT.
FT   DOMAIN        36    272       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM     273    294       PROBABLE.
FT   TRANSMEM     299    320       PROBABLE.
FT   TRANSMEM     332    354       PROBABLE.
FT   DOMAIN       355    444       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM     445    465       PROBABLE.
FT   CARBOHYD      50     50       POTENTIAL.
FT   CARBOHYD     127    127       POTENTIAL.
FT   CARBOHYD     245    245       POTENTIAL.
FT   DISULFID     188    202       BY SIMILARITY.
SQ   SEQUENCE   465 AA;  53550 MW;  963AF632 CRC32;


  Query Match             34.1%;  Score 444;  DB 1;  Length 465;
  Best Local Similarity   35.6%;  Pred. No. 4.3e-32;
  Matches   90;  Conservative   45;  Mismatches   62;  Indels   56;  Gaps    5;

Qy       1 FTGVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESA 60
           | |: | |||  |  ||:::||||||::||| ||   |:|:|  :| :||||||||  ::
Db     240 FVGLRNSTEISHTISGDYIIMTIFFDLSRRMGYFTIQTYIPCILTVVLSWVSFWINKDAV 299

Qy      61 PARTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIY 120
           |||||||||:|||||||  | :||: |:|||:||:| :::::||:| | ||:|:  |::
Db     300 PARTSLGITTVLTMTTLSTIARKSLPKVSYVTAMDLFVSVCFIFVFAALMEYGTLHYFTS 359

Qy     121 N----------QTKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGS 169
```

```
           |          ::|   || |       | :     :     | :: :  | :  ||
Db     360 NNKGKTTRDRKLKSKTSVSPGL-------HAGSTLIPMNNISMPQGEDDYGYQCL--EGK 410

Qy     170 DGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGRLCI 229
           |      |:                              :||   ||   :|::||: |
Db     411 D------CAT----------------------------FFCCFEDCRTGSWREGRIHI 434

Qy     230 HVYRLDNYSRVVF 242
             : ::|:|||: |
Db     435 RIAKIDSYSRIFF 447


RESULT  12
GAA6_CHICK
ID   GAA6_CHICK     STANDARD;      PRT;   465 AA.
AC   Q90845;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRA6.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EMBRYONIC BRAIN;
RX   MEDLINE; 96373714.
RA   BAHN S., HARVEY R.J., DARLISON M.G., WISDEN W.;
RT   "Conservation of gamma-aminobutyric acid type A receptor alpha 6
RT   subunit gene expression in cerebellar granule cells.";
RL   J. Neurochem. 66:1810-1818(1996).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X94343; CAA64069.1; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    465       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6
FT                                 SUBUNIT.
FT   DOMAIN        20    242       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM     243    264       PROBABLE.
FT   TRANSMEM     269    290       PROBABLE.
FT   TRANSMEM     302    324       PROBABLE.
FT   DOMAIN       325    421       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM     422    443       PROBABLE.
FT   CARBOHYD      31     31       POTENTIAL.
FT   CARBOHYD     128    128       POTENTIAL.
FT   CARBOHYD     141    141       POTENTIAL.
FT   DISULFID     156    170       BY SIMILARITY.
SQ   SEQUENCE   465 AA;  51717 MW;  B74B26D1 CRC32;


  Query Match             26.7%;  Score 348;  DB 1;  Length 465;
  Best Local Similarity   33.5%;  Pred. No. 1.2e-23;
```

```
  Matches   87;  Conservative   39;  Mismatches   70;  Indels   64;  Gaps    7;

Qy       3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
           | :  :| | :  |::::||::|:: |: ||   | | |  :| :|| ||||| || ||
Db     212 GQTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPA 271

Qy      63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
           ||  |||:|||||||   :| : |:||| ||:|::||:|| | | ||:||| :|:    |
Db     272 RTVFGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQ 331

Qy     123 TKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFV-----CQI---VTTEGSDGEER 174
           |:       |  |  :|| |   | | |       |       | :   | :  |  ::
Db     332 TQ-------RAMRKAARAAALAAALSAATVPAEDEIVSHSDSNCNLKKRVNSVTSQADQS 384

Qy     175 P-----SCSAQQ-------PPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTW 222
           |     | || |       ||:| :|                                |   |::
Db     385 PEASIVSNSASQCQPVSAPPPAPPAP-------------------------PPVGGTS- 418

Qy     223 QQGRLCIHVYRLDNYSRVVF 242
                 ::| |||::|
Db     418 ----------KIDQYSRILF 427


RESULT  13
GAA4_RAT
ID   GAA4_RAT       STANDARD;      PRT;   552 AA.
AC   P28471;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRA4.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92008629.
RA   WISDEN W., HERB A., WIELAND H., KEINAENEN K., LUEDDENS H.,
RA   SEEBURG P.H.;
RT   "Cloning, pharmacological characteristics and expression pattern of
RT   the rat GABAA receptor alpha 4 subunit.";
RL   FEBS Lett. 289:227-230(1991).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L08493; AAC42032.1; -.
DR   EMBL; S55933; AAB19902.1; -.
DR   PIR; S17551; S17551.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36    552       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4
FT                                 SUBUNIT.
FT   DOMAIN       36    258       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    259    280       PROBABLE.
FT   TRANSMEM    285    306       PROBABLE.
FT   TRANSMEM    318    340       PROBABLE.
FT   DOMAIN      341    521       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    522    541       PROBABLE.
FT   CARBOHYD     47     47       POTENTIAL.
FT   CARBOHYD    144    144       POTENTIAL.
FT   CARBOHYD    157    157       POTENTIAL.
FT   DISULFID    172    186       BY SIMILARITY.
SQ   SEQUENCE   552 AA;  60951 MW;  62956C8F CRC32;


  Query Match             26.2%;  Score 341;  DB 1;  Length 552;
  Best Local Similarity   36.4%;  Pred. No. 6.1e-23;
  Matches   76;  Conservative   31;  Mismatches   78;  Indels   24;  Gaps    3;

Qy       3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
           | :  :| | :  |:::|||::|:: |: ||   | |:|  :| :|| |||||  || ||
Db     228 GQTVSSETIKSITGEYIVMTVYFHLRRKMGYFMIQTYIPCIMTVILSQVSFWINKESVPA 287

Qy      63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
           ||  |||:|||||||   :| : |:||| ||:|::||:|| | | ||:||| :|:    |
Db     288 RTVFGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNIQ 347

Qy     123 ------------TKAHASPKLRHPRINS---RAHARTRARSRACARQHQEAFV------- 161
                       :  |:| |:     :     ||    | |  |  | |: |
Db     348 MQKAKKKISKPPPEVPAAPVLKEKHTETSLQNTHANLNMRKRTNALVHSESDVNSRTEVG 407

Qy     161 --CQIVTTEGSDGEERPSCSAQQPPSPGS 187
                 |     |  |        |:| |
Db     408 NHSSKTTAAQESSETTPKAHLASSPNPFS 436


RESULT  14
GAA4_HUMAN
ID   GAA4_HUMAN     STANDARD;      PRT;   554 AA.
AC   P48169;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRA4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN CORTEX;
RA   YANG W., DREWE J.A., LAN N.C.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U30461; AAB52519.1; -.
DR   MIM; 137141; -.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 1.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
```

```
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36    554       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4
FT                                 SUBUNIT.
FT   DOMAIN        36    258       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM     259    280       PROBABLE.
FT   TRANSMEM     285    306       PROBABLE.
FT   TRANSMEM     318    340       PROBABLE.
FT   DOMAIN       341    523       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM     524    543       PROBABLE.
FT   CARBOHYD      47     47       POTENTIAL.
FT   CARBOHYD     144    144       POTENTIAL.
FT   CARBOHYD     157    157       POTENTIAL.
FT   DISULFID     172    186       BY SIMILARITY.
SQ   SEQUENCE   554 AA;  61640 MW;  49E8E56A CRC32;


  Query Match             25.8%;  Score 336;  DB 1;  Length 554;
  Best Local Similarity   38.3%;  Pred. No. 1.7e-22;
  Matches   77;  Conservative   37;  Mismatches   69;  Indels   18;  Gaps    5;

Qy       3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
           | :  :| | :  |:::|||::|:: |: ||   | |:|  :| :|| ||||| || ||
Db     228 GQTVSSETIKSITGEYIVMTVYFHLRRKMGYFMIQTYIPCIMTVILSQVSFWINKESVPA 287

Qy      63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
           ||  |||:|||||||   :| : |:|||:||:|::||:|| | | ||:||| :|:    |
Db     288 RTVFGITTVLTMTTLSISARHSLPKVSYLTAMDWFIAVCFAFVFSALIEFAAVNYFTNIQ 347

Qy     123 ------------TKAHASP--KLRHPRINSR-AHARTRARSRACARQHQEAFVCQIVTTE 167
                       :  |:|  : :||    :  :|    | |  |  | |: |     ||
Db     348 MEKAKRKTSKPPQEVPAAPVQREKHPEAPLQDTNANLNMRKRTNALVHSESDVGN--RTE 405

Qy     168 GSDGEERPSCSAQQPPSPGSP 188
             :  : |   |:  | |:|
Db     406 VGNHSSKSSTVVQE-SSKGTP 425


RESULT  15
GAA6_RAT
ID   GAA6_RAT       STANDARD;      PRT;   453 AA.
AC   P30191;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6 SUBUNIT PRECURSOR (GABA(A)
DE   RECEPTOR).
GN   GABRA6 OR GABRA-6.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 90348963.
RA   LUEDDENS H., PRITCHETT D., KHLER M., KILLISCH I., KEINAENEN K.,
RA   MONYER H., SPRENGEL R., SEEBURG P.H.;
RT   "Cerebellar GABAA receptor selective for a behavioural alcohol
RT   antagonist.";
RL   Nature 346:648-651(1990).
CC   -!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE
CC       VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
CC       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
CC       CHANNEL.
CC   -!- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
CC       RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: ONLY FOUND IN CEREBELLAR GRANULE CELLS.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L08495; AAC42034.1; -.
DR   EMBL; X55742; CAA39273.1; -.
DR   PIR; S11087; S11087.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PFAM; PF00065; neur_chan; 2.
KW   Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    453       GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6
FT                                 SUBUNIT.
FT   DOMAIN       20    242       EXTRACELLULAR (PROBABLE).
FT   TRANSMEM    243    264       PROBABLE.
FT   TRANSMEM    269    290       PROBABLE.
FT   TRANSMEM    301    324       PROBABLE.
FT   DOMAIN      325    419       CYTOPLASMIC (PROBABLE).
FT   TRANSMEM    420    441       PROBABLE.
FT   CARBOHYD     31     31       POTENTIAL.
FT   CARBOHYD    128    128       POTENTIAL.
FT   CARBOHYD    141    141       POTENTIAL.
FT   DISULFID    156    170       BY SIMILARITY.
SQ   SEQUENCE   453 AA;  51184 MW;  0ED8616E CRC32;


  Query Match             25.8%;  Score 336;  DB 1;  Length 453;
  Best Local Similarity   30.5%;  Pred. No. 1.4e-22;
  Matches   78;  Conservative   43;  Mismatches   77;  Indels   58;  Gaps    4;

Qy       3 GVSNKTEIITTPVGDFMVMTIFFNVSRRFGYVAFQNYVPSSVTTMLSWVSFWIKTESAPA 62
           | :  :| | :  |::::||::|:: |: ||   | | |  :| :|| |||||  || ||
Db     212 GQTVSSETIKSNTGEYVIMTVYFHLQRKMGYFMIQIYTPCIMTVILSQVSFWINKESVPA 271

Qy      63 RTSLGITSVLTMTTLGTFSRKNFPRVSYITALDFYIAICFVFCFCALLEFAVLNFLIYNQ 122
           ||  |||:|||||||   :| : |:||| ||:|::||:||'| | ||:||| :|:    |
Db     272 RTVFGITTVLTMTTLSISARHSLPKVSYATAMDWFIAVCFAFVFSALIEFAAVNYFTNLQ 331

Qy     123 TKAHASPKLRHPRINSRAHARTRARSRACARQHQEAFVCQIVTTEGS------------- 170
           ::             :  |:| |:      :  |:   :||    |
Db     332 SQ------------KAERQAQTAAKPPVAKSKTTESLEAEIVVHSDSKYHLKKRISSLTL 379

Qy     170 ---DGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCKRFKKYFCMVPDCEGSTWQQGR 226
               |    :: |  | :|  |  |                          :|   |::
Db     380 PIVPSSEASKVLSRTPILPSTPVTPPLL------------------LPAIGGTS----- 416

Qy     227 LCIHVYRLDNYSRVVF 242
             ::| |||::|
Db     416 ------KIDQYSRILF 425


Search completed: March 11, 2000, 06:26:40
Job time: 43 sec
```